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	MAMMA1001161	4.3	5.27	19.53	18.34	10.8	14.8	
	MAMMA1001162	1.98	1.77	3.16	5.25	5.13	2.25	
	MAMMA1001181	2.44	2.28	4.87	5.06	4.74	3.62	
5	MAMMA1001186	2	2.66	4.66	5.38	5.48	3.9	
	MAMMA1001189	2.23	3.68	7.17	11	11.17	9.9	*
	MAMMA1001191	2.54	2.07	5.49	4.37	3.89	2.97	+
	MAMMA1001198	368.47	416.05	784.82	647.17	738.61	605.52	
10	MAMMA1001202	11.78	11.85	30.06	34.39	28.74	25.16	
	MAMMA1001203	2.57	3.01	7.15	8.72	6.26	5.56	
	MAMMA1001206	1.91	3.28	4.5	3.69	6.66	2.65	
	MAMMA1001208	2.66	2.93	3.31	3.82	4.95	3.19	
	MAMMA1001215	2.9	3.08	6.55	3.49	8.09	4.74	
15	MAMMA1001220	2.63	3.03	7.25	7.16	7.17	6.03	
	MAMMA1001222	1.25	1.18	4.18	2.18	5.85	0.53	
	MAMMA1001223	2.48	3.32	6.53	4.95	6.51	4.1	
	MAMMA1001232	2.82	4.27	8.08	12.22	8.82	9.57	
	MAMMA1001234	1.25	3.27	3.17	5.05	3.91	3.26	
20	MAMMA1001237	1.22	1.56	4.21	1.94	3.66	2.09	
	MAMMA1001243	2.18	2.28	4.06	4.05	4.89	1.99	
	MAMMA1001244	1.22	1.16	2.86	2.96	4.79	2.22	
	MAMMA1001249	2.3	1.89	5.93	5.19	5.8	3.75	
25	MAMMA1001256	3	3.09	8.29	5.89	7.83	8.01	
	MAMMA1001259	4.38	3.25	7.15	7.94	9.24	6.63	
	MAMMA1001260	1.76	2.71	5.42	6.51	5.33	7.33	
	MAMMA1001262	2.1	4.11	5.28	7.86	8.04	6.25	*
	MAMMA1001268	2	2.16	4.59	2.56	4.23	2.48	+
30	MAMMA1001271	4.84	5.78	17.37	18.29	14.24	15.67	
	MAMMA1001274	2.88	3.06	6.17	6.22	8.55	7.93	
	MAMMA1001280	2.09	1.48	4.36	1.84	3.78	1.73	
	MAMMA1001283	1.63	1.71	6.34	6.88	5.63	4.83	
	MAMMA1001284	2.27	2	8.67	5.08	9.09	9.51	
35	MAMMA1001286	13.83	9.72	17.39	12.15	11.83	14.63	
	MAMMA1001289	17.63	13.49	23.32	21.02	26.39	36.8	
	MAMMA1001292	3	3.01	5.94	7.26	6.31	6.85	*
	MAMMA1001296	3.55	3.76	12.61	14.11	12.37	12.8	+
	MAMMA1001298	1.26	1.7	6.26	4.25	6.78	4.07	
40	MAMMA1001305	0.86	1.59	4.43	2.49	4.07	2.63	
	MAMMA1001309	0.61	0.9	2.7	1.84	3	1.49	
	MAMMA1001310	1.72	2.17	3.64	4.81	7.38	4.42	
	MAMMA1001322	0.99	1.54	1.83	2.83	1.77	2.13	
	MAMMA1001324	1.3	1.12	3.16	2.03	2.83	1.94	
45	MAMMA1001330	3.35	2.65	9.53	7.93	9.75	5.36	
	MAMMA1001333	3.1	3.74	10.23	9.88	11.4	9.07	
	MAMMA1001334	5.53	4.17	4.83	10.97	8.23	10.16	**
	MAMMA1001337	2.49	3.54	6.6	6.99	9.16	8.05	*
	MAMMA1001341	1.21	1.14	3.48	1.54	5.66	1.41	+
50	MAMMA1001343	2.37	1.89	8.07	8.17	9.75	10.95	
	MAMMA1001344	9.59	9.07	11.75	13.63	11.67	15.98	
	MAMMA1001346	1.34	1.25	3.9	2.05	3.9	2.94	
	MAMMA1001383	3.07	3.61	8.52	8.3	9.02	9.38	
	MAMMA1001388	1.62	1.93	5.34	3.38	6.11	4.58	
55	MAMMA1001396	4.2	2.12	8.12	11.39	10.42	8.68	

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	MAMMA1001397	2.59	2.27	5.79	8.33	8.96	7.78	*	+
	MAMMA1001401	26.87	16.48	32.72	43.47	57.55	45.66	*	+
5	MAMMA1001408	1.06	1.06	2.57	0.65	4.22	1.19		
	MAMMA1001411	1.65	1.26	3.84	4.38	3.33	3.51		
	MAMMA1001414	3.12	3.85	5.74	12.58	10.67	15.28	**	+
	MAMMA1001415	2.45	3.16	11.93	14.57	20.15	13.69	*	+
	MAMMA1001418	0.66	2.2	5.36	3.57	6.04	4.46		
10	MAMMA1001419	0.8	2.43	4.93	6.03	7.01	3.92		
	MAMMA1001420	0.96	3.09	4.5	3.23	4.11	3.41		
	MAMMA1001426	20.24	32.21	42.42	44.31	39.63	38.75		
	MAMMA1001428	1.94	2.83	6.35	3.8	6.93	4.33		
15	MAMMA1001432	1.19	2.33	8.19	5.62	6.19	6.68		
	MAMMA1001435	1.43	0.78	3.32	3.48	3.67	2.64		
	MAMMA1001442	1.96	3.94	7.41	8.18	8.6	6.63		
	MAMMA1001446	2.17	2.57	6.71	6.9	7.34	7.97		
	MAMMA1001450	1.22	2.05	3.58	2.81	4.18	2.39		
20	MAMMA1001452	1.99	1.78	5.92	8.38	6.19	4.83		
	MAMMA1001465	3.93	3.25	13.61	16.65	14.6	13.82		
	MAMMA1001476	1.63	1.09	4.25	5.87	5.95	4.64	*	+
	MAMMA1001478	2.28	2.12	5.98	3.55	6.27	4.19		
	MAMMA1001479	3.11	4.71	8.32	5.58	6.74	6.21		
25	MAMMA1001487	1.1	1.14	3.84	4.73	3.26	2.08		
	MAMMA1001498	1.93	3.41	7.78	6.17	7.45	5.64		
	MAMMA1001501	0.88	1.97	4.49	2.8	4.77	2.36		
	MAMMA1001502	1.82	1.91	6.48	3.29	6.29	6.26		
	MAMMA1001510	0.48	0.78	2.92	0.54	3.04	1.19		
30	MAMMA1001522	1.03	1.29	3.94	5.05	4.9	3.39		
	MAMMA1001529	0.72	2.06	3.22	3.74	4.07	2.57		
	MAMMA1001532	1.74	1.86	4.27	3.79	5.71	3.12		
	MAMMA1001533	0.61	1.31	2.9	1.52	3.06	1.64		
	MAMMA1001534	0.44	2.59	2.4	1.48	3.64	1.14		
35	MAMMA1001535	1.38	1.91	3.99	2.12	3.98	2.38		
	MAMMA1001547	2.8	2.89	7.77	9.23	8.22	6.22		
	MAMMA1001551	1.1	1.48	4.46	2.23	2.88	2.99		
	MAMMA1001569	1.27	1.68	3.41	2.03	3.41	1.94		
	MAMMA1001575	1.48	2.41	3.42	4.01	4.43	2.81		
40	MAMMA1001576	4.79	8.23	9.65	14.75	9.39	17.03		
	MAMMA1001584	0.89	2.48	3.33	3.11	4	3.09		
	MAMMA1001586	1.43	2.41	3.34	3.78	3.31	1.84		
	MAMMA1001590	2.96	2.53	5.55	5.44	6.47	6.04		
45	MAMMA1001599	4.64	7.15	16.79	15.8	15.18	15.06		
	MAMMA1001600	1.45	2.22	4.73	2.98	4.68	2.11		
	MAMMA1001604	1.03	1.76	3.62	2.35	4.01	1.64		
	MAMMA1001606	1.64	2.04	5.15	3.58	5.45	4.27		
	MAMMA1001609	1.31	2.37	4.36	3.05	5.43	1.59		
50	MAMMA1001614	2.91	3.57	6.15	5.94	6.11	4.14		
	MAMMA1001615	3.98	2.61	10.12	8.87	8.29	8.41		
	MAMMA1001619	7.73	7.8	14.29	16.33	12.93	14.61		
	MAMMA1001620	2.53	2.41	7.98	5.77	7.13	4.54		
	MAMMA1001623	4.11	4.58	9.3	7.34	9.28	6.75		
55	MAMMA1001626	0.83	1.98	2.52	3.24	3.93	1.93		
	MAMMA1001627	1.11	1.98	3.57	2.63	3.68	1.63		

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	MAMMA1001630	2.02	3.08	7.83	7.49	7.53	4.29		
	MAMMA1001633	2.64	3.12	8.8	12.09	9.59	6.16		
	MAMMA1001634	2.83	2.7	6.11	8.69	8.27	6.9	*	+
5	MAMMA1001635	5.65	2.39	9.52	7.92	8.3	8.37		
	MAMMA1001649	1.61	1.63	4.71	2.95	4.62	2.53		
	MAMMA1001654	8.14	9.45	39	43.4	55	46.79		
	MAMMA1001660	19.61	17.92	37.43	40.94	27.03	34		
	MAMMA1001663	1.9	4.73	9.42	9.59	9.56	6.58		
10	MAMMA1001670	1.12	2.66	3.97	3.65	4.09	2.62		
	MAMMA1001671	1.08	1.42	3.56	1.37	4.64	1.77		
	MAMMA1001679	6.85	6.37	13.89	11.48	17.04	13.91		
	MAMMA1001683	2.15	3.29	9.6	6.58	6.53	6.96		
	MAMMA1001686	1.25	1.34	3.77	1.39	2.97	3.06		
15	MAMMA1001688	113.39	113.61	245.56	392.2	458.41	413	**	+
	MAMMA1001689	1.01	3.76	4.1	5.04	3.79	4.44		
	MAMMA1001692	1.97	2.59	5.37	3.66	5.3	3.88		
	MAMMA1001711	1.99	3.64	8.65	4.35	5.51	6.1		
	MAMMA1001715	1.31	1.64	3.95	4.64	4.87	4.13		
20	MAMMA1001730	2.01	2.15	2.5	2.8	4.42	2.83		
	MAMMA1001735	44.73	48.32	102.35	94.99	156.23	119.88		
	MAMMA1001740	0.64	1.6	4.59	2.06	3.91	1.95		
	MAMMA1001743	9.84	11.15	33.16	41.97	51.62	49.6	*	+
25	MAMMA1001744	0.63	0.72	0.86	1.1	1.72	1.71	*	+
	MAMMA1001745	1.41	2.15	6.15	3.27	4.46	3.93		
	MAMMA1001751	1.38	2.41	3.24	2.85	4.51	4.32		
	MAMMA1001752	4.7	4.78	9.75	6.12	9.61	8.4		
	MAMMA1001754	7.25	7.89	7.34	11.04	9.63	9.39	*	+
30	MAMMA1001757	1.21	1.1	2.32	2.21	3.25	2.43		
	MAMMA1001760	3.87	4.52	20.01	22.91	24.2	27.59	*	+
	MAMMA1001764	2.62	2.36	5.97	7.13	10.17	6.51		
	MAMMA1001767	1.22	1.55	2.13	1.61	2.96	1.55		
	MAMMA1001768	0.57	1.18	4.25	4.74	4.72	4.37		
35	MAMMA1001769	2.48	2.83	9.22	9.3	9.81	8.94		
	MAMMA1001771	2.66	1.58	3.74	2.86	5.85	6.77		
	MAMMA1001773	2.7	3.53	3.87	4	6.29	7.61		
	MAMMA1001778	0.88	1.92	3.14	3.13	4.21	3.61		
	MAMMA1001783	2.01	2.1	11.25	11.63	18.46	13.04		
40	MAMMA1001785	3	3.52	8.85	10.56	13.38	11	*	+
	MAMMA1001788	0.49	0.86	1.21	0.72	1.72	1.11		
	MAMMA1001790	1.68	1.67	5.1	2.37	3.73	3.93		
	MAMMA1001800	0.83	0.99	1.47	1.5	2.24	3.25		
	MAMMA1001804	1.02	1.41	3.18	2.37	4.16	2.4		
45	MAMMA1001806	2.13	2.78	6.4	3.15	5.5	4.72		
	MAMMA1001812	1.46	1.33	5.52	4.21	5.86	5.05		
	MAMMA1001815	0.33	1.76	3.07	1.22	3.67	1.24		
	MAMMA1001817	3.19	3.38	9.5	6.78	10.89	13.3		
	MAMMA1001818	1.68	2.08	3.41	3.94	8.52	3.41		
50	MAMMA1001819	2.57	4.12	5.82	8.7	10.29	7.87	*	+
	MAMMA1001820	2.68	4.51	8.27	7.51	10.98	6.07		
	MAMMA1001824	1.66	2.83	8.36	7.55	9.8	7.11		
	MAMMA1001832	6.72	7.99	11.85	20.17	21.28	17.21	**	+
55	MAMMA1001836	1.74	1.66	5.08	4.79	8.19	4.88		

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	MAMMA1001837	2.61	2	5.84	7.1	9.19	5.37		
	MAMMA1001848	1.02	1.61	3.3	2.81	5.33	3.18		
5	MAMMA1001850	3.79	4.51	9.31	9.98	9.93	14.19		
	MAMMA1001851	1.49	2.33	4.98	4.97	4.12	4.02		
	MAMMA1001852	2.98	4	9.68	6.4	7.56	6.8		
	MAMMA1001854	2.56	3.11	9.16	10.59	10.64	9.98		
	MAMMA1001858	3.11	2.22	5.28	9.93	7.91	8.87	**	+
10	MAMMA1001864	1.69	1.91	4.09	8.91	6.18	4.37		
	MAMMA1001868	0.71	0.92	2.64	1.68	2.58	0.91		
	MAMMA1001874	1.2	0.87	2.52	1.06	3.48	1.17		
	MAMMA1001878	3.1	3.46	10.86	7.7	13.37	6.77		
	MAMMA1001880	2.67	2.99	7.24	5.58	7.17	8.12		
15	MAMMA1001885	1.14	1.93	6.19	4.7	5.54	4.58		
	MAMMA1001890	3.54	3.95	12.93	13.59	13.29	12.2		
	MAMMA1001893	3.74	3.42	6.25	6.59	5.49	5.58		
	MAMMA1001901	1.13	1.5	5.4	4.53	5.72	2.67		
	MAMMA1001907	2.57	1.62	6.43	4.15	7.36	6.34		
20	MAMMA1001908	3.2	3.36	8.35	11.83	12.96	12.46	*	+
	MAMMA1001919	0.23	0.97	3.3	2.24	3.9	2.07		
	MAMMA1001931	0.76	1.65	4.04	3.36	5.89	3.25		
	MAMMA1001937	2.27	3.15	5.5	6.44	5.06	3.78		
25	MAMMA1001951	1.74	2.57	6.47	6.48	6.15	4.83		
	MAMMA1001956	3.02	3.48	9.72	8.52	7.66	6.76		
	MAMMA1001957	3.39	3.51	9.15	7.88	9.47	7.66		
	MAMMA1001960	3.1	3.34	7.24	12.06	9.14	6.1		
	MAMMA1001963	0.57	0.78	2.14	1.3	2.36	1.06		
30	MAMMA1001969	1.7	3.43	10.86	8.54	11.14	8.74		
	MAMMA1001970	2.86	3.04	8.48	13.11	6.59	6.64		
	MAMMA1001978	0.57	1.85	1.76	2.42	3.87	1.53		
	MAMMA1001992	2.07	2.04	5.65	6.79	6.75	5.09		
	MAMMA1001994	7.97	3.65	11	18.83	13.23	17.17	*	+
35	MAMMA1002008	3.28	3.77	6.42	3.43	4.06	1.24		
	MAMMA1002009	1.46	2.94	5.17	5.73	7.57	4.06		
	MAMMA1002011	1.77	1.71	4.26	6.5	6.45	3.37		
	MAMMA1002022	1.51	2.1	5.92	6.64	7.42	5.2		
	MAMMA1002024	9.79	9.67	19.03	17.61	16.96	22.43		
40	MAMMA1002032	2.78	2.41	7.25	5.29	6.16	8.07		
	MAMMA1002033	3.23	3.95	7.73	11.24	7.23	6.62		
	MAMMA1002041	2.87	2.25	3.18	4.74	5.39	1.71		
	MAMMA1002042	2.54	2.34	5.66	5.65	5.78	3.76		
	MAMMA1002045	2.33	3.51	7.28	8.39	5.05	4.44		
45	MAMMA1002047	2.58	2.98	8.83	8.7	8.9	6.89		
	MAMMA1002056	2.01	5.78	11.14	11.35	10.64	9.14		
	MAMMA1002058	1.67	2.61	8.19	4.84	4.66	4.27		
	MAMMA1002060	1.08	2.08	1.41	2.5	4.09	1.2		
	MAMMA1002065	1.81	2.75	6.04	7.19	5.19	3.26		
50	MAMMA1002068	2.43	1.84	5.29	4.98	5.6	4.47		
	MAMMA1002070	4.5	2.92	4.15	2.58	5.23	2.81		
	MAMMA1002078	1.32	1.43	2.94	1.12	4.4	1.07		
	MAMMA1002080	7.98	9.71	13.38	14.92	20.84	14.26		
	MAMMA1002082	2.54	4.96	13.04	9.67	8.15	7.78		
55	MAMMA1002084	1.78	3.47	3.38	4.68	4.48	3.6		

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	MAMMA1002087	1.12	2.15	5.37	3.6	4.67	2.36		
	MAMMA1002091	3.79	3.22	4.32	7.18	6.76	6.41	**	+
	MAMMA1002093	0.72	1.4	4.31	2.74	4.39	2.33		
5	MAMMA1002095	2.4	3.22	7.5	4.73	7.52	4.54		
	MAMMA1002108	1.84	1.02	2.63	1.87	3.24	1.31		
	MAMMA1002112	2.94	3.4	7.03	12.79	16.02	11.28	**	+
	MAMMA1002118	1.02	1.61	2.24	1.41	3.18	2.01		
10	MAMMA1002119	0.76	2.15	3.61	1.51	3.12	2.54		
	MAMMA1002125	1.79	2.61	6.95	4.52	4.19	4.11		
	MAMMA1002126	3.72	4.25	9.79	10.08	9.02	11.03		
	MAMMA1002128	0.9	2.36	3.07	2.7	3.49	2.88		
	MAMMA1002132	3.78	3.24	11.42	6.18	9.05	6.81		
15	MAMMA1002140	1.46	1.87	3.68	2.18	3.24	2.33		
	MAMMA1002142	3.13	3.43	7.06	5.18	7.62	5.46		
	MAMMA1002143	5.42	2.27	7.96	7.98	9.87	13.23		
	MAMMA1002145	1.47	1.34	3.3	2.9	4.02	2.64		
	MAMMA1002147	0.81	1.59	2.9	2.71	4.4	3		
20	MAMMA1002153	0.99	1.92	5.55	3.52	6.41	4.75		
	MAMMA1002155	2.11	1.93	6.76	4.4	6.46	4.46		
	MAMMA1002156	0.81	0.8	1.94	0.67	2.63	0.78		
	MAMMA1002158	1.38	1.83	5.12	4.09	7.73	5.2		
	MAMMA1002164	2.01	2.09	5.86	3.17	3.18	4.04		
25	MAMMA1002165	4.04	4.29	7.25	8.65	8.1	6.81		
	MAMMA1002170	1.01	1.48	154.53	2.65	3.24	4.11		
	MAMMA1002174	1.66	2.9	5.88	4.55	7.78	8.58		
	MAMMA1002175	3.27	3.3	7.02	6.95	6.64	7.22		
	MAMMA1002180	8.59	6.53	35.97	55.49	48.49	51.08	*	+
30	MAMMA1002198	3.11	2.3	9.33	7.6	11.22	7.13		
	MAMMA1002205	2.93	1.66	6.15	6.3	8.04	7.54		
	MAMMA1002206	4.6	3.59	8.14	12.4	13.97	11.74	**	+
	MAMMA1002209	1.7	1.93	4.03	4.43	4.23	4.57		
	MAMMA1002215	4.17	2.72	15.2	11.05	12.43	17.14		
35	MAMMA1002219	1.57	1.96	4.99	4.84	6.34	5.96		
	MAMMA1002224	3.18	2.9	8.13	5.49	7.25	5.86		
	MAMMA1002229	3.74	2.21	8.83	8.48	9.26	6.82		
	MAMMA1002230	2.02	2.21	6.63	5.31	8.91	6.58		
	MAMMA1002233	3.01	1.6	6.03	4.21	7.91	6.14		
40	MAMMA1002234	3.05	3.06	6.7	8.6	10.45	10.76	*	+
	MAMMA1002236	4.13	3.68	14.08	26.56	20.38	24.71	*	+
	MAMMA1002243	0.97	2.48	3.48	3.28	3.43	2.96		
	MAMMA1002250	1.06	2.09	5.2	3.95	6.82	6.01		
	MAMMA1002253	2.77	2.39	3.45	4.84	6.18	3.37		
45	MAMMA1002267	17.17	19.95	51.7	130.02	108.53	115.75	**	+
	MAMMA1002268	1.72	2.28	5.82	6.92	11.3	6.52		
	MAMMA1002269	0.89	0.73	2.25	2.32	2.58	1.67		
	MAMMA1002282	0.86	1.09	4.95	5.87	5.31	6.81		
	MAMMA1002292	2.71	2.25	7.77	10.57	10.52	11.53	*	+
50	MAMMA1002293	3.71	3.31	12.31	8.54	10.47	12.05		
	MAMMA1002294	0.9	1.71	4.61	3.68	6.03	4.2		
	MAMMA1002297	1.53	3.25	7.45	5.77	7.8	6.91		
	MAMMA1002298	1.48	1.4	3.98	3.85	3.11	2.46		
55	MAMMA1002299	1.5	1.69	3.16	3.91	2.97	2.2		

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	MAMMA1002308	1.39	1.35	6.55	4.5	3.11	2.54		
	MAMMA1002310	3.56	3.84	12.73	9.92	12.66	11.48		
5	MAMMA1002311	2.52	2.13	6.82	9.61	9.66	6.9	*	+
	MAMMA1002312	1.63	2.22	5.19	3.51	8.45	2.55		
	MAMMA1002317	2.08	2.55	4.89	4.08	3.85	4.09		
	MAMMA1002319	0.8	2.78	3.51	2.68	3.97	2.85		
	MAMMA1002322	2.48	3.23	7.84	12.21	10.02	8.55	*	+
10	MAMMA1002329	1.64	1.67	2.93	2.9	3.3	2.76		
	MAMMA1002332	2.17	2.38	4.58	5.98	4.14	3.05		
	MAMMA1002333	1.7	1.74	4.19	5.35	5.07	3.54		
	MAMMA1002335	1.75	2.72	8.53	6.93	11.32	4.23		
	MAMMA1002339	2.09	2.42	7.34	5.21	7.5	5.14		
15	MAMMA1002347	1.7	2.3	6.39	5.5	5.32	4.64		
	MAMMA1002351	2.08	2.68	5.74	3.03	4.48	4.84		
	MAMMA1002352	1.27	2.28	3.66	3.53	4.63	2.8		
	MAMMA1002353	4.46	2.5	5.84	5.95	4.19	4		
	MAMMA1002355	3.97	3.38	8.37	7.98	7.31	8.57		
20	MAMMA1002356	2.18	1.49	4.36	5.43	4.13	3.75		
	MAMMA1002359	3.95	3.35	16.09	23.81	24.53	19	*	+
	MAMMA1002360	0.93	1.73	3.77	2.48	3.2	1.67		
	MAMMA1002361	2.01	2.64	4.53	4.17	4.95	4.03		
	MAMMA1002362	2.33	2.33	3.36	5.31	5.51	3.99	*	+
25	MAMMA1002367	2.97	3.64	14.63	18.34	21.06	21.56	*	+
	MAMMA1002371	2.28	3.75	8.3	6.15	6.74	5.88		
	MAMMA1002380	1.81	2.26	4.9	4.71	5.76	3.55		
	MAMMA1002384	2.14	1.53	4.73	4.48	5.36	4.05		
	MAMMA1002385	1.19	2.05	5.63	3.34	4.8	2.47		
30	MAMMA1002390	1.41	2.04	3.75	5.48	5.4	3.43		
	MAMMA1002392	1.94	3.1	6.1	4.06	5.95	3.32		
	MAMMA1002396	4.87	3.49	12.87	10.79	12.9	8.08		
	MAMMA1002399	4.42	5.13	10.69	10.95	8.66	4.57		
	MAMMA1002400	3	2.22	4.69	3.11	4.36	3.53		
35	MAMMA1002409	51.57	55.16	63.3	77.54	80.62	77.88	**	+
	MAMMA1002411	1.08	1.88	4.13	3.43	5.49	1.92		
	MAMMA1002413	2.02	3.01	9.19	5.93	7.17	6.75		
	MAMMA1002417	1.83	2.24	4.87	3.45	4.25	2.63		
	MAMMA1002427	1.5	2.38	4.54	4.78	5.56	3.41		
40	MAMMA1002428	2.47	2.26	5.38	4.46	5.11	4.28		
	MAMMA1002433	1.74	2.18	6.84	6.72	6.96	6.22		
	MAMMA1002434	2.94	2.4	7.38	5.34	4.65	5.03		
	MAMMA1002446	1.39	2.34	5.62	3.98	5.84	5.96		
	MAMMA1002447	2.51	1.38	6.4	5.11	6.26	5.45		
45	MAMMA1002454	7.77	9.16	18.07	21.71	17.12	18.35		
	MAMMA1002461	2.06	4.11	7.7	4.92	5.41	6.47		
	MAMMA1002463	3.28	3.32	8.09	6.98	7.82	5.39		
	MAMMA1002464	16.58	16.77	20.05	19.41	20.41	18.09		
50	MAMMA1002466	9.48	9.89	14.22	14.58	15.75	13.93		
	MAMMA1002470	1.39	1.51	5.13	3.54	5.01	3.73		
	MAMMA1002475	0.72	1.85	5.03	3.86	5.17	4.65		
	MAMMA1002480	0.66	1.21	2.31	1.68	2.84	2.03		
	MAMMA1002485	29.98	27.24	46.09	64.83	74.9	80.68	**	+
55	MAMMA1002494	2	2	4.11	4.48	5.12	5.13	*	+

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	MAMMA1002498	0.97	2.57	3.16	2.07	3.18	1.55		
	MAMMA1002524	3.04	2.96	6.43	5.18	7.34	6.1		
	MAMMA1002530	2.5	3.24	4.88	3.17	4.41	2.55		
5	MAMMA1002538	2.34	2.38	5.62	5.46	5.13	4.91		
	MAMMA1002545	2.37	2.64	6.26	4.56	6.49	4.56		
	MAMMA1002554	1.96	1.42	5.43	5.3	6.01	7.81		
	MAMMA1002556	1.3	1.9	3.6	3.73	5.75	3.89		
10	MAMMA1002561	2.3	2.99	7.19	8.13	10.46	7.98		
	MAMMA1002565	1.22	2.15	3.52	2.57	4.51	2.55		
	MAMMA1002566	0.98	1.87	6.21	1.65	4.7	3.9		
	MAMMA1002571	0.53	1.8	3.06	1.43	3.1	4.3		
	MAMMA1002573	2.14	1.86	7.06	4.54	5.66	5.97		
15	MAMMA1002576	118.77	131.84	363.97	348.62	471.73	358.66		
	MAMMA1002584	3.52	2.27	11.91	12.86	17.82	13.46		
	MAMMA1002585	0.76	1.86	4.38	1.85	3.6	5.26		
	MAMMA1002586	1.98	2.55	3.85	4.12	5.02	3.3		
	MAMMA1002589	1.08	1.26	2.44	2.36	5.06	3.19		
20	MAMMA1002590	1.01	1.57	5.87	2.58	6.75	4.57		
	MAMMA1002593	2.48	2.48	4.89	4.18	4.07	3.04		
	MAMMA1002597	2.47	2.52	7.25	8.06	9.48	8.78	*	+
	MAMMA1002598	12.12	13.52	30.83	37.28	48.14	38.91	*	+
	MAMMA1002603	1.2	1.39	3.69	3.25	6.24	4.35		
25	MAMMA1002612	3.51	3.39	12.6	7.66	7.78	9.76		
	MAMMA1002617	4.3	3.41	10.15	6.3	7.29	10.05		
	MAMMA1002618	1.68	2.27	4.02	2.76	3.59	3.91		
	MAMMA1002619	2.96	2.8	5.24	3.22	5.88	3.49		
30	MAMMA1002622	2.51	2.12	8.02	7.1	7.18	7.15		
	MAMMA1002623	2.31	2.21	6.27	5.89	6.17	6.19		
	MAMMA1002625	1.32	1.3	3.23	2.3	6.42	2.6		
	MAMMA1002627	0.98	0.82	2.93	0.6	1.29	0.21		
	MAMMA1002629	1.8	2.23	6.09	5.03	6.74	7.02		
35	MAMMA1002631	1	1.86	3.61	3.07	4.55	2.97		
	MAMMA1002633	6.61	7.44	21.47	19.33	24.55	21.53		
	MAMMA1002636	1.02	2.46	6.97	6.79	8.77	9.25		
	MAMMA1002637	1.05	1.4	4.66	3.39	4.85	4.28		
	MAMMA1002646	1.69	0.8	3.32	2.33	2.86	1.53		
40	MAMMA1002648	10.51	14.07	21.18	42.29	31.45	39.76	**	+
	MAMMA1002650	1.33	0.56	1.62	1.76	2.08	0.57		
	MAMMA1002652	1.76	2.82	7.31	7.5	7.41	9.79		
	MAMMA1002655	1.7	2.11	3.65	2.54	4.23	3.78		
	MAMMA1002662	0.84	2.24	4.33	3.57	5.68	4.13		
45	MAMMA1002665	3.61	3.57	10.05	13.42	17.97	19.59	*	+
	MAMMA1002671	2.84	3.63	10.17	17.04	16.47	19.3	**	+
	MAMMA1002673	1.32	2.14	4.93	4.07	5.03	2.82		
	MAMMA1002684	2.95	3.11	3.84	6.61	8.19	7.54	**	+
	MAMMA1002685	0.68	1.49	2.57	2.05	3.74	2.97		
50	MAMMA1002692	1.28	1.96	5.45	2.46	4.14	3.62		
	MAMMA1002693	1.84	4.18	8	4.63	7.68	6.61		
	MAMMA1002698	0.99	1.91	4.05	2.92	4.42	3.3		
	MAMMA1002699	2	2.35	4.43	4.05	5.22	3.64		
55	MAMMA1002701	2.41	2.56	8.46	6.72	8.94	8.93		
	MAMMA1002708	1.51	1.55	5.38	4.08	6.16	6.18		

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	MAMMA1002711	1.58	2.08	7.04	4.37	7.35	5.81		
	MAMMA1002712	3.05	3.13	6.98	4.88	7.12	7.39		
5	MAMMA1002716	0.56	1.75	3.39	2.38	6.29	2.9		
	MAMMA1002721	2.11	2.01	5.57	3.72	6.34	4.59		
	MAMMA1002723	2.43	2.46	4.91	3.85	5.98	4.88		
	MAMMA1002727	3.85	5.55	5.78	5.29	4.45	6.22		
	MAMMA1002728	21.35	22.03	57.81	49.09	54.73	65.13		
10	MAMMA1002742	4.12	4.39	10.35	7.92	8.63	7.61		
	MAMMA1002743	4.12	3.89	6.17	13.81	14.09	13.46	**	+
	MAMMA1002744	2.07	3.15	9.18	9.33	12.98	13.16		
	MAMMA1002746	0.93	1.28	3.09	2.29	4.31	1.68		
	MAMMA1002748	2.71	2.65	4.52	7.15	5.86	4.72	*	+
15	MAMMA1002754	1.12	2.41	5.56	5.05	5.65	6.26		
	MAMMA1002758	0.71	1.66	2.55	1.57	4.41	1.69		
	MAMMA1002762	11.3	11.14	36.64	38.42	34.23	48.71		
	MAMMA1002764	1.83	3.2	5.95	5.11	6.06	4.26		
	MAMMA1002765	1.19	1.63	4.29	4.63	5.26	2.67		
20	MAMMA1002769	7.4	6.44	13.04	13.78	8.03	12.41		
	MAMMA1002771	1.41	2.41	3.31	3.54	5.39	4.39		
	MAMMA1002775	4.56	4.48	19.79	22.54	29.77	24.29	*	+
	MAMMA1002780	2.59	1.83	3.03	2.11	4.89	3.78		
	MAMMA1002782	1.43	2.49	3.85	2.51	4.79	4.11		
25	MAMMA1002795	1.89	2.03	3.46	6.45	7.68	5.35	**	+
	MAMMA1002796	4.35	3.97	7.51	7.2	8.09	8.17		
	MAMMA1002805	6.61	11.12	16.52	15.95	24.7	16.5		
	MAMMA1002806	1.47	2.02	3.51	2.28	4.62	2.17		
	MAMMA1002807	1.63	2.4	6.77	6.78	9.66	6.4		
30	MAMMA1002814	3.43	3.52	7.92	9.58	12.39	10.66	*	+
	MAMMA1002817	1.28	1.56	2.87	2.89	5.43	2.91		
	MAMMA1002820	1.66	1.93	2.61	2.52	4.77	2.21		
	MAMMA1002830	67.67	70.46	130.59	165.92	139.33	187.18	*	+
35	MAMMA1002833	4.16	2.88	9.4	8.22	10.68	10.58		
	MAMMA1002835	0.77	1.87	4.03	1.73	3.97	2.79		
	MAMMA1002838	1.85	2.66	5.31	2.91	4.44	3.93		
	MAMMA1002842	1	3.83	3.84	3.32	4.63	5.15		
	MAMMA1002843	1.72	2.92	2.33	4.09	4.81	3		
40	MAMMA1002844	3.05	3.64	6.52	5.26	7.3	4.09		
	MAMMA1002845	1.25	1.57	2.45	3.59	3.55	4.67	*	+
	MAMMA1002857	92.1	106.97	208.17	209.17	202.29	249.13		
	MAMMA1002858	317.94	188.78	378.89	560.7	620.76	724.33	**	+
	MAMMA1002863	2.17	2.83	6.91	3.51	5.12	3.96		
45	MAMMA1002868	2.73	3.7	6.26	6.35	9.53	10.25	*	+
	MAMMA1002869	5.43	6.83	26.64	22.68	30.03	29.85		
	MAMMA1002871	0.61	1.7	1.78	1.9	3.8	1.97		
	MAMMA1002875	1.9	2.59	3.99	4.48	6.35	4.06		
	MAMMA1002879	8.42	9.2	14.19	22.55	23.63	27.96	**	+
50	MAMMA1002880	1.23	2.02	2.12	1.48	5.42	2.03		
	MAMMA1002881	1.21	1.43	1.84	3.01	5.43	2.46		
	MAMMA1002885	0.96	1.59	2.71	2.6	3.26	1.59		
	MAMMA1002886	2.63	2.52	3.9	6.01	5.37	7.05	**	+
	MAMMA1002887	1.28	1.83	2.78	2.98	5.14	4.32	*	+
55	MAMMA1002890	0.79	1.7	4.05	4.39	4.8	4.01		

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	MAMMA1002892	1.35	2.45	4.98	6.64	6.24	5.84	*	+
	MAMMA1002893	4.52	3.58	5.4	7.6	8.03	8.43	**	+
	MAMMA1002895	1.43	1.31	3.28	1.81	3.89	1.64		
5	MAMMA1002898	0.53	1.67	4.15	2.69	4.72	1.42		
	MAMMA1002905	1.32	1.58	2.51	4.1	5.01	3.87	**	+
	MAMMA1002906	15.12	10.76	15.42	19.47	13.76	15.58		
	MAMMA1002908	0.99	1.24	4.28	3.53	4.24	4.07		
	MAMMA1002909	1.92	2.64	5.67	6.82	8.18	6.57	*	+
10	MAMMA1002918	2.75	2.69	5.42	5.27	7.26	6.58		
	MAMMA1002925	92.88	85.77	163.7	127.31	122.97	178.98		
	MAMMA1002926	6.08	6.31	16.25	16.64	19.48	19.9		
	MAMMA1002930	1.21	1.59	5.67	4.88	8.91	4.21		
15	MAMMA1002937	4.91	3.87	30.71	40.45	75.17	61.59	*	+
	MAMMA1002938	1.67	1.86	2.42	2.35	3.2	3.56		
	MAMMA1002941	0.49	1.48	2.78	2.53	3.59	2.24		
	MAMMA1002947	2.24	2.59	4.55	6	6.8	7.94	*	+
	MAMMA1002964	1.73	2.9	5.91	6.91	7.24	7.16	*	+
20	MAMMA1002967	1.94	1.59	2.28	2.9	4.19	2.79		
	MAMMA1002970	2.72	1.77	6	7.59	7.28	8.96	*	+
	MAMMA1002971	1.52	1.6	2.9	2.51	7.27	3.93		
	MAMMA1002972	1	1.32	2.95	1.74	4.56	2.12		
	MAMMA1002973	1.38	2.45	6.73	4.36	6.72	6.78		
25	MAMMA1002979	55.6	60.16	121.72	134.02	101.19	107.19		
	MAMMA1002982	0.53	1.98	2.28	2.04	3.28	1.9		
	MAMMA1002987	1.56	2.11	5.56	3.14	5.55	4.14		
	MAMMA1003003	0.77	2.18	4.78	4.46	6.47	5.08		
	MAMMA1003004	1.65	1.86	3.7	3.64	3.59	3.16		
30	MAMMA1003007	0.69	1.16	2.73	1.88	3.7	2.32		
	MAMMA1003011	1.56	1.8	3.67	3.77	5.41	3.94		
	MAMMA1003013	3.67	5.57	39.41	47.56	59.11	54.29	*	+
	MAMMA1003015	1.16	1.8	2.21	2.54	2.9	2.19		
	MAMMA1003019	0.6	1.61	2.1	3.12	4.61	2.63		
35	MAMMA1003020	2.96	4.19	5.34	11.31	10.33	10.09	**	+
	MAMMA1003026	1.29	1.56	2.95	2.66	4.25	2.25		
	MAMMA1003031	0.61	1.71	5.64	4.13	5.85	5.89		
	MAMMA1003033	1.34	1.65	4.13	2.84	5.11	3.64		
	MAMMA1003035	1.66	2.5	5.44	5.12	7.03	4.9		
40	MAMMA1003039	0.95	0.75	3.31	2.15	4.73	2.48		
	MAMMA1003040	1.38	2.54	5.32	4.57	7.47	7.43		
	MAMMA1003044	2.36	2.96	6.52	4.29	6.41	5.99		
	MAMMA1003047	1.82	3.67	7.61	5.74	7.05	7.13		
	MAMMA1003049	0.47	1.72	2.03	1.08	1.56	1.45		
45	MAMMA1003055	1.24	1.67	4.92	3.77	5.14	3.44		
	MAMMA1003056	0.9	0.91	1.85	1.22	2.26	1.02		
	MAMMA1003057	2.53	3.34	6.76	7.25	9.2	5.01		
	MAMMA1003066	1.65	2.06	4.73	4.1	7.08	5.07		
	MAMMA1003075	1.11	1.71	3.16	1.85	4.37	2.32		
50	MAMMA1003089	1.69	2.11	7.13	7.85	8.66	7.43		
	MAMMA1003092	1.25	1.79	3.21	2.62	4.08	1.76		
	MAMMA1003095	2.27	3.33	5.4	7.24	8.57	5.34		
	MAMMA1003099	1.88	2.51	4.95	4.09	6.45	4.35		
55	MAMMA1003102	1.33	2.04	2.88	3.2	3.27	2.39		

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	MAMMA1003104	0.64	1.07	3.17	2.15	3.25	1.56		
	MAMMA1003113	4.22	4.21	6.98	9.22	7.02	7.07		
	MAMMA1003126	12.93	14.72	20.89	19.28	12	15.63		
5	MAMMA1003127	2.95	3.14	5.91	3.88	6.12	5.19		
	MAMMA1003131	2.82	3.51	4.86	3.82	5.91	5.88		
	MAMMA1003135	3.66	4.65	7.61	2.33	4.04	2.64		
	MAMMA1003140	0.73	2.01	3.59	2.3	3.32	1.89		
	MAMMA1003146	2.08	2.24	3.89	3.17	5.09	3.3		
10	MAMMA1003150	1.18	1.8	3.01	3.37	4.29	3.45	*	+
	MAMMA1003154	0.54	1.41	2.29	2.21	3.57	2.34		
	MAMMA1003155	8.08	9.18	20.88	21.41	17.68	20.56		
	MAMMA1003157	5.94	4.82	6.07	5.18	7.05	7.89		
	MAMMA1003163	1.74	1.69	4.23	2.55	5.46	3.08		
15	MAMMA1003164	2.94	4.56	6.23	4.08	9.9	8.18		
	MAMMA1003166	3.62	3.5	5.77	6.24	8.66	6.12		
	NB9N31000010	2.5	3.88	7.58	9.63	12.26	9.5	*	+
	NB9N31000016	0.73	2.8	5.21	4.04	4.41	3.15		
20	NB9N31000043	8.1	8.88	19.71	12.51	12.3	12.64		
	NB9N31000045	167.24	153.32	255.96	401.78	320.53	296.06	*	+
	NB9N31000054	7.29	4.42	11.75	11.15	11.87	13.43		
	NB9N31000076	2.31	1.94	3.51	4.5	6.35	4.44	*	+
	NB9N31000086	2.62	2.65	6.23	3.61	9.71	7.69		
25	NT2RM1000001	2.56	2.45	6.24	5.7	7.05	6.32		
	NT2RM1000018	3.84	4.69	10.6	6.58	9.09	6.92		
	NT2RM1000032	1.12	2.64	3.88	2.28	4.92	3.21		
	NT2RM1000035	1.72	3.68	5.53	5.44	5.21	5.98		
	NT2RM1000037	1.38	2.98	2.75	2.41	4.15	2.11		
30	NT2RM1000039	3.45	5.13	5.9	6.51	7.26	8.4	*	+
	NT2RM1000042	33.96	32.7	65.25	57.46	67.15	64.39		
	NT2RM1000055	0.85	1.74	3.34	1.16	3.55	1.16		
	NT2RM1000059	3.26	3.16	7.66	4.69	5.97	5.78		
	NT2RM1000062	1.13	1.21	1.9	3.47	4.33	2.46	*	+
35	NT2RM1000065	23.8	16.41	34.06	36.15	35.1	51.38		
	NT2RM1000066	4.13	4.31	8.98	7.23	10.95	9.81		
	NT2RM1000071	49.63	37.81	86.71	73.04	63.32	84.05		
	NT2RM1000080	1.37	2.04	3.8	5.1	5.94	4.5	*	+
	NT2RM1000086	4.04	4.65	4.08	5.01	6.23	5.58	*	+
40	NT2RM1000092	6.17	6.93	15.76	14.48	25.91	15.13		
	NT2RM1000118	0.63	1.12	1.22	0.63	1.7	0.44		
	NT2RM1000119	1.32	2.27	1.96	1.84	3.38	2.99		
	NT2RM1000121	1.13	1.84	1.76	2.92	3.84	2.78	*	+
	NT2RM1000122	3.5	3.78	7.34	5.5	8.86	9.57		
45	NT2RM1000127	0.69	1.34	1.47	2.14	3.36	3.32	*	+
	NT2RM1000131	0.71	1.7	1.47	1.36	3.02	2.53		
	NT2RM1000132	3.2	4.88	4.83	6.86	6.46	6.31	*	+
	NT2RM1000153	1.75	1.9	3.68	2.38	4.45	4.84		
	NT2RM1000184	72.82	77.46	151.91	106.39	163.07	125.55		
50	NT2RM1000186	1.55	1.46	4.32	2.67	4.72	3.94		
	NT2RM1000187	3.11	1.96	5.16	10.09	9.1	8.78	**	+
	NT2RM1000199	1.12	1.37	2.11	2.41	3.51	2.72	*	+
	NT2RM1000213	1.32	1.75	2.38	2.66	2.71	2.22		
55	NT2RM1000215	10.95	11.07	17.21	19.51	22.84	15.14		

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	NT2RM1000218	9.72	9.95	23.71	26.94	24.74	29.21		
	NT2RM1000224	8.8	8.63	15.2	15.51	21.29	17.61		
5	NT2RM1000236	30.38	24.19	61.14	72.86	82.44	71.5	*	+
	NT2RM1000242	0.23	1.17	1.32	0.39	2.27	0.12		
	NT2RM1000244	1.41	1.48	3.43	6.9	3.69	6.7	*	+
	NT2RM1000252	1.75	1.5	3.4	3.4	3.06	3.18		
	NT2RM1000256	7.88	5.89	9.46	26.12	29.45	36.8	**	+
10	NT2RM1000257	1.98	3.01	5.09	4.64	6.83	6.65		
	NT2RM1000260	7.9	7.01	13.32	9.18	12.49	11.77		
	NT2RM1000269	3.87	2.87	5.12	6.63	9.78	3.87		
	NT2RM1000271	0.71	0.8	1.87	0.46	2.47	0.51		
	NT2RM1000272	117.67	92.26	202.95	249.32	333.98	356.74	*	+
15	NT2RM1000273	10.03	9.45	20.12	22.32	16.68	15.76		
	NT2RM1000274	63.11	66.41	123.01	137.14	91.97	104.48		
	NT2RM1000280	3.95	4.18	8.18	6.71	8.72	7.93		
	NT2RM1000295	0.49	1	2.2	1.12	3.16	0.87		
	NT2RM1000300	1.51	1.87	2.78	3.63	5.75	3.09		
20	NT2RM1000304	58.38	98.72	161.87	187.58	185.55	204.78	*	+
	NT2RM1000314	1.8	2.12	3.6	3.84	4.07	4.33		
	NT2RM1000318	12.6	14.04	20.81	35.01	29.96	29.8	**	+
	NT2RM1000335	2.76	2.57	4.34	6.29	5.41	4.09		
	NT2RM1000341	0.46	1.27	1.95	1.41	2.33	0.99		
25	NT2RM1000350	3.04	3.47	5.52	7.32	5.63	6.44		
	NT2RM1000354	0.55	1.31	1.31	5.43	7.2	5.72	**	+
	NT2RM1000355	30.24	31.5	56.85	74.62	50.25	61.33		
	NT2RM1000361	3.63	3.87	7.23	14.39	20.29	18.78	**	+
	NT2RM1000365	0.58	1.08	1.71	1.27	1.82	0.52		
30	NT2RM1000372	14.99	19.56	30.06	42.71	46.67	45.44	**	+
	NT2RM1000377	2.04	2.18	9.66	13.38	14.74	13.48	*	+
	NT2RM1000388	0.35	1.57	3.01	2.2	3.8	2.42		
	NT2RM1000394	0.45	1.31	1.87	1.43	2.72	0.69		
	NT2RM1000399	0.53	1.57	3.25	1.98	3.2	1.81		
35	NT2RM1000407	1.13	1.52	2.17	1.02	2.7	1.51		
	NT2RM1000421	0.84	0.57	2.78	1.06	1.77	1.13		
	NT2RM1000422	20.65	23.31	54.69	87.5	82.91	79.47	*	+
	NT2RM1000430	1.22	1.57	2.01	3.2	3.67	2.95	**	+
	NT2RM1000462	1.55	2.33	7.32	5.59	7.28	8.16		
40	NT2RM1000499	1.36	2.09	4.74	5	6.16	6.37	*	+
	NT2RM1000512	12.49	13.22	19.22	10.54	14.15	19.84		
	NT2RM1000519	33.96	37.54	55.78	31.14	29.25	47.55		
	NT2RM1000527	7.97	8.92	37.68	55.15	60.19	46.68	*	+
	NT2RM1000539	3.45	3.59	12.93	15.52	17.01	18.1	*	+
45	NT2RM1000542	0.85	1.05	2.99	1.17	2.35	1.02		
	NT2RM1000553	3.7	2.42	22.32	42.83	42.96	34.5	*	+
	NT2RM1000555	11.3	11.6	23.97	34.11	29.67	22.76		
	NT2RM1000558	2.09	5.34	9.74	9.56	16.24	14.29		
	NT2RM1000563	1.47	2.42	3.36	4.07	5.58	3.95	*	+
50	NT2RM1000566	0.88	1.57	3.5	3.62	6.01	2.79		
	NT2RM1000570	96.92	77.32	137.63	167.35	105.47	174.1		
	NT2RM1000571	13.21	11.87	22.51	43.87	40.18	28.45	*	+
	NT2RM1000574	0.84	2.15	2.55	2.15	3.07	1.67		
55	NT2RM1000580	1.37	2.18	4.07	5.15	7.98	2.96		

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	NT2RM1000620	2.61	2.95	8.2	8.35	9.58	7.26		
	NT2RM1000623	1.25	1.2	2.38	1.75	2.81	0.62		
	NT2RM1000630	0.79	2.28	2.39	1.68	3.51	1.67		
5	NT2RM1000633	30.97	39.36	36.34	54.43	44.6	43.59	*	+
	NT2RM1000634	1.91	4.16	8.12	2.56	7.05	5.57		
	NT2RM1000642	3.85	5.37	8.13	8.21	8.56	8.52		
	NT2RM1000647	41.3	39.09	62.11	57.72	68.29	62.69		
10	NT2RM1000648	2.49	2.65	4.61	6.14	5.63	4.51		
	NT2RM1000650	2.46	3.05	7.6	5.4	6.07	6		
	NT2RM1000661	4.48	5.7	15.82	15.48	13.45	13.18		
	NT2RM1000666	1	1.77	1.99	1.37	2.8	0.71		
	NT2RM1000669	3.51	2.76	4.67	3.63	5.42	3.28		
15	NT2RM1000672	2.23	3.95	7.81	3.98	8.47	7.22		
	NT2RM1000681	99.53	86.09	118.7	105.41	90.59	124.14		
	NT2RM1000691	2.02	2.61	5.74	3.61	7.69	3.76		
	NT2RM1000698	1.11	1.43	4	6.42	6.29	4.11	*	+
	NT2RM1000699	1.85	2.86	3.17	3.67	4.35	4.15	*	+
20	NT2RM1000702	3.71	4.64	9.47	9.31	9.72	11.4		
	NT2RM1000703	11.56	12.36	25.24	26.72	20.42	21.06		
	NT2RM1000704	24.48	23	32.91	46.54	24.13	40.82		
	NT2RM1000725	60.92	59.45	88.28	94.89	82.36	105.67		
25	NT2RM1000726	1.85	2.02	5.75	1.97	4.8	4		
	NT2RM1000731	1.11	2.24	4.98	2.45	3.47	3.43		
	NT2RM1000741	1.38	1.87	3.16	2.69	4.15	2.9		
	NT2RM1000742	2.61	4.6	7.41	9.55	10.94	9.84	*	+
	NT2RM1000744	2.1	3.61	7.14	4.05	5.24	5.05		
30	NT2RM1000746	2.25	2.47	2.95	2.22	4.01	3.89		
	NT2RM1000747	23.34	23.92	46.23	44.66	50.12	55.15		
	NT2RM1000752	3.83	2.36	4.62	3.95	4.88	3.46		
	NT2RM1000767	4.14	7.27	35.27	25.27	38.02	28.81		
	NT2RM1000770	2.97	3.08	6.36	4.71	6.71	5.67		
35	NT2RM1000772	0.76	0.7	1.07	1.34	1.69	0.44		
	NT2RM1000779	13.03	12.11	42.22	53.91	45.61	66.73	*	+
	NT2RM1000780	1.16	2.9	3.74	3.09	4.32	3.01		
	NT2RM1000781	1.07	0.98	1.71	2.58	4.4	1.93		
	NT2RM1000789	5.28	5.15	29.74	29.63	46.72	36.53		
40	NT2RM1000800	2.87	2.63	6.37	5.66	9.57	6.96		
	NT2RM1000802	2.44	2.99	7.5	4.34	5.47	4.82		
	NT2RM1000811	1.78	1.6	2.13	2.26	4.96	2.76		
	NT2RM1000826	6.06	6.36	13.34	14.42	20.73	20.98	*	+
	NT2RM1000829	3.91	2.87	6.39	6.73	8.48	8.41	*	+
45	NT2RM1000831	81.54	64.45	185.14	182.43	179.79	197.27		
	NT2RM1000833	14.58	13.33	42.25	76.74	73.25	67.48	**	+
	NT2RM1000834	4.06	3.09	6.2	8.49	9.42	10.49	**	+
	NT2RM1000841	12.34	10.01	21.15	34.98	36.63	30.81	**	+
	NT2RM1000848	4.79	4.42	6.44	9.36	12.74	10.45	**	+
50	NT2RM1000850	2.66	3.42	13.41	8.55	11.79	9.74		
	NT2RM1000852	1.34	1.94	3.23	3.01	5.76	2.61		
	NT2RM1000853	1.19	2.85	2.15	3.11	3.26	3.23		
	NT2RM1000855	29.27	24.82	45.19	52.48	45.32	58.45		
	NT2RM1000857	4.63	5	10.67	8.76	11.3	10.76		
55	NT2RM1000858	7.3	7.6	15.86	9.09	11.56	10.93		

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	NT2RM1000867	19.42	15.85	28.1	32.52	35.03	24.06		
	NT2RM1000874	3.15	2.65	7.03	5.17	9.62	5.31		
5	NT2RM1000882	2.36	1.37	3.71	5.39	9.31	5.45	*	+
	NT2RM1000883	5.21	3.34	7.42	5.18	11.3	7.9		
	NT2RM1000885	3.86	4.43	9.4	7.59	8.15	9.8		
	NT2RM1000893	3.15	3.41	8.14	7.73	6.17	8.39		
	NT2RM1000894	3.29	4.4	6.18	8.14	6.11	6.61		
10	NT2RM1000898	3.72	7.33	10.02	13.4	17.51	12.41	*	+
	NT2RM1000899	1.02	2.22	3.07	3.68	7.49	4.69		
	NT2RM1000905	11.92	17.41	30.36	37.19	45.16	37.3	*	+
	NT2RM1000910	7.5	8.78	20.16	36.37	36.98	37.5	**	+
	NT2RM1000914	6.46	7.69	19.74	14.28	17.33	17.77		
15	NT2RM1000919	6.1	3.92	9.91	14.61	17.49	15.37	**	+
	NT2RM1000921	0.72	1.9	3.69	2.79	4.27	3.32		
	NT2RM1000922	4.7	6.11	8.09	9.03	5.21	6.36		
	NT2RM1000924	0.89	3.03	3.04	3.08	2.89	3		
	NT2RM1000927	1.35	1.78	2.85	3.07	4.72	3.46		
20	NT2RM1000951	7.95	11.33	26.73	32.33	34.46	31.18	*	+
	NT2RM1000956	7.91	6.36	13.35	23.61	27.46	21.91	**	+
	NT2RM1000960	12.48	10.27	29.06	34.95	37.47	38.96	*	+
	NT2RM1000961	3.28	3.61	7.45	9.44	13.18	8.11		
	NT2RM1000962	4.14	3.5	8.18	7.59	10.15	9.86		
25	NT2RM1000973	16.71	15.79	29.32	31.15	11.56	27.73		
	NT2RM1000978	0.57	1.46	1.58	0.95	2.64	0.44		
	NT2RM1000982	2.34	2.29	3.52	3.57	4.94	4.54	*	+
	NT2RM1000991	1.61	1.78	4.25	3.88	5.56	5.23		
30	NT2RM1000994	6.36	6.16	12.57	16.52	16.64	14.53	*	+
	NT2RM1001002	5.11	6.69	15.34	21.78	22.69	22.28	*	+
	NT2RM1001003	5.42	5.15	11.98	16.24	9.06	8.46		
	NT2RM1001008	1.4	2.22	2.48	1.83	4.34	4.33		
	NT2RM1001011	6.29	5.43	7.86	14.4	10.46	14.72	*	+
35	NT2RM1001013	2.9	2.75	4.75	8.29	7.96	5.81	*	+
	NT2RM1001017	1	1.82	3.44	3.28	4.86	3.92		
	NT2RM1001018	65.15	74.45	146.86	134.65	125.46	113.93		
	NT2RM1001026	1.37	2.64	3.17	2.99	4.61	3.31		
	NT2RM1001028	0.98	1.73	2.91	1.74	1.89	0.76		
40	NT2RM1001043	4.47	3.64	8.42	11.43	12.7	8.01		
	NT2RM1001044	2.23	3.17	4.92	5.03	5.51	3.93		
	NT2RM1001059	1.47	3.72	4.12	4.05	6.11	3.02		
	NT2RM1001063	4.11	3.29	6.1	4.22	5.64	5.6		
	NT2RM1001066	0.86	1.85	2.44	2.23	3.99	2.85		
45	NT2RM1001072	1.8	2.8	4.33	1.94	3.74	1.52		
	NT2RM1001074	1.66	2.38	5.18	5.18	4.19	2.67		
	NT2RM1001076	1.39	2.2	4.94	3.43	4.42	1.72		
	NT2RM1001082	1.79	2.6	5.23	5.31	5.92	4.57		
	NT2RM1001085	1.25	1.65	2.81	1.16	3.27	1.17		
50	NT2RM1001092	3.82	4.2	5.57	9.34	7.94	9.82	**	+
	NT2RM1001102	1.7	2.3	4.4	2.49	5.94	4.64		
	NT2RM1001103	4.37	3.88	7.18	6.25	10.28	8.08		
	NT2RM1001105	1.77	2.02	4.63	2.49	5.11	3.51		
	NT2RM1001112	2.68	2.66	3.69	3.85	4.75	2.43		
55	NT2RM1001115	1.44	1.57	4.72	3	6.46	3.73		

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	NT2RM1001122	2.84	3.35	7.3	9.43	9.75	9.54	*	+
	NT2RM1001136	0.88	1.41	2.71	2.31	3.87	1.59		
5	NT2RM1001139	3.9	3.7	5.38	5.33	11.18	6.77		
	NT2RM2000003	2.45	3.33	2.4	4.5	6.29	4.88	*	+
	NT2RM2000006	2.34	2.95	7.25	5.12	7.11	6.24		
	NT2RM2000010	12.79	13.03	22.53	20.2	17.11	21.83		
	NT2RM2000013	8.1	9.44	50.36	68.75	95.32	74.36	*	+
10	NT2RM2000030	4.8	2.21	23.41	26.33	32.15	28.69		
	NT2RM2000032	2.76	2.92	8.53	10.01	12.19	10.67	*	+
	NT2RM2000039	3.94	4.67	4.75	6.42	5.78	4.99		
	NT2RM2000042	3.5	4.9	11.69	17.71	17.4	15.02	*	+
	NT2RM2000092	1	2.38	1.98	1.29	4.69	2.25		
15	NT2RM2000093	8.37	6.63	11.41	9.02	12.23	10.18		
	NT2RM2000101	9.2	9.94	40	61.09	76.38	69.62	*	+
	NT2RM2000104	6.82	8.02	46.75	51.34	68.83	43.48		
	NT2RM2000124	1.54	2.23	6.33	7.73	8.84	8.47	*	+
20	NT2RM2000155	5.08	3.77	5.8	9.45	11.58	12.51	**	+
	NT2RM2000191	3.33	5.68	28.62	26.54	34.38	31.6		
	NT2RM2000192	1.03	1.29	2.45	6.3	4.75	3.83	*	+
	NT2RM2000239	1.92	2.79	3.09	2.85	5.02	3.1		
	NT2RM2000240	32.78	29.59	74.35	61.15	60.54	61.71		
25	NT2RM2000241	4.49	5.9	6.35	8.24	11.72	6.78		
	NT2RM2000250	1.29	1.54	4.16	2.09	5.05	2.54		
	NT2RM2000259	3.06	3.42	3.59	6.38	8.44	6.74	**	+
	NT2RM2000260	2.53	2.05	3.12	4.23	4.07	5.79	*	+
	NT2RM2000265	0.91	1.55	0.99	1.43	2.4	1.09		
30	NT2RM2000287	4.7	4.23	10.82	10.69	11.54	14.73		
	NT2RM2000306	12.24	9.36	10.48	23.63	14	20.79	*	+
	NT2RM2000312	19.4	17.81	25.01	38.39	31.27	24.8		
	NT2RM2000322	1.93	1.82	4.48	3.79	7.05	3.32		
	NT2RM2000343	7.74	8.38	41.34	63.81	79.6	71.12	*	+
35	NT2RM2000359	3.67	2.86	4.95	4.93	9.55	4.72		
	NT2RM2000362	20.09	18.2	62.29	94.88	111.25	95.66	*	+
	NT2RM2000363	1.08	1.89	2.97	4.2	4.32	3.33	*	+
	NT2RM2000368	2.84	2.4	4.74	6.15	5.98	5.29	*	+
	NT2RM2000371	76.64	65.68	119.32	135.82	125	44.64		
40	NT2RM2000374	1.68	1.92	5.75	3.34	4.8	3.58		
	NT2RM2000387	8.98	9.83	11.92	20.02	25.18	17.11	*	+
	NT2RM2000393	1.7	1.63	3.75	3.31	7.65	3.28		
	NT2RM2000395	1.07	1.51	1.98	1.72	4.34	2.23		
	NT2RM2000402	12.38	11	15.78	25.15	18.31	22.51	*	+
45	NT2RM2000405	1.33	1.25	2.2	1.52	3.08	3.16		
	NT2RM2000407	0.76	1.78	2.49	1.89	2.72	2.89		
	NT2RM2000410	0.79	1.94	2.23	1.98	2.84	2.09		
	NT2RM2000420	3.09	2.52	4.43	4.24	4.5	3.26		
50	NT2RM2000422	3.22	2.44	5.81	3.61	6.17	2.87		
	NT2RM2000423	1.91	1.96	5.69	3.89	7.64	4.18		
	NT2RM2000452	3.46	3.18	4.31	7.35	8.65	9.57	**	+
	NT2RM2000469	3.28	3.28	4.44	1.87	2.33	2.46	*	-
	NT2RM2000490	6.03	6.03	9.18	5.55	6.16	6.9		
55	NT2RM2000497	3.29	3.29	4.59	3.15	5.48	2.43		
	NT2RM2000502	4.69	4.69	10.24	5.87	7.08	7.02		

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	NT2RM2000504	7.37	7.37	12.93	10.83	4.49	11.2	
	NT2RM2000514	2.75	2.75	6.23	3.11	3.32	3.8	
5	NT2RM2000522	1.9	1.9	3.27	1.94	1.18	1.13	
	NT2RM2000540	6.02	6.02	9.53	9.12	8.96	8.14	
	NT2RM2000556	2.09	2.09	2.8	1.24	2.33	0.93	
	NT2RM2000565	3.35	3.35	6.02	3.27	4.14	3.72	
	NT2RM2000566	6.59	6.59	15.8	9.09	9.21	9.57	
10	NT2RM2000567	2.16	2.16	5.64	2	5.67	3.82	
	NT2RM2000569	4.69	4.69	7.93	5.77	8.18	4.7	
	NT2RM2000577	11.08	11.08	15.39	11.79	14.95	14.48	
	NT2RM2000581	4.64	4.64	6.49	5.98	7.97	6.85	
	NT2RM2000582	5.23	5.23	10.34	8.34	9.14	7.19	
15	NT2RM2000588	21.84	21.84	65.91	40.15	44.01	45.21	
	NT2RM2000589	3.98	3.98	11.35	7.96	7.6	8.64	
	NT2RM2000594	1.87	1.87	4.38	1.62	2.71	1.92	
	NT2RM2000599	6.34	6.34	16.12	17.82	14.5	15.44	
20	NT2RM2000609	4.61	4.61	6.77	3.76	5.81	5.48	
	NT2RM2000612	3.52	3.52	6.4	5.93	7.47	4.55	
	NT2RM2000622	16.6	16.6	56.24	53.07	75.02	55.48	
	NT2RM2000623	2.66	2.66	7.1	7.92	6.03	5.58	
	NT2RM2000624	4.18	4.18	10.6	7.33	14.39	7.56	
25	NT2RM2000632	2.8	2.8	6.73	4.1	6.4	4.73	
	NT2RM2000635	3.42	3.42	8.09	5.41	6.29	5.31	
	NT2RM2000636	2.61	2.61	6.28	3.99	4.39	3.72	
	NT2RM2000639	3.73	3.73	8.26	5.42	7.79	5.99	
	NT2RM2000649	6.03	6.03	9.69	9.4	9.17	8.05	
30	NT2RM2000658	6.49	6.49	13.18	15.17	14.66	15.83	* +
	NT2RM2000660	11.45	11.45	18.34	17.03	7.1	20.16	
	NT2RM2000669	3.6	3.6	6.51	5.28	4.28	6.69	
	NT2RM2000689	31.07	31.07	59.7	37.03	16.51	70.9	
	NT2RM2000691	2.09	2.09	5.73	4.83	7.13	4.27	
35	NT2RM2000714	3.41	3.41	10.97	11.46	14.54	11.3	
	NT2RM2000718	4.08	4.08	7.15	2.88	5.42	4.33	
	NT2RM2000732	5.38	5.38	14.81	9.49	14.18	8.25	
	NT2RM2000735	3.72	3.72	6.16	4.27	6.55	6.49	
	NT2RM2000740	2.26	2.26	6.2	4.27	3.01	3.71	
40	NT2RM2000743	2.26	2.26	7.89	5.65	3.24	3.89	
	NT2RM2000772	6.43	6.43	8.48	5.24	6.72	9.47	
	NT2RM2000773	8.17	8.17	19.56	19.18	17.96	18.29	
	NT2RM2000776	13.96	13.96	17.16	24.24	9.95	26.76	
	NT2RM2000784	6.64	6.64	8.8	8.74	9.02	10.5	
45	NT2RM2000795	4.35	4.35	13.56	7.44	8.66	10.45	
	NT2RM2000796	2.27	2.27	4.64	1.71	2.31	1.38	
	NT2RM2000798	25.81	25.81	160.08	158.19	136.83	188.99	
	NT2RM2000801	45.09	45.09	161.29	160.44	152.13	189.56	
50	NT2RM2000821	7.53	7.53	12.33	7.37	7.77	11.87	
	NT2RM2000829	5.76	5.76	13.01	8.05	10.13	11.75	
	NT2RM2000837	3.29	3.29	7.28	4.27	6.08	4.18	
	NT2RM2000924	9.96	9.96	36.74	43.24	57.8	35.84	
	NT2RM2000930	10.64	10.64	18.29	24.45	27.78	28.34	** +
55	NT2RM2000937	4.35	4.35	8.62	5.08	6.66	6.56	
	NT2RM2000939	1.12	1.12	2.37	2.67	1.84	1.82	

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	NT2RM2000942	124.8	124.8	253.61	161.4	118.61	210.11		
	NT2RM2000951	1.01	1.01	2.6	2.13	3.12	1.6		
5	NT2RM2000952	2.53	2.53	5.31	5.98	6.41	6.86	*	+
	NT2RM2000966	19.69	19.69	111.88	95.61	137.32	135.9		
	NT2RM2000973	23.45	23.45	16.81	39.12	39.51	33.8	**	+
	NT2RM2000983	10.07	10.07	18.59	30.68	39.13	27.52	*	+
	NT2RM2000984	6.48	6.48	7.71	4.88	5.64	5.26	*	-
10	NT2RM2000994	8.27	8.27	16.47	13.2	8.36	21.81		
	NT2RM2001004	6.01	6.01	48.58	47.51	54.15	46.8		
	NT2RM2001022	101.09	101.09	350.92	239.63	304.37	490.04		
	NT2RM2001035	10.75	10.75	24.98	24.17	24.54	34.51		
	NT2RM2001038	5.77	5.77	9.86	10.48	11.75	7.9		
15	NT2RM2001043	4.45	4.45	10.02	5.1	7.41	6.74		
	NT2RM2001050	2.71	2.71	6.89	4.72	5.83	4.03		
	NT2RM2001055	3.78	3.78	5.89	4.24	6.31	4.7		
	NT2RM2001065	6.17	6.17	15.91	8.51	12.12	14.21		
	NT2RM2001075	39.81	39.81	188.21	154.65	156.72	168.68		
20	NT2RM2001083	2.23	2.23	5.57	4.01	5.8	3.01		
	NT2RM2001100	10.38	10.38	93.67	95.8	113.9	97.52		
	NT2RM2001105	6.34	6.34	8.27	11.35	5.34	11.8		
	NT2RM2001109	6.81	6.81	9.4	11.88	12.47	14.53	*	+
	NT2RM2001110	7.67	7.67	21.63	21.2	30.71	23.29		
25	NT2RM2001126	6.1	6.1	6.53	5.32	6.44	7.27		
	NT2RM2001131	5.52	5.52	40.22	21.93	29.37	20.14		
	NT2RM2001141	1.64	1.64	6.84	7.09	6.4	5.45		
	NT2RM2001152	1.63	1.63	3.27	4.42	5.77	3.02		
	NT2RM2001177	3.42	3.42	7.23	10.28	7.25	8.24		
30	NT2RM2001194	2.74	2.74	7.51	6.68	5.77	8.17		
	NT2RM2001195	3.7	3.7	8.8	6.37	7.13	6.89		
	NT2RM2001196	5.24	5.24	6.35	5.19	6.46	4.64		
	NT2RM2001201	14.45	14.45	25.36	20.02	21.68	22.38		
35	NT2RM2001221	4.22	4.22	8.61	11.69	13.61	16.63	*	+
	NT2RM2001238	2.87	2.87	5.65	3.91	3.88	1.96		
	NT2RM2001243	5.39	5.39	8.98	9.81	6.13	6.53		
	NT2RM2001244	3.91	3.91	10.63	6.58	9.24	6.41		
	NT2RM2001247	14.94	14.94	121.59	110.47	140.27	118.79		
40	NT2RM2001256	3.84	3.84	5.23	3.15	3.26	2.96		
	NT2RM2001269	4.4	4.4	5.98	4.8	5.63	4.74		
	NT2RM2001278	5.28	5.28	7.37	8.45	8.56	5.35		
	NT2RM2001291	3.05	3.05	5.18	3.24	4.62	2.9		
	NT2RM2001294	12.47	12.47	24.39	20.08	15.43	17.81		
45	NT2RM2001295	2.56	2.56	8.82	4.54	4.43	4.99		
	NT2RM2001302	2.38	2.38	4.55	2.3	4.5	2.81		
	NT2RM2001306	3.51	3.51	7.62	4.1	4.46	5.14		
	NT2RM2001312	2.34	2.34	3.72	1.92	2.84	1.68		
	NT2RM2001319	2.76	2.76	3.93	3.61	5.29	4.11		
50	NT2RM2001324	3.73	3.73	8.29	5.48	4.9	5.71		
	NT2RM2001345	8.53	8.53	10.01	6.83	11.12	14.14		
	NT2RM2001360	4.02	4.02	6.36	5.67	5.9	5.46		
	NT2RM2001370	5.75	5.75	14.53	8.56	9.86	11.69		
	NT2RM2001391	1.79	1.79	6.07	1.85	5.04	1.65		
55	NT2RM2001393	4.49	4.49	6.39	5.12	7.91	7.14		

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	NT2RM2001420	2.94	2.94	4.61	2.61	3.62	3.14		
	NT2RM2001423	5.44	5.44	9.53	8.64	11.95	11.36		
	NT2RM2001424	5.88	5.88	15.09	11.77	10.31	11.63		
5	NT2RM2001482	2.24	2.24	6.48	3.5	6.06	3.63		
	NT2RM2001499	1.4	1.4	5.81	2.84	4.3	2.17		
	NT2RM2001504	3.63	3.63	6.99	3.2	4.54	1.68		
	NT2RM2001524	2.51	2.51	5.81	2.34	2.22	3.51		
10	NT2RM2001530	2.56	2.56	4.42	2.68	4.35	3.52		
	NT2RM2001533	5.06	5.06	9.09	8.2	9.18	7.84		
	NT2RM2001540	5.77	5.77	8.36	14.57	17.99	27.1	*	+
	NT2RM2001544	2.4	2.4	6.12	3.7	3.72	2.31		
	NT2RM2001547	6.6	6.6	15.29	8.44	7.61	8.24		
15	NT2RM2001558	1.53	1.53	3.44	1.76	4.87	1.71		
	NT2RM2001575	2.45	2.45	4.57	3.36	4.38	2.29		
	NT2RM2001582	2.99	2.99	4.98	2.2	5.16	3.06		
	NT2RM2001588	3.69	3.69	8.8	6.39	9.14	6.6		
	NT2RM2001592	2.66	2.66	6.2	3.1	5.24	4.64		
20	NT2RM2001603	4.74	4.74	8.7	10.42	12.03	11.77	*	+
	NT2RM2001605	1.74	1.74	4.52	3.08	1.51	2.39		
	NT2RM2001611	2.28	2.28	8.63	3.74	3.34	3.51		
	NT2RM2001613	14.91	14.91	32.53	21.51	13.13	27.42		
	NT2RM2001626	2.45	2.45	3.08	2.1	4.28	2.06		
25	NT2RM2001632	4.93	4.93	7.07	4.67	4.88	5.42		
	NT2RM2001633	4.45	4.45	10.39	3.74	5.15	5.43		
	NT2RM2001635	4.33	4.33	9.54	4.3	5.81	4.7		
	NT2RM2001636	4.88	4.88	7.35	12.75	18.11	13.34	**	+
	NT2RM2001637	1.25	1.25	6.48	4.18	3.68	2.51		
30	NT2RM2001639	3.98	3.98	9.32	4.67	4.33	3.29		
	NT2RM2001641	1.63	1.63	4.69	4.84	6.02	2.71		
	NT2RM2001643	2.78	2.78	7.46	4.79	4.4	2.83		
	NT2RM2001648	12.97	12.97	18.91	20.13	17.07	25.5		
35	NT2RM2001652	6.32	6.32	5.65	4.29	8.13	4.46		
	NT2RM2001659	5.78	5.78	9.17	5.73	5.28	6.95		
	NT2RM2001660	3.44	3.44	3.86	2.08	2.29	2.63	**	-
	NT2RM2001664	1.24	1.24	6.12	4.51	4.89	4.8		
	NT2RM2001668	3.72	3.72	8.16	7.66	5.72	7.02		
40	NT2RM2001670	1.62	1.62	4.11	2.88	3.96	3.56		
	NT2RM2001671	2.67	2.67	5.57	3.9	6.46	4.85		
	NT2RM2001675	1.94	1.94	4.28	1.97	3.73	0.64		
	NT2RM2001681	2.47	2.47	5.91	3.13	4.64	3.39		
	NT2RM2001685	4.58	4.58	5.68	1.29	2.72	1.14	**	-
45	NT2RM2001688	5.46	5.46	4.14	3.11	3.82	2.46	*	-
	NT2RM2001695	15.09	15.09	35.18	17.41	19.26	34.51		
	NT2RM2001696	2.74	2.74	6.64	7.15	6.7	6.8		
	NT2RM2001698	1.44	1.44	3	4.06	3.49	1.65		
	NT2RM2001699	1.63	1.63	5.03	4.19	3.75	5.48		
50	NT2RM2001700	1.65	1.65	4.13	2.56	3.37	3.91		
	NT2RM2001704	2.68	2.68	5.46	3.89	3.85	3.99		
	NT2RM2001706	4.29	4.29	6.77	3.33	3.13	3.32		
	NT2RM2001714	6.48	6.48	6.64	5.62	7.33	5.18		
	NT2RM2001716	0.97	0.97	3.7	3.03	5.49	2.92		
55	NT2RM2001718	1.91	1.91	3.47	5	3.5	3		

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	NT2RM2001723	2.09	2.09	5.48	5.1	5.21	5.71		
	NT2RM2001727	3.08	3.08	6.25	7.51	7.28	5.7		
5	NT2RM2001730	3.52	3.52	7.15	5.04	5.43	3.85		
	NT2RM2001738	4.56	4.56	6.2	6.71	10.25	9.08	*	+
	NT2RM2001743	2.95	2.95	5.81	4.39	5.02	4.46		
	NT2RM2001753	5.98	5.98	7.55	5.72	6.09	4.54		
	NT2RM2001755	0.89	0.89	2.82	2.4	2.83	2.67		
10	NT2RM2001760	14.77	14.77	33.17	27.49	25.48	36.23		
	NT2RM2001765	1.35	1.35	1.71	2.45	3.12	2.03	*	+
	NT2RM2001767	12.04	12.04	120.66	148.84	168.4	146.29	*	+
	NT2RM2001768	2.1	2.1	3.59	3.41	4.21	3.05		
	NT2RM2001771	4.82	4.82	5.65	7.15	5.97	5.05		
15	NT2RM2001778	2.89	2.89	4.09	2.34	3.24	1.48		
	NT2RM2001782	5.32	5.32	7.32	4.96	7.71	7.57		
	NT2RM2001784	0.84	0.84	2.19	2.81	2.5	1.41		
	NT2RM2001785	1.35	1.35	4.11	5.5	5.02	2.76		
20	NT2RM2001792	6.03	6.03	8.53	5.49	5.54	5.76		
	NT2RM2001795	3.97	3.97	6.15	7.62	5.96	8.9		
	NT2RM2001797	2.82	2.82	3.78	5	5.94	2.71		
	NT2RM2001800	3.46	3.46	4.26	5.01	4.03	5.24		
	NT2RM2001803	3.5	3.5	6.61	4.46	7.34	2.44		
25	NT2RM2001805	3.65	3.65	3.21	2.53	4.2	1.71		
	NT2RM2001806	7.34	7.34	17.96	15.62	15.23	21.11		
	NT2RM2001813	1.54	1.54	2.05	2.54	1.88	2.32		
	NT2RM2001814	2.46	2.46	4.71	3.52	2.89	4.42		
	NT2RM2001818	1.21	1.21	2.66	0.97	1.48	0.27		
30	NT2RM2001823	1.4	1.4	3.24	1.87	2.46	1.37		
	NT2RM2001825	14.79	14.79	36.08	34.68	34.2	35.81		
	NT2RM2001832	5.93	5.93	6.1	5.19	5.48	2.93		
	NT2RM2001839	67.48	67.48	123.46	152.63	157.11	121.35		
	NT2RM2001840	3.04	3.04	7.13	4.61	5.11	5.37		
35	NT2RM2001851	3.92	3.92	7.61	3.78	4.74	6.49		
	NT2RM2001855	8.21	8.21	11.51	10.22	12.06	15.41		
	NT2RM2001867	2.82	2.82	5.01	2.83	5.62	3.74		
	NT2RM2001869	60.8	60.8	90.58	101.19	79.67	105.32		
	NT2RM2001879	3.01	3.01	6.99	2.55	3.19	2.66		
40	NT2RM2001883	1.52	1.52	3.26	0.98	2.28	0.73		
	NT2RM2001886	1.57	1.57	4.56	2.48	3.51	2.42		
	NT2RM2001887	3.78	3.78	7.66	4.48	4.97	5.73		
	NT2RM2001896	274.2	274.2	378.57	325.68	216.52	497.31		
	NT2RM2001902	1.92	1.92	4.28	1.31	2.92	2.14		
45	NT2RM2001903	16.25	16.25	42.55	35.47	31.71	37.22		
	NT2RM2001930	2.11	2.11	6.3	2.3	5.86	5.44		
	NT2RM2001935	4.16	4.16	5.04	3.16	4.42	5.87		
	NT2RM2001936	2.81	2.81	4.9	2.99	3.44	4		
	NT2RM2001939	3.56	3.56	3.34	1.82	3.01	3.16		
50	NT2RM2001941	1.84	1.84	4.29	2.84	2.82	2.72		
	NT2RM2001950	4.66	4.66	10	6.01	6	8.69		
	NT2RM2001952	2.67	2.67	4.78	2.49	4.55	5.37		
	NT2RM2001976	11.48	11.48	18.2	14.58	11.46	35.27		
	NT2RM2001982	1.85	1.85	3.91	2.04	2.47	1.88		
55	NT2RM2001983	4.45	4.45	8.36	4.18	6.49	7.54		

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	NT2RM2001984	7.74	7.74	8.88	20.06	27.05	22.95	**	+
	NT2RM2001989	2.72	2.72	3.68	2.99	4.26	3.7		
	NT2RM2001996	7.51	7.51	8.09	4.8	8.01	5.29		
5	NT2RM2001997	3.65	3.65	7.29	3.18	5.09	6.78		
	NT2RM2001998	2.24	2.24	5.07	3.33	6.53	3.96		
	NT2RM2001999	4.86	4.86	7.69	6.88	6.02	4.01		
	NT2RM2002003	11.33	11.33	18.17	10.15	11	14.9		
	NT2RM2002004	1.99	1.99	5.79	2.51	2.09	1.9		
10	NT2RM2002009	5.35	5.35	9.03	9.85	11.04	11.09	*	+
	NT2RM2002014	2.62	2.62	3	3.65	4.47	4.03	**	+
	NT2RM2002019	25.1	25.1	38.52	19.47	14.2	16.35		
	NT2RM2002029	12.92	12.92	19.01	10.82	4.88	14.74		
15	NT2RM2002030	4.15	4.15	5.8	13.54	9.71	21.98	*	+
	NT2RM2002034	22.05	22.05	31.76	24.83	20.89	21.04		
	NT2RM2002049	7.4	7.4	12.12	9.76	10.42	13.22		
	NT2RM2002055	2.8	2.8	8.01	1.91	4.03	2.52		
	NT2RM2002072	9.26	9.26	12.88	12.28	19.12	12.82		
20	NT2RM2002088	4.82	4.82	13.85	11.35	11.7	15.28		
	NT2RM2002091	4.98	4.98	8.44	5.92	3.82	4.61		
	NT2RM2002100	3.26	3.26	6.05	4.82	4.24	3.19		
	NT2RM2002109	1.31	1.31	3.57	2.57	4.88	4.92		
	NT2RM2002126	21.41	21.41	32.24	35.28	22.31	31.52		
25	NT2RM2002128	3.7	3.7	5.17	2.74	3.86	2.41		
	NT2RM2002129	6.43	6.43	11.48	8.53	13.03	10.66		
	NT2RM2002142	5.72	5.72	9.74	5.26	8.91	6.4		
	NT2RM2002144	3.27	3.27	3.76	1.85	1.73	1.62	**	-
	NT2RM2002145	2.63	2.63	8.69	6.1	5.18	5.98		
30	NT2RM2002153	2.61	2.61	6.37	6.31	7.62	5.75		
	NT2RM2002163	0.97	0.97	3.41	1.87	3.4	0.64		
	NT2RM2002170	3.28	3.28	7.03	6.62	7.5	7.65		
	NT2RM2002178	3.99	3.99	3.67	3.5	5.48	2.9		
	NT2RM2002179	7.82	7.82	8.69	6.17	8.15	6.02		
35	NT2RM2002270	4.51	4.51	4.56	2.28	1.76	1.67	**	-
	NT2RM2002326	2.47	2.47	3.86	2.13	3.69	2.34		
	NT2RM2002337	1.88	1.88	3.97	5.4	4.22	4.79	*	+
	NT2RM2002339	2.83	2.83	6.29	5.26	5.22	3.85		
	NT2RM2002345	5.16	5.16	6.03	4.04	4.2	4.21	*	-
40	NT2RM2002368	2.43	2.43	5.86	6.05	7.01	4.96		
	NT2RM2002381	2.23	2.23	5.16	3.47	3.65	2.8		
	NT2RM2002424	4.64	4.64	7.1	6.69	8.5	6.3		
	NT2RM2002450	4.17	4.17	3.87	2.29	2.39	1.87	**	-
45	NT2RM2002482	3.93	3.93	4.65	2.66	3.2	3.79		
	NT2RM2002492	9.39	9.39	24.31	29.13	24.65	29.29		
	NT2RM2002575	3.26	3.26	5.23	5.99	6.03	5.07		
	NT2RM2002580	4.23	4.23	4.68	4.82	7.79	7.42		
	NT2RM2002592	7.7	7.7	12.59	13.07	15.28	14.69	*	+
50	NT2RM2002608	27.33	27.33	45.49	57.07	65.96	48.3	*	+
	NT2RM2002615	6.01	6.01	9.38	13.15	20.32	14.42	*	+
	NT2RM2002622	14.35	14.35	16.22	18.38	24.99	13.44		
	NT2RM2002630	4.86	4.86	6.63	8.05	7.37	6.7		
	NT2RM2002634	1.72	1.72	4.66	4.71	4.6	3.94		
55	NT2RM2002645	27.02	27.02	68.46	30.66	14.59	31.46		

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	NT2RM2002646	12.09	12.09	25.03	29.45	22.88	34.8		
	NT2RM2002647	7.68	7.68	17.56	19.5	17.74	23.44		
5	NT2RM2002652	5.11	5.11	4.71	4.3	6.43	3.73		
	NT2RM2002692	4.59	4.59	4.48	2.5	2.86	2.02	**	-
	NT2RM2002721	30.26	30.26	46.01	62.71	84.18	61.02	*	+
	NT2RM2002748	18.37	18.37	43.62	87.35	119.27	102.35	**	+
	NT2RM2002764	2.28	2.28	5.3	5.05	5.95	4.07		
10	NT2RM2002772	3.15	3.15	9.32	9.66	7.81	5.44		
	NT2RM2002811	5.79	5.79	12.3	14.01	9.18	10.45		
	NT2RM2002818	2.03	2.03	7.94	5.86	5.42	7.13		
	NT2RM2002879	4.21	4.21	7.17	8.39	7.87	9.11	*	+
15	NT2RM2002979	11.79	11.79	19.66	24.49	23.23	21.79	*	+
	NT2RM2002981	4.42	4.42	3.78	3.58	4.95	2.63		
	NT2RM2002995	5.13	5.13	3.29	3.42	3.74	3.5		
	NT2RM2003031	1.37	1.37	2.63	3	2.58	1.9		
	NT2RM2003042	4.1	4.1	10.77	10.59	6.02	6.07		
20	NT2RM2003044	1.88	1.88	4.11	2.13	5.11	1.2		
	NT2RM2003090	4.4	4.4	7.64	9.36	7.91	10.68	*	+
	NT2RM2003095	11.98	11.98	25.25	15.63	16.43	19.04		
	NT2RM2003116	11.16	11.16	16.09	17.96	21.43	22.08	*	+
	NT2RM2003222	3.98	3.98	3.63	2.67	3.64	2.35		
25	NT2RM2003224	11.29	11.29	15.33	24.29	29.77	20.76	*	+
	NT2RM2003250	14.18	14.18	86.06	85.79	96.6	94.15		
	NT2RM2003258	4.59	4.59	6.32	6.54	5.11	5.69		
	NT2RM2003262	5.07	5.07	7.33	5.06	7.76	5.72		
	NT2RM4000023	2.15	2.15	7.02	3.57	4.91	4.29		
30	NT2RM4000024	2.28	2.28	6.78	3.17	4.98	4.33		
	NT2RM4000027	4.74	4.74	7.77	4.85	6.94	11.32		
	NT2RM4000030	2.95	2.95	5.73	3.16	4.9	2.64		
	NT2RM4000033	2.51	2.51	4.77	2.36	3.89	4.61		
	NT2RM4000034	1.93	1.93	5.35	3.74	4.84	6.09		
35	NT2RM4000046	1.37	1.37	3.79	1.57	3.5	2.32		
	NT2RM4000052	1.82	1.82	3.55	1.72	2.96	1.98		
	NT2RM4000054	10.43	10.43	13.85	12.07	12.83	24.7		
	NT2RM4000061	1.65	1.65	4.17	1.66	4.54	0.83		
	NT2RM4000074	15.83	15.83	43.57	27.9	34.24	30.79		
40	NT2RM4000085	5.35	5.35	10.1	8.41	10.19	10.17		
	NT2RM4000086	3.06	3.06	4.5	3.84	5.25	3.71		
	NT2RM4000100	6.62	6.62	15.05	12.74	15.6	14.84		
	NT2RM4000101	3.77	3.77	9.11	7.17	7.71	8.78		
	NT2RM4000102	32.35	32.35	42.47	27.24	19.34	70.54		
45	NT2RM4000104	2.78	2.78	7.13	3.41	5.12	4.3		
	NT2RM4000115	2.87	2.87	6.1	3.91	5.86	4.08		
	NT2RM4000129	2.17	2.17	4.75	2.62	3.48	2.18		
	NT2RM4000139	3.17	3.17	3.31	3.58	4.82	6.49		
	NT2RM4000149	2.74	2.74	1.49	2.41	2.55	7.32		
50	NT2RM4000155	2.73	2.73	5.5	2.13	4.51	3.71		
	NT2RM4000156	5.94	5.94	16.74	20.45	21	21.96	*	+
	NT2RM4000167	1.36	1.36	2.58	2.61	4.34	1.75		
	NT2RM4000169	9.95	9.95	36.53	29.12	24.89	23.57		
	NT2RM4000191	4.29	4.29	7.56	5.49	5.57	5.66		
55	NT2RM4000197	2.73	2.73	4.78	1.83	3.86	2.2		

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	NT2RM4000198	3.38	3.38	7.42	5.26	5.45	4.21		
	NT2RM4000199	2	2	3.51	2.8	4	3.76		
5	NT2RM4000200	0.67	0.67	3.19	2.25	1.84	1.2		
	NT2RM4000202	1	1	3.24	2.11	2.42	1.84		
	NT2RM4000210	1.46	1.46	3.72	2.41	3.08	2.21		
	NT2RM4000215	2.54	2.54	5.43	3.3	4.09	3.06		
	NT2RM4000220	6.42	6.42	10.52	8.68	11.08	15.14		
10	NT2RM4000229	3.26	3.26	6.62	1.46	2.34	1.76		
	NT2RM4000231	6.37	6.37	7.06	6.13	7.85	6.24		
	NT2RM4000233	4.83	4.83	17.3	11.9	14.34	13.4		
	NT2RM4000244	2.35	2.35	5.22	3.86	4.14	5.17		
	NT2RM4000251	3.85	3.85	10.97	4.82	6.52	4.59		
15	NT2RM4000255	2.28	2.28	4.7	3.79	4.89	1.42		
	NT2RM4000265	2.23	2.23	5.69	4.29	8.21	1.99		
	NT2RM4000283	18.14	18.14	26.21	37.17	39.88	44.79	**	+
	NT2RM4000284	13.85	13.85	33.72	31.96	42.88	40.67		
	NT2RM4000290	6.31	6.31	7.76	3.77	4.92	4	*	-
20	NT2RM4000295	2.36	2.36	2.16	2.32	2.13	0.88		
	NT2RM4000306	3.79	3.79	7.76	7.1	6.14	5.02		
	NT2RM4000307	5.04	5.04	9.13	9.95	9.99	11.72	*	+
	NT2RM4000309	2.48	2.48	5.34	3.92	6.52	5.52		
	NT2RM4000313	3.92	3.92	9.61	5.75	7.77	8.52		
25	NT2RM4000318	3.38	3.38	6.87	4.35	6.36	3.28		
	NT2RM4000324	4.93	4.93	5.93	2.79	4.98	2.12		
	NT2RM4000326	5.32	5.32	4.61	2.59	2.45	2.01	**	-
	NT2RM4000327	4.97	4.97	10.95	7.94	10.32	7.71		
	NT2RM4000344	5.46	5.46	16.67	11.16	10.17	19.18		
30	NT2RM4000349	3.68	3.68	9.99	11.87	10.88	13.8	*	+
	NT2RM4000354	1.65	1.65	3.13	4.2	4.31	3.1		
	NT2RM4000356	1.5	1.5	3.11	2.5	4.07	1.64		
	NT2RM4000366	15.75	15.75	44.48	38.81	44.07	58.06		
	NT2RM4000368	3.04	3.04	5.9	4.36	5.48	3.48		
35	NT2RM4000373	6.49	6.49	12.29	12.72	15.96	16.47	*	+
	NT2RM4000386	4.92	4.92	4.71	3.81	4.57	4.6		
	NT2RM4000395	2.7	2.7	4.69	6.36	6.51	5.68	*	+
	NT2RM4000414	1	1	2.76	2.38	2.9	2.19		
	NT2RM4000417	1.66	1.66	2.83	3.9	3.95	3.25	*	+
40	NT2RM4000421	2.99	2.99	5.17	4.96	5.47	4.13		
	NT2RM4000425	10.56	10.56	26.8	26.49	31.48	45.28		
	NT2RM4000433	2.78	2.78	5.39	1.67	2.21	1.79		
	NT2RM4000436	3.8	3.8	9.47	11.84	16.75	16.38	*	+
45	NT2RM4000444	4.51	4.51	12.97	7.29	8.54	7.38		
	NT2RM4000457	3.35	3.35	8.69	13.35	12.38	13.25	*	+
	NT2RM4000471	1.73	1.73	4.01	4.17	4.87	2.49		
	NT2RM4000472	2.2	2.2	7.62	6.64	7.61	5.39		
	NT2RM4000486	2.98	2.98	5.92	6.85	7.54	6		
50	NT2RM4000490	3.85	3.85	6.41	7.16	5.1	5.86		
	NT2RM4000496	3.68	3.68	3.86	2.16	2.36	2.04	**	-
	NT2RM4000505	26.85	26.85	60.33	68.9	80.59	70.67	*	+
	NT2RM4000511	22.8	22.8	45.35	64.6	89.95	75.97	*	+
	NT2RM4000514	2.61	2.61	6.75	10.47	7.53	9.25	*	+
55	NT2RM4000515	3.75	3.75	8.81	7.27	7.94	4.66		

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	NT2RM4000517	34.51	34.51	74.2	76.45	53.07	79.47	
	NT2RM4000520	2.24	2.24	3.08	3.21	3.3	5.49	
	NT2RM4000531	2.76	2.76	5.71	4.41	5.5	4.22	
5	NT2RM4000532	3.03	3.03	5.56	2.72	3.54	2.39	
	NT2RM4000533	3.55	3.55	5.43	4.73	6.98	3.23	
	NT2RM4000534	5.17	5.17	2.92	2.73	4.62	1.94	
	NT2RM4000563	5.21	5.21	16.69	17.05	16.8	19.36	
	NT2RM4000566	1.79	1.79	4.6	7.14	5.27	7.91	*
10	NT2RM4000568	10.48	10.48	19.4	28.18	22.91	33.06	* +
	NT2RM4000585	1.97	1.97	2.52	0.82	1.99	1.26	
	NT2RM4000587	3.88	3.88	6.15	6.66	5.75	5.15	
	NT2RM4000590	3.73	3.73	4.12	1.64	2.48	2.3	** -
	NT2RM4000593	4.46	4.46	7.83	10.21	12.36	7.45	
15	NT2RM4000595	3.94	3.94	3.91	2.27	4.36	2.45	
	NT2RM4000603	4.18	4.18	6.98	6.95	7.23	7.26	
	NT2RM4000611	9.81	9.81	18.02	17.1	17.38	25.49	
	NT2RM4000616	2.05	2.05	6.19	2.73	4.14	4.53	
20	NT2RM4000621	26.04	26.04	70.86	57.5	62.2	59.07	
	NT2RM4000648	2.78	2.78	7.83	2.66	2.67	3.88	
	NT2RM4000649	5.53	5.53	11.03	7.34	8.4	13.12	
	NT2RM4000658	3.22	3.22	8.18	4.22	6.14	8.14	
	NT2RM4000661	57.68	57.68	140.68	141.09	135.49	177.49	
25	NT2RM4000673	3.02	3.02	5.72	3.69	3.8	4.59	
	NT2RM4000674	2.23	2.23	4.27	2.89	2.63	2.99	
	NT2RM4000689	3.81	3.81	6.47	5.34	6.36	7.74	
	NT2RM4000698	14.85	14.85	20.92	25.12	23.66	26.39	* +
	NT2RM4000700	2.39	2.39	5.53	2.41	6.95	5.61	
30	NT2RM4000701	10.07	10.07	54.36	61.81	67.75	63.17	
	NT2RM4000712	3.5	3.5	7.9	5.97	8.03	9.55	
	NT2RM4000717	2.14	2.14	6.66	3.67	2.94	4.3	
	NT2RM4000733	4.37	4.37	7.8	4.16	6.93	11.03	
	NT2RM4000734	2.17	2.17	5.92	2.35	5.23	4.7	
35	NT2RM4000741	2.14	2.14	6.11	3.59	4.75	4.66	
	NT2RM4000744	1.76	1.76	7.05	2.76	4.4	10.18	
	NT2RM4000749	15.53	15.53	23.13	26.26	27.8	34.67	* +
	NT2RM4000751	2.88	2.88	6.54	6.23	6.11	5.94	
	NT2RM4000752	4.11	4.11	4.88	4.78	5.12	38.58	
40	NT2RM4000760	3.5	3.5	9.69	4.54	6.31	5.26	
	NT2RM4000761	237.9	237.9	478.3	219.65	302.54	336.34	
	NT2RM4000764	66.05	66.05	178	212.33	205.98	232.75	* +
	NT2RM4000768	6.11	6.11	11.21	15.56	10.14	21.17	
45	NT2RM4000778	1.6	1.6	4.7	4.27	5.18	6.18	
	NT2RM4000779	4.52	4.52	8.28	6.87	7.19	7.33	
	NT2RM4000787	2.55	2.55	7.49	3.64	4.9	4.53	
	NT2RM4000790	2.99	2.99	5.03	5.47	5.82	12.06	
	NT2RM4000795	1.99	1.99	3.67	2.36	1.2	2.51	
50	NT2RM4000796	3.26	3.26	5.86	4.29	3.48	4.28	
	NT2RM4000798	1.77	1.77	5.53	3.72	3.08	3.47	
	NT2RM4000800	4.15	4.15	8.16	8.7	9.44	9.06	
	NT2RM4000813	3.31	3.31	8.79	7.14	7.95	10.09	
	NT2RM4000820	4.89	4.89	9.14	5.39	6.27	5.44	
55	NT2RM4000827	7.1	7.1	18.55	16.3	15.8	17.88	

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	NT2RM4000830	3.27	3.27	7.35	5.28	7.8	8.38	
	NT2RM4000833	2.51	2.51	6.84	4.48	3.35	4.87	
	NT2RM4000841	4	4	15	10.57	8.84	10.1	
5	NT2RM4000846	1.66	1.66	8.83	4.74	6.83	5.09	
	NT2RM4000848	2.61	2.61	5.75	4.15	6.32	3.12	
	NT2RM4000852	3.89	3.89	9.81	8.16	8.67	8.29	
	NT2RM4000855	5.12	5.12	7.64	5.99	6.08	7.19	
10	NT2RM4000859	11.18	11.18	16.28	16.48	19.12	17.62	
	NT2RM4000868	3.06	3.06	6.47	5.23	6.91	7.05	
	NT2RM4000870	4	4	9.82	7.06	3.87	6.59	
	NT2RM4000879	1.67	1.67	6	4.15	3.31	3.11	
	NT2RM4000882	18.99	18.99	28.36	20.33	16.5	12.55	
15	NT2RM4000887	2.16	2.16	6.01	3.53	4.91	1.6	
	NT2RM4000895	2.33	2.33	5.33	3.16	5.9	3.08	
	NT2RM4000897	5.78	5.78	6.99	8.89	9.73	7.02	
	NT2RM4000901	5.22	5.22	6.41	4.37	6.2	6.12	
	NT2RM4000950	4.04	4.04	5.09	3.57	4.06	2.91	
20	NT2RM4000965	2.89	2.89	4.54	5.98	4.04	6.18	
	NT2RM4000971	2.49	2.49	4.78	4.84	4.29	7.62	
	NT2RM4000979	5.16	5.16	12.71	10.23	10.46	7.87	
	NT2RM4000987	1.9	1.9	4.59	3.64	4.22	3.21	
	NT2RM4000989	2.51	2.51	5.17	4.2	5.16	4.99	
25	NT2RM4000991	3.1	3.1	4.83	2.87	3.53	8.73	
	NT2RM4000992	3.39	3.39	5.41	3.6	4.54	3.19	
	NT2RM4000996	6.22	6.22	7.86	7.14	8	7.28	
	NT2RM4000997	3.53	3.53	13.96	9.81	10.96	10.89	
	NT2RM4001001	26.06	26.06	55.43	37.67	34.22	54.29	
30	NT2RM4001002	5.13	5.13	11.03	11.54	11.33	19.44	
	NT2RM4001016	1.63	1.63	2.73	4.07	5.31	3.76	*
	NT2RM4001025	65.77	65.77	133.97	148.39	181.87	171.5	* +
	NT2RM4001027	2.49	2.49	3.66	1.67	1.77	4.31	
	NT2RM4001032	2.55	2.55	6.74	4.94	5.46	3.84	
35	NT2RM4001047	3.87	3.87	3.7	2.61	2.73	2.7	** -
	NT2RM4001049	3.97	3.97	10.12	18.29	20.63	26.25	** +
	NT2RM4001051	2.72	2.72	12.54	11.17	10.12	13.68	
	NT2RM4001052	14.95	14.95	72.14	75.49	75.01	79.12	
	NT2RM4001053	14.96	14.96	39.3	41.36	28.95	25.87	
40	NT2RM4001054	3.13	3.13	5.17	5.34	5.69	5.01	
	NT2RM4001059	3.65	3.65	6.37	4.91	3.52	4.48	
	NT2RM4001071	4.03	4.03	7.35	6.8	7.34	6.55	
	NT2RM4001084	8.04	8.04	6.52	9.49	10.53	9.53	* +
45	NT2RM4001092	12.61	12.61	109.97	76.93	98.78	73.14	
	NT2RM4001100	6.72	6.72	20.93	22.35	15.18	18.98	
	NT2RM4001116	1.17	1.17	2.5	2.77	2.96	2.16	
	NT2RM4001119	1.74	1.74	4.82	4.72	4.22	4.15	
	NT2RM4001140	2.65	2.65	7.49	8.27	7.78	9.03	
50	NT2RM4001148	6.59	6.59	13.68	12.1	12.92	15.83	
	NT2RM4001151	3.7	3.7	4.31	1.94	3.65	1.68	
	NT2RM4001155	5.51	5.51	6.36	3.55	5.37	4.63	
	NT2RM4001157	1.68	1.68	4.95	4.86	2.81	3.82	
	NT2RM4001160	1.57	1.57	3.39	2.99	1.9	2.41	
55	NT2RM4001163	42.35	42.35	86.27	106.63	52.13	98.56	

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	NT2RM4001187	2.64	2.64	7.25	3.96	4.87	5.2
	NT2RM4001191	3.2	3.2	9.95	8.59	6.36	8.72
5	NT2RM4001200	3.83	3.83	6.35	5.52	4.41	4.11
	NT2RM4001203	9.93	9.93	20.29	22.65	25.36	21.82
	NT2RM4001204	3.23	3.23	3.59	3.17	2.83	2.6
	NT2RM4001217	4.62	4.62	12.16	11.26	13.39	13.72
	NT2RM4001245	7.31	7.31	17.14	13.76	14.49	17.16
10	NT2RM4001247	3.23	3.23	9.1	5.73	6.57	5.03
	NT2RM4001256	2.51	2.51	6.39	3.57	5.48	4.14
	NT2RM4001258	8.2	8.2	24.68	25.02	24.16	22.89
	NT2RM4001267	3.43	3.43	4.83	3.93	4.3	8.08
	NT2RM4001273	4.23	4.23	8.38	7.39	6.96	8.77
15	NT2RM4001281	4	4	10.54	10.15	9.05	10
	NT2RM4001286	345.27	345.27	526.77	215.2	220.51	552.53
	NT2RM4001290	23.51	23.51	61.5	56.51	48.6	59.58
	NT2RM4001309	2.64	2.64	6.81	3.17	5.42	4.05
	NT2RM4001313	2.63	2.63	8.62	3.81	6.36	7.03
20	NT2RM4001316	3.14	3.14	6.12	3.39	3.85	5.25
	NT2RM4001320	2.4	2.4	6.43	2.83	3.16	5.6
	NT2RM4001321	3.98	3.98	8.62	6.17	7.03	6.24
	NT2RM4001325	2.54	2.54	5.2	4.76	2.93	5.25
	NT2RM4001333	8.65	8.65	18.06	8.57	10.76	9.51
25	NT2RM4001340	4.81	4.81	12.27	6.99	7.72	11.24
	NT2RM4001344	4.09	4.09	4.69	3.04	3.44	4.93
	NT2RM4001347	6.49	6.49	9.8	10.53	9.72	17.71
	NT2RM4001357	7.59	7.59	12.09	8.58	11.68	9.37
	NT2RM4001360	2.79	2.79	5.11	3.82	2.85	3.07
30	NT2RM4001371	4.71	4.71	8.57	6.58	13.16	12.93
	NT2RM4001377	8.01	8.01	13.74	8.66	9.23	10.58
	NT2RM4001382	17.31	17.31	56.74	35.57	28.32	38.22
	NT2RM4001384	2.17	2.17	4.11	2.35	3.34	3.75
	NT2RM4001400	3.78	3.78	5.76	4.87	4.66	5.07
35	NT2RM4001409	2.55	2.55	6.82	4.82	4.63	5.27
	NT2RM4001410	5.48	5.48	21.69	17.34	21.09	18.91
	NT2RM4001411	2.66	2.66	6.5	5.86	6.64	6.77
	NT2RM4001412	1.75	1.75	3.33	2.39	2.52	2.79
	NT2RM4001414	2.18	2.18	4.83	2.45	2.4	3.77
40	NT2RM4001436	8.35	8.35	16.65	10.45	10.13	15.55
	NT2RM4001437	2.77	2.77	8.85	8.31	11.26	7.67
	NT2RM4001444	11.57	11.57	25.93	21.1	18.36	18.42
	NT2RM4001454	3.62	3.62	7.89	6.16	5.03	4.79
	NT2RM4001455	5.85	5.85	22.19	18.03	25.08	26.16
45	NT2RM4001483	4.37	4.37	8.77	4.97	5.43	6.46
	NT2RM4001489	3.12	3.12	7.04	3.64	4.19	5.46
	NT2RM4001495	1.35	1.35	5.13	2.85	3.29	3.37
	NT2RM4001499	1.74	1.74	4.98	3.65	2.77	3.3
	NT2RM4001515	0.95	0.95	3.38	2.65	5.38	3.41
50	NT2RM4001519	1.86	1.86	4.6	2.24	4.38	2.85
	NT2RM4001522	3.8	3.8	7.66	5.36	7.42	9.13
	NT2RM4001523	5.46	5.46	9.11	4.82	7.58	5.79
	NT2RM4001550	11.9	11.9	17.38	16.49	16.76	15.01
55	NT2RM4001553	7.88	7.88	13.4	23.26	23.53	23.87 ** +

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	NT2RM4001554	0.86	0.86	1.74	1.85	1.11	2.2		
	NT2RM4001557	2.5	2.5	6.33	5.05	3.36	4.89		
	NT2RM4001565	1.87	1.87	4.05	2.46	3.34	3.23		
5	NT2RM4001566	3.23	3.23	8.57	8.91	10.49	11.42		
	NT2RM4001569	1.47	1.47	5.4	3.35	4.15	1.56		
	NT2RM4001579	6.57	6.57	16.69	19.23	23.83	18.22		
	NT2RM4001582	4.06	4.06	5.97	2.16	3.17	2.67	*	-
10	NT2RM4001589	21.51	21.51	37.16	42.45	55.76	47.57	*	+
	NT2RM4001592	1.37	1.37	2.96	3.02	2.14	3.71		
	NT2RM4001594	1.98	1.98	4.09	5.4	5.24	5.67	*	+
	NT2RM4001597	2.65	2.65	5.64	5.17	4.97	4.33		
	NT2RM4001605	2.7	2.7	6.18	5.71	5.92	5.93		
15	NT2RM4001609	23.65	23.65	45	61.08	78.89	77.31	*	+
	NT2RM4001610	48.1	48.1	69.16	132.54	132.39	115.22	**	+
	NT2RM4001611	3.31	3.31	4.56	2.33	2.32	2.02	*	-
	NT2RM4001618	7.05	7.05	7.95	6.68	8.98	12.95		
	NT2RM4001622	13.53	13.53	19.88	14.67	24.67	28.46		
20	NT2RM4001624	1.6	1.6	3.02	3.92	2.66	4.43		
	NT2RM4001625	4.89	4.89	39.6	41.63	47.1	46.46		
	NT2RM4001629	3.82	3.82	8.82	12.09	12.08	13.38	*	+
	NT2RM4001632	15.28	15.28	24.55	31.07	26.16	25.6		
	NT2RM4001642	3.29	3.29	4.17	2.89	3.62	2.1		
25	NT2RM4001647	4.44	4.44	6.83	4.04	5.48	4.67		
	NT2RM4001650	4.96	4.96	4.94	2.66	2.87	3.79	**	-
	NT2RM4001662	2.18	2.18	5.47	8.31	6.54	9.39	*	+
	NT2RM4001666	2.28	2.28	6.5	6.24	6.17	8.14		
30	NT2RM4001670	3.52	3.52	10.77	11.16	10.82	14.91		
	NT2RM4001682	12.66	12.66	31.6	33.03	26.04	37.07		
	NT2RM4001710	6.7	6.7	38.5	40.58	58.41	40.31		
	NT2RM4001712	4.06	4.06	7.61	10.19	10.7	9.98	*	+
	NT2RM4001714	10.88	10.88	19.37	18.67	19.3	17.65		
35	NT2RM4001715	10.77	10.77	11.6	13.55	16.86	12.99		
	NT2RM4001727	3.41	3.41	5.92	4.83	5.89	7.6		
	NT2RM4001731	2.6	2.6	10.72	13.46	11.23	11.73		
	NT2RM4001735	12.84	12.84	21.53	22.01	20.88	34.93		
	NT2RM4001739	2.46	2.46	7.3	8.13	5.17	7.14		
40	NT2RM4001741	14.41	14.41	29.88	26.98	27.21	32.35		
	NT2RM4001746	3.65	3.65	6.76	6.89	6.5	5.33		
	NT2RM4001754	3.16	3.16	4.17	3.39	3.62	3.84		
	NT2RM4001757	5.02	5.02	5.78	4.7	6.31	7.97		
	NT2RM4001758	1	1	0.76	1.98	0.65	1.46		
45	NT2RM4001768	4.83	4.83	10.19	8.48	6.91	7.83		
	NT2RM4001775	3.23	3.23	2.76	1.9	1.85	1.71	**	-
	NT2RM4001776	2.56	2.56	4.77	2.47	2.68	2.69		
	NT2RM4001783	2.88	2.88	3.22	3.12	3.48	3.68		
	NT2RM4001793	4.67	4.67	11.44	12.02	9.6	10.75		
50	NT2RM4001810	3.31	3.31	4.46	3.33	3.63	3.11		
	NT2RM4001813	3.9	3.9	4.15	4.71	4.19	5.36		
	NT2RM4001818	4.06	4.06	11.34	10.43	8.67	10.53		
	NT2RM4001819	2.35	2.35	5.6	2.37	3.02	4.58		
	NT2RM4001823	1.76	1.76	4.48	2.47	4.04	4.27		
55	NT2RM4001828	5.01	5.01	11.49	5.67	7.54	7.51		

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	NT2RM4001835	9.75	9.75	18.65	21.12	16.5	26.55		
	NT2RM4001836	3.27	3.27	8.32	3.65	3.54	5.58		
5	NT2RM4001841	7.94	7.94	15.82	20.15	20.96	23.33	*	+
	NT2RM4001842	2.1	2.1	4.44	3.5	3.35	4.85		
	NT2RM4001843	5.65	5.65	14.54	13.34	12.25	14.94		
	NT2RM4001856	4.42	4.42	7.16	7.65	4.71	16.83		
	NT2RM4001858	5.91	5.91	15.86	16.09	17.03	16.93		
10	NT2RM4001861	2.91	2.91	9.57	6.31	8.66	9.28		
	NT2RM4001863	8.06	8.06	9.5	15.16	15.68	11.77	*	+
	NT2RM4001865	5.04	5.04	11.25	7.44	10.24	9.03		
	NT2RM4001869	5.1	5.1	5.96	5.22	8.45	21.88		
	NT2RM4001873	9.62	9.62	18.43	13.33	15.49	19.21		
15	NT2RM4001876	2.24	2.24	6.94	3.65	4.39	7.25		
	NT2RM4001880	3.6	3.6	8.57	5.13	5.41	7.67		
	NT2RM4001885	5.71	5.71	11.11	7.11	6.56	11.98		
	NT2RM4001889	10.25	10.25	18.24	16.31	15.85	21.33		
	NT2RM4001894	2.61	2.61	6.07	3.58	3.65	3.49		
20	NT2RM4001897	7.87	7.87	20.24	18.41	20.4	23.46		
	NT2RM4001899	3.36	3.36	7.43	4.92	8.19	8.54		
	NT2RM4001905	3	3	4.84	3.3	4.53	7.1		
	NT2RM4001922	2.55	2.55	6.05	3.97	4.84	5.11		
25	NT2RM4001930	2.64	2.64	8.9	2.88	6.53	6.38		
	NT2RM4001938	2.65	2.65	4.91	5.09	5.65	6.43		
	NT2RM4001940	2.73	2.73	6.17	5.91	4.46	5.48		
	NT2RM4001942	37.36	37.36	32.02	53.86	59.28	82.77	*	+
	NT2RM4001953	4.65	4.65	9.68	5.04	6.79	4.91		
	NT2RM4001965	4.96	4.96	8.82	10.18	8.54	8.39		
30	NT2RM4001966	3	3	5.14	6.3	7.45	8.19	*	+
	NT2RM4001969	2.22	2.22	7.29	5.01	2.95	4.5		
	NT2RM4001974	1.19	1.19	4.61	1.89	2.96	4.83		
	NT2RM4001979	2.09	2.09	6.37	3.39	4.65	7.36		
35	NT2RM4001980	4.3	4.3	7.59	7.58	8.02	9.33		
	NT2RM4001984	2.31	2.31	5.36	2.68	3.49	4.57		
	NT2RM4001987	3.36	3.36	9.66	2.92	4.6	5.01		
	NT2RM4002013	6.62	6.62	15.13	13.47	17.16	19.8		
	NT2RM4002018	2.31	2.31	5.15	4.09	5.53	7.1		
40	NT2RM4002033	3.19	3.19	8.16	4.91	3.27	5.93		
	NT2RM4002034	1.89	1.89	6.19	4.82	4.38	4.03		
	NT2RM4002044	7.71	7.71	17.9	18.75	12.3	18.5		
	NT2RM4002047	3.88	3.88	5.19	2.68	5.38	9.2		
	NT2RM4002054	4.54	4.54	6.97	2.56	4.3	3.89		
45	NT2RM4002055	13.72	13.72	74.75	60.51	91.27	61.53		
	NT2RM4002059	23.73	23.73	31.85	48.05	63.09	52.61	**	+
	NT2RM4002061	3.72	3.72	5.32	3.59	3.69	4.81		
	NT2RM4002062	1.9	1.9	5.41	3.66	2.84	4.26		
	NT2RM4002063	2.21	2.21	8.1	7.64	7.35	3.79		
50	NT2RM4002066	2.07	2.07	5.29	4.42	6.32	4.07		
	NT2RM4002067	2.51	2.51	4.27	3.07	5.19	4.41		
	NT2RM4002073	3.73	3.73	7.24	5.51	7.69	5.16		
	NT2RM4002074	5.19	5.19	7.35	5.67	7.47	4.49		
	NT2RM4002075	5.13	5.13	5.9	3.16	3.18	2.91	**	-
55	NT2RM4002076	3.13	3.13	3.05	1.94	2.52	1.71	*	-

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	NT2RM4002078	10.3	10.3	28.06	23.95	20.81	26.64		
	NT2RM4002081	10.47	10.47	30.87	19.18	17.8	18.22		
	NT2RM4002082	1.25	1.25	3.02	3.85	2.58	1.23		
5	NT2RM4002093	2.82	2.82	3.9	4.79	4.66	4.79	*	+
	NT2RM4002109	4.42	4.42	11.51	13.95	15.12	15.21	*	+
	NT2RM4002115	2.86	2.86	4.51	4.81	4.8	2.52		
	NT2RM4002118	4.48	4.48	6.14	4.3	4.86	4.27		
10	NT2RM4002128	3.78	3.78	4.57	2.84	3.31	3.13	*	-
	NT2RM4002137	3.96	3.96	8.14	10.27	7.51	8.92		
	NT2RM4002139	3.78	3.78	8.98	7.03	7.84	7.87		
	NT2RM4002140	4.04	4.04	9.45	8.87	7.81	10.17		
	NT2RM4002145	5.99	5.99	17.51	25.81	31.07	24.47	*	+
15	NT2RM4002146	4.51	4.51	8.23	8.56	9	8.92		
	NT2RM4002161	2.33	2.33	4.97	1.38	3.15	5.3		
	NT2RM4002174	4.86	4.86	8.02	3.12	4.53	6.15		
	NT2RM4002178	7.3	7.3	24.43	28.61	33.13	29.27	*	+
	NT2RM4002180	3.47	3.47	11.93	9.27	10.02	11.28		
20	NT2RM4002185	5.94	5.94	35.51	31.59	32.34	31.69		
	NT2RM4002189	1.6	1.6	3.24	3.68	5.59	4.91	*	+
	NT2RM4002194	9.3	9.3	25.94	37.2	29.64	38.23	*	+
	NT2RM4002198	6.09	6.09	7.61	9.37	8.4	10.04	*	+
	NT2RM4002205	4.01	4.01	9.05	6.76	7.86	8.76		
25	NT2RM4002213	5.36	5.36	8.79	8.05	11.99	14.41		
	NT2RM4002216	7.35	7.35	12.58	16.58	23.93	18.16	*	+
	NT2RM4002226	3.84	3.84	9.71	20.85	16.65	16.5	**	+
	NT2RM4002237	4.19	4.19	10.13	10.37	7.64	13.22		
	NT2RM4002240	1.96	1.96	3.64	3.73	3.71	7.59		
30	NT2RM4002251	2.11	2.11	6.2	7.87	5.48	5.17		
	NT2RM4002256	4.38	4.38	10.68	10.7	9.46	9.64		
	NT2RM4002262	2.85	2.85	6.25	3.34	4.43	9.66		
	NT2RM4002266	3.93	3.93	4.76	2.76	3.55	4.47		
	NT2RM4002276	11.23	11.23	15.55	16.5	28.25	20.64		
35	NT2RM4002278	1.89	1.89	4.59	4.33	3.99	5.11		
	NT2RM4002281	17.71	17.71	59.08	62.68	51.19	59.89		
	NT2RM4002287	2.08	2.08	3.84	2.46	4.21	3.32		
	NT2RM4002294	3.19	3.19	6.99	6.28	6.09	8.69		
	NT2RM4002298	18.59	18.59	60.14	86.09	89.9	88.75	*	+
40	NT2RM4002301	3.2	3.2	6.85	4.63	5.94	4.02		
	NT2RM4002306	4.71	4.71	8.24	4.99	5.31	4.2		
	NT2RM4002323	3.9	3.9	4.06	4.11	4.39	3.11		
	NT2RM4002334	11.54	11.54	20.76	17.92	20.72	16.95		
45	NT2RM4002339	1.78	1.78	3.52	1.33	1.3	1.38		
	NT2RM4002344	2.36	2.36	5.74	2.87	3.57	7.92		
	NT2RM4002345	3.56	3.56	10.59	5.06	4.63	7.5		
	NT2RM4002352	2.04	2.04	7.67	3.99	5.14	3.74		
	NT2RM4002362	20.38	20.38	24.92	11.23	14.32	15.17	*	-
50	NT2RM4002373	2.1	2.1	3.96	3.21	2.55	3.63		
	NT2RM4002374	2.28	2.28	4.39	2.29	3.58	4.3		
	NT2RM4002376	4.02	4.02	6.03	3.31	2.97	5.52		
	NT2RM4002383	2.8	2.8	8.49	4.76	5.79	4.28		
	NT2RM4002390	3.03	3.03	6.01	4.06	5.27	7.37		
55	NT2RM4002398	5.16	5.16	43.18	33.97	50.73	30.41		

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	NT2RM4002409	2.11	2.11	5.93	3.37	4.29	1.9	
	NT2RM4002414	4.73	4.73	6.21	7.37	9.12	14.53	
5	NT2RM4002438	2.07	2.07	5.28	3.03	4.38	7.18	
	NT2RM4002440	2.99	2.99	6.92	5.78	5.32	9.49	
	NT2RM4002446	2.23	2.23	6.08	2.95	4.45	5.7	
	NT2RM4002450	3.36	3.36	10.01	6.15	7.75	7.24	
	NT2RM4002452	2.13	2.13	6.3	3.67	5.15	7.23	
10	NT2RM4002457	2.68	2.68	4.44	2.66	3.26	4.52	
	NT2RM4002458	3.06	3.06	5.77	3.32	5.34	4.04	
	NT2RM4002460	2.43	2.43	3.68	1.57	2.45	1.43	
	NT2RM4002464	5.4	5.4	12.62	14.39	13.72	14.3	
	NT2RM4002479	4.66	4.66	6.69	4.91	7.98	11.54	
15	NT2RM4002482	4.26	4.26	16.18	10.19	11.5	12.2	
	NT2RM4002489	6.74	6.74	16.91	8.79	5.81	11.68	
	NT2RM4002493	1.35	1.35	3.22	1.96	3.51	2.73	
	NT2RM4002499	34.96	34.96	72.9	59.42	52.07	54.3	
	NT2RM4002504	5.15	5.15	10.68	10.57	13.51	9.8	
20	NT2RM4002506	4.77	4.77	9.4	4.93	7.59	8.53	
	NT2RM4002510	2.03	2.03	3.27	1.66	2.97	2.48	
	NT2RM4002527	1.57	1.57	3.14	1.83	2.31	4.47	
	NT2RM4002532	2.45	2.45	7.75	5.88	3.37	5.19	
	NT2RM4002534	1.79	1.79	4.8	2.1	3.45	2.94	
25	NT2RM4002535	2.5	2.5	6.51	5.89	8.1	6.37	
	NT2RM4002554	3.29	3.29	5.31	3.31	5.47	3.12	
	NT2RM4002558	6.91	6.91	32.57	32.58	41.54	25.61	
	NT2RM4002565	5.38	5.38	13.6	8.22	9.85	10.53	
	NT2RM4002567	3.34	3.34	5.43	4.21	4.49	7.22	
30	NT2RM4002571	4.48	4.48	15.61	11.95	16.47	15.24	
	NT2RM4002572	5.57	5.57	17.2	13.7	9.59	13.48	
	NT2RM4002577	7.76	7.76	15.25	6.59	5.87	5.65	
	NT2RM4002583	1.08	1.08	3.58	2.28	4.83	2.44	
	NT2RM4002584	1.64	1.64	5.67	3.24	5.74	5.56	
35	NT2RM4002593	3.29	3.29	5.17	2.75	3.91	4.61	
	NT2RM4002594	11.26	11.26	46.5	38.21	55.32	43.58	
	NT2RM4002604	4.83	4.83	4.64	1.77	2.03	2.89	** -
	NT2RM4002614	3.48	3.48	3.48	2.52	3.66	2.81	
40	NT2RM4002616	1.07	1.07	2.73	2.88	2.71	2.38	
	NT2RM4002623	1.39	1.39	4.89	3.92	3.72	5.06	
	NT2RM4002634	1.41	1.41	4.38	3.42	4.91	2.96	
	NT2RM4002636	2.22	2.22	3.93	3.92	4.18	4.12	
	NT2RP1000002	8.82	8.82	52.94	75.1	92.89	81.45	* +
45	NT2RP1000006	4.68	4.68	6.28	4.25	4.48	2.56	
	NT2RP1000015	4.86	4.86	5.27	2.74	1.99	2.28	** -
	NT2RP1000018	5.45	5.45	5	5.55	4.83	4.96	
	NT2RP1000034	18.22	18.22	49.95	38.04	30.76	50.07	
	NT2RP1000035	1.93	1.93	3.2	5.26	3.23	3.96	
50	NT2RP1000040	1.77	1.77	3.33	2.93	3.28	4.28	
	NT2RP1000042	1.3	1.3	3.44	1.99	3.22	2.38	
	NT2RP1000048	3.6	3.6	10.24	7.25	9.9	9	
	NT2RP1000050	2.21	2.21	4.71	2.89	4	3.57	
	NT2RP1000056	4.03	4.03	3.74	1.09	0.61	1.96	** -
55	NT2RP1000058	3.49	3.49	2.03	1.84	2.07	2.48	

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	NT2RP1000063	1.77	1.77	3.65	4.09	4	3.83		
	NT2RP1000068	1.89	1.89	3.99	3.12	3.33	2.43		
	NT2RP1000072	22.9	22.9	74.07	82.91	66.26	95.85		
5	NT2RP1000073	2.18	2.18	2.45	2.68	3.69	3.86	*	+
	NT2RP1000078	2.72	2.72	3.17	2.93	2.3	3.13		
	NT2RP1000079	4.13	4.13	5.32	3.6	4.48	2.5		
	NT2RP1000080	4.99	4.99	8.13	9.46	12.46	9.46	*	+
	NT2RP1000086	4.15	4.15	3.63	1.31	2.1	3.75		
10	NT2RP1000087	1.3	1.3	4.36	3.51	3.21	3.45		
	NT2RP1000089	4.5	4.5	9.98	12.69	11.3	14.93	*	+
	NT2RP1000090	45.76	45.76	96.6	94.37	53.44	93.42		
	NT2RP1000100	2.17	2.17	4.05	5.23	4.13	3.66		
	NT2RP1000101	3.44	3.44	5.22	4.41	2.88	4.81		
15	NT2RP1000111	3.24	3.24	5.56	4.51	3.9	3.69		
	NT2RP1000112	3.29	3.29	4.08	1.85	3.33	3		
	NT2RP1000124	5.57	5.57	4.96	3.11	5.73	5.5		
	NT2RP1000125	7.28	7.28	19.39	13.69	10.68	16.86		
	NT2RP1000129	1.81	1.81	4.35	5.14	3.91	4.27		
20	NT2RP1000130	2.31	2.31	4.11	5.31	5.62	16.86		
	NT2RP1000154	7.5	7.5	15.63	17.16	12.72	16.37		
	NT2RP1000163	2.42	2.42	3.51	2.72	2.99	3.59		
	NT2RP1000170	3.42	3.42	4.2	4.96	5.17	5.85	*	+
25	NT2RP1000174	3.5	3.5	3.42	1.3	2.38	2.12	**	-
	NT2RP1000181	6.14	6.14	7.22	10.97	14.98	9.38	*	+
	NT2RP1000191	1.08	1.08	5.61	4.94	3.59	5.71		
	NT2RP1000202	1.06	1.06	1.66	2.02	1.2	2.24		
	NT2RP1000239	1.53	1.53	4.1	2.15	0.94	2.07		
30	NT2RP1000243	2.37	2.37	2.04	1.31	1.14	1.64	**	-
	NT2RP1000255	1.94	1.94	3.02	2.11	2.26	1.78		
	NT2RP1000259	5.27	5.27	9.55	5.53	6.33	4.29		
	NT2RP1000261	2.76	2.76	4.4	2.07	1.64	2.64		
	NT2RP1000269	5.16	5.16	5.01	7.7	10.51	7.39	*	+
35	NT2RP1000271	7.79	7.79	15.88	13.16	15.11	18.48		
	NT2RP1000272	7.71	7.71	13.07	10.72	11.74	11.3		
	NT2RP1000279	2.19	2.19	5.24	2.23	3.91	2.62		
	NT2RP1000290	6.61	6.61	9.02	12.65	13.52	9.92	*	+
	NT2RP1000293	6.86	6.86	10.91	9.75	8.45	10.92		
40	NT2RP1000300	12.42	12.42	11.93	9.96	11.37	10.2	*	-
	NT2RP1000324	5.16	5.16	6	4.69	5.92	6.97		
	NT2RP1000325	54.42	54.42	101.4	70.46	57.52	78.6		
	NT2RP1000326	4.01	4.01	7.67	3.82	4.56	7.85		
	NT2RP1000331	12.16	12.16	24.08	12.19	10.5	20.1		
45	NT2RP1000333	4.18	4.18	7.52	6.66	6.53	6.98		
	NT2RP1000336	1.45	1.45	4.45	1.35	3.76	1.78		
	NT2RP1000347	3.05	3.05	8.75	7.26	8.31	6.38		
	NT2RP1000348	2.11	2.11	4.14	2.76	3	2.75		
	NT2RP1000349	2.12	2.12	3.92	3	4.39	4.11		
50	NT2RP1000353	40.87	40.87	83.5	51.49	47.8	66.02		
	NT2RP1000356	39.53	39.53	93.37	50.3	56.48	74.42		
	NT2RP1000357	3.89	3.89	9.63	8.43	8.7	8.72		
	NT2RP1000358	2.85	2.85	6.11	4.23	3.04	5.09		
55	NT2RP1000360	11.04	11.04	19.39	12.08	18.42	19.44		

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	NT2RP1000363	13.09	13.09	15.39	13.13	13.38	10.01		
	NT2RP1000376	1.81	1.81	3.8	2.09	1.9	2.24		
5	NT2RP1000386	118	118	191.31	146.98	187.97	155.47		
	NT2RP1000407	0.72	0.72	3.16	0.58	0.89	1.2		
	NT2RP1000409	2.05	2.05	5.39	2.84	6.59	3.83		
	NT2RP1000413	4.78	4.78	8.03	5.86	8.89	10.19		
	NT2RP1000416	1.5	1.5	2.01	0.93	3.17	0.7		
10	NT2RP1000418	2.27	2.27	6.69	5.08	6.67	4.85		
	NT2RP1000420	1.77	1.77	5.19	7.32	7.64	3.7		
	NT2RP1000434	1.48	1.48	4.39	1.27	3.12	1		
	NT2RP1000439	5.02	5.02	9.31	20.62	28.73	24.75	**	+
	NT2RP1000443	1.8	1.8	3.46	2.24	1.61	1.63		
15	NT2RP1000447	2.21	2.21	5.57	2.49	2.87	3.1		
	NT2RP1000448	1.39	1.39	3.58	3.09	4.4	1.41		
	NT2RP1000451	4.2	4.2	6.37	5.72	7.27	7.04		
	NT2RP1000458	15.1	15.1	10.53	19.73	8.72	23.03		
	NT2RP1000460	7.55	7.55	13.82	8.76	11.49	8.62		
20	NT2RP1000465	4.58	4.58	20.97	20.41	19.98	22.46		
	NT2RP1000468	3.25	3.25	4.64	3.82	4.1	4.45		
	NT2RP1000470	2.38	2.38	5.67	3.99	2.35	3.8		
	NT2RP1000477	1.11	1.11	3.81	1.1	0.84	0.83		
	NT2RP1000478	4.53	4.53	12.55	19.87	18.75	20.39	*	+
25	NT2RP1000481	1.23	1.23	3.89	2.48	4.09	1.2		
	NT2RP1000493	2.44	2.44	3.8	1.74	3.83	0.87		
	NT2RP1000513	13.07	13.07	16.37	17.06	17.57	18.97	*	+
	NT2RP1000522	6.13	6.13	12.69	13.13	13.08	10.32		
	NT2RP1000533	3.72	3.72	6.17	2.92	4.49	2.17		
30	NT2RP1000544	1.53	1.53	2.45	1.38	1.24	1.44		
	NT2RP1000547	0.88	0.88	2.45	2	1.63	1.23		
	NT2RP1000551	1.7	1.7	2.62	2.13	3.2	1.1		
	NT2RP1000567	1.66	1.66	4.29	2.54	4.29	1.77		
	NT2RP1000574	1.99	1.99	4.28	1.5	3.43	1.38		
35	NT2RP1000577	3.14	3.14	6.01	3.16	5.31	2.05		
	NT2RP1000579	4.64	4.64	6.24	3.27	3.97	2.04		
	NT2RP1000581	5.22	5.22	3.58	2.07	1.61	0.93	**	-
	NT2RP1000593	1.74	1.74	4.39	2.48	3.28	2.3		
	NT2RP1000604	3.85	3.85	7.75	17.25	13.78	16.39	**	+
40	NT2RP1000609	1.15	1.15	2.21	2.84	2.61	1.55		
	NT2RP1000613	1.12	1.12	2.56	1.82	4.29	0.82		
	NT2RP1000622	5.94	5.94	15.9	14.91	19.42	15.46		
	NT2RP1000627	9.18	9.18	18.96	23.88	21.9	14.86		
45	NT2RP1000629	4.18	4.18	5.9	5.92	5.32	3.17		
	NT2RP1000630	6.54	6.54	7.84	7.21	7.67	7.92		
	NT2RP1000639	0.64	0.64	0.31	1.53	2.04	0.28		
	NT2RP1000640	130.14	130.14	307.77	227.5	176.05	232.29		
	NT2RP1000646	4.14	4.14	9.59	10.19	11.87	12.15	*	+
50	NT2RP1000659	2.65	2.65	7	8.91	7.99	6.04		
	NT2RP1000674	13.48	13.48	28.08	43.62	45.82	56.95	**	+
	NT2RP1000677	3.9	3.9	10.76	11.84	10.19	9.87		
	NT2RP1000679	2.38	2.38	3.76	2.3	2.35	1.05		
	NT2RP1000688	4.72	4.72	3.34	2.76	2.73	1.83	*	-
55	NT2RP1000689	1.44	1.44	1.86	2.03	1.22	1.13		

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	NT2RP1000695	1.11	1.11	2.5	2.09	2.44	1.52		
	NT2RP1000701	0.89	0.89	1.08	2.62	2.74	1.71	*	+
	NT2RP1000702	1.12	1.12	2.28	3.74	4.07	3.15	*	+
5	NT2RP1000713	2.29	2.29	2.79	2.8	3.56	2.38		
	NT2RP1000721	4.14	4.14	4.49	4.48	3.92	3.78		
	NT2RP1000730	3.5	3.5	4.83	2.61	4.5	2.41		
	NT2RP1000733	6.08	6.08	6.56	4.91	8.12	5.65		
10	NT2RP1000738	3.18	3.18	8.04	5.16	5.71	7.11		
	NT2RP1000739	1.11	1.11	2.65	4.02	3.09	2.86		
	NT2RP1000740	1.41	1.41	3.13	3.63	3.57	3.77	*	+
	NT2RP1000746	1.15	1.15	3.58	2.28	3.74	1.37		
	NT2RP1000750	4	4	8.31	10.25	10.72	9.39	*	+
15	NT2RP1000751	33.15	33.15	59.65	67.84	64.22	66.55		
	NT2RP1000767	3.8	3.8	3.64	1.7	2.62	0.62	*	-
	NT2RP1000769	9.31	9.31	13.98	7.42	8.59	7.19		
	NT2RP1000780	0.86	0.86	1.01	1.87	1.13	0.89		
	NT2RP1000782	4.25	4.25	12.21	10.24	7.96	9.13		
20	NT2RP1000796	3.17	3.17	2.69	4.23	2.99	2.86		
	NT2RP1000797	12.31	12.31	22.78	19.44	18.64	21.78		
	NT2RP1000800	1.13	1.13	3.74	2.46	2.66	1.46		
	NT2RP1000825	2.38	2.38	2.91	1.04	1.88	0.87	*	-
	NT2RP1000833	2.5	2.5	2.85	0.92	2.39	1.26		
25	NT2RP1000834	35.44	35.44	66.57	73.98	90.28	71.45		
	NT2RP1000836	1.83	1.83	3.43	1.01	2.39	1.04		
	NT2RP1000837	3.36	3.36	6.66	3.22	4.71	3.67		
	NT2RP1000846	1.29	1.29	5.48	1.67	2.84	1.4		
	NT2RP1000847	1.99	1.99	5.49	2.15	5.12	1.64		
30	NT2RP1000851	4.67	4.67	9.32	6.18	7.94	6.72		
	NT2RP1000856	14.31	14.31	17.46	20.38	23.22	19.37	*	+
	NT2RP1000860	2.09	2.09	4.54	4.02	2.74	4.04		
	NT2RP1000902	5.31	5.31	11.6	6.94	9.91	7.34		
	NT2RP1000903	2.45	2.45	6.26	4.04	3.42	4.24		
35	NT2RP1000905	1.76	1.76	4.87	5.36	5.66	10		
	NT2RP1000915	5.51	5.51	10.01	6.72	8.59	9.91		
	NT2RP1000916	2.31	2.31	5.51	1.78	3.82	2.09		
	NT2RP1000921	9.38	9.38	8.73	8.23	9.13	7.92		
	NT2RP1000943	5.14	5.14	10.76	8.51	8.55	7.2		
40	NT2RP1000944	1.59	1.59	2.21	1.78	1.74	1.15		
	NT2RP1000947	8.5	8.5	14.91	16.51	15.04	14.22		
	NT2RP1000954	2.11	2.11	4.96	2.74	5.55	3.04		
	NT2RP1000958	6.48	6.48	14.73	4.54	10.17	10.21		
	NT2RP1000959	124.81	124.81	209.45	128.43	72.65	206.1		
45	NT2RP1000966	9.96	9.96	12.96	14.28	15.36	21.39		
	NT2RP1000974	2.46	2.46	5.38	3.98	6.08	3.71		
	NT2RP1000980	3.07	3.07	5.5	4.04	4.53	4.02		
	NT2RP1000981	4.3	4.3	8.09	5.68	7.26	5.27		
	NT2RP1000988	6.45	6.45	10.46	9.62	6.44	7.87		
50	NT2RP1001002	2.8	2.8	7.36	3.94	4.57	4.3		
	NT2RP1001004	4.72	4.72	8.25	3.65	4.9	5.37		
	NT2RP1001007	1.42	1.42	3.42	1.69	3.84	2.03		
	NT2RP1001011	1.94	1.94	5.93	3.82	5.46	4.83		
55	NT2RP1001013	4.45	4.45	9.41	5.92	8.62	5.04		

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	NT2RP1001014	2.21	2.21	5.89	3.76	6.64	3.49	
	NT2RP1001020	1.87	1.87	4.11	2.08	3.75	2.36	
	NT2RP1001023	62.79	62.79	145.09	101.48	105.86	143.96	
5	NT2RP1001027	18.11	18.11	82.66	51.63	59.05	68.9	
	NT2RP1001031	1.83	1.83	3.31	2.05	3.53	2.25	
	NT2RP1001033	2.43	2.43	6.09	5.68	5.98	4.27	
	NT2RP1001042	2.94	2.94	6.47	2.99	3.85	2.04	
10	NT2RP1001045	15.95	15.95	23.24	40.66	47.04	44.53	** +
	NT2RP1001073	6.64	6.64	10.57	8.32	10.46	7.33	
	NT2RP1001079	2.91	2.91	6.37	2.16	2.58	1.48	
	NT2RP1001080	2.16	2.16	4.89	6.88	4.2	4.56	
	NT2RP1001113	1.07	1.07	3.64	3.55	3.94	3.26	
15	NT2RP1001159	21.42	21.42	43.84	22.89	23.31	34.25	
	NT2RP1001173	1.7	1.7	3.07	1.38	4.28	1.52	
	NT2RP1001176	7.4	7.4	10.13	13	9.31	13.95	
	NT2RP1001177	5.31	5.31	5.75	3.01	5.5	2.02	
	NT2RP1001185	6.42	6.42	9.37	3.79	4.63	2.73	* -
20	NT2RP1001199	3.9	3.9	7.67	6.93	5.22	3.28	
	NT2RP1001205	7.78	7.78	19.46	16.66	12.64	23.28	
	NT2RP1001215	1.82	1.82	5.02	3.79	4.12	3.15	
	NT2RP1001225	4.54	4.54	7.96	7.56	8.77	6.31	
25	NT2RP1001245	7.27	7.27	10.86	19.68	21.03	22.13	** +
	NT2RP1001247	2.04	2.04	4.01	1.77	2.89	1.67	
	NT2RP1001248	2.81	2.81	6.79	3.94	4.63	2.4	
	NT2RP1001253	5.02	5.02	6.39	4.48	4.38	3.32	
	NT2RP1001286	6.18	6.18	7.69	3.79	3.88	4.12	** -
30	NT2RP1001294	2.4	2.4	4.47	3.6	2.73	4.18	
	NT2RP1001302	2.46	2.46	4.51	4.89	2.9	5.39	
	NT2RP1001310	15.54	15.54	34.01	21.13	20.75	27.15	
	NT2RP1001311	1.9	1.9	3.22	2.66	3.16	2.38	
	NT2RP1001313	2.6	2.6	7.72	5.45	7.85	5.78	
35	NT2RP1001324	2.47	2.47	5.3	3.34	4.17	2.35	
	NT2RP1001349	3.3	3.3	6.29	3.63	3.92	2.14	
	NT2RP1001361	19.41	19.41	18.28	23.28	28.33	24.16	* +
	NT2RP1001379	3.82	3.82	9.52	4.97	7.97	7.06	
	NT2RP1001385	2.06	2.06	4.51	4.09	3.89	4.4	
40	NT2RP1001395	4.96	4.96	7.86	6.01	6.32	8.13	
	NT2RP1001410	8.75	8.75	20.39	15.74	15.66	9.94	
	NT2RP1001424	2.39	2.39	3.34	3	3	1.73	
	NT2RP1001432	4.33	4.33	3.86	2.19	1.76	2.05	** -
	NT2RP1001449	6.23	6.23	7.5	6.29	8.21	4.63	
45	NT2RP1001457	4.09	4.09	4.21	2.11	2.26	2.63	** -
	NT2RP1001459	21.54	21.54	132.97	90.96	107.97	81.08	
	NT2RP1001466	5.73	5.73	14.97	11.31	9.39	10.99	
	NT2RP1001475	2.45	2.45	6.31	5.98	6.67	3.9	
	NT2RP1001482	3.93	3.93	9.18	15.88	13.03	8.2	
50	NT2RP1001494	1.61	1.61	4.6	4.34	4.18	2.25	
	NT2RP1001500	3.39	3.39	8.13	8.09	8.65	7.42	
	NT2RP1001517	5.11	5.11	7.37	4.41	5.38	2.36	
	NT2RP1001540	4.74	4.74	5.03	4.6	4.86	3.11	
	NT2RP1001543	1.02	1.02	1.83	1.49	1.12	0.98	
55	NT2RP1001546	22.51	22.51	51.51	34.99	22.76	33.42	

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	NT2RP1001550	9.33	9.33	21.4	14.35	12.21	13.42		
	NT2RP1001553	2.07	2.07	6.07	5.69	6.04	4.45		
	NT2RP1001555	36.28	36.28	58.55	41.1	53.63	54.35		
5	NT2RP1001563	2.28	2.28	3.44	2.07	2.24	1.31		
	NT2RP1001569	9.43	9.43	16	17.31	18.21	13.04		
	NT2RP1001584	15.6	15.6	19.66	28.1	32.53	25.83	**	+
	NT2RP1001599	1.18	1.18	1.95	1.27	1.19	1.24		
	NT2RP1001616	5	5	11.95	9.49	6.7	8.95		
10	NT2RP1001654	11.78	11.78	18.07	16.27	16.54	18.38		
	NT2RP1001665	2.77	2.77	4.72	2.73	2.05	2.05		
	NT2RP1001679	76.31	76.31	195.7	199.2	240.87	222.46		
	NT2RP1001681	10.11	10.11	15.1	20.39	21.03	23.99	**	+
	NT2RP1001694	3.58	3.58	3.82	2.45	2.38	1.97	**	-
15	NT2RP2000001	5.23	5.23	5.53	4.17	4.54	3.74	**	-
	NT2RP2000006	3.49	3.49	7.32	4.12	3.88	3.4		
	NT2RP2000007	3.18	3.18	6.56	4.68	5.66	4.92		
	NT2RP2000008	2.77	2.77	6.72	3.66	5.3	4.9		
20	NT2RP2000010	2.89	2.89	5.59	2.99	5.06	2.5		
	NT2RP2000011	7.08	7.08	17.96	14.55	14.74	15.15		
	NT2RP2000027	2.28	2.28	7.42	4.52	4.89	3.61		
	NT2RP2000028	22.93	22.93	62.54	46.48	51.47	53.47		
	NT2RP2000032	2.5	2.5	5.85	3.11	3.71	6.42		
25	NT2RP2000040	11.57	11.57	23.92	14.38	14.5	23.1		
	NT2RP2000042	5.28	5.28	10.32	6.89	7.21	12.64		
	NT2RP2000045	5.7	5.7	9.42	5.27	6.45	6.3		
	NT2RP2000051	3.16	3.16	6.29	9.23	9.96	9.53	**	+
	NT2RP2000054	2.55	2.55	6.42	3.81	5.42	2.53		
30	NT2RP2000056	3.68	3.68	6.23	5.67	6.89	5.8		
	NT2RP2000057	60.79	60.79	174.83	212.63	239.81	221.98	*	+
	NT2RP2000067	3.1	3.1	3.86	2.98	4.36	5.72		
	NT2RP2000070	2.91	2.91	6.27	5.7	5.95	8.21		
	NT2RP2000076	1.66	1.66	4.45	2.98	3.58	3.23		
35	NT2RP2000077	1.67	1.67	4.73	2.43	4.94	3.14		
	NT2RP2000079	3.76	3.76	9.24	5.15	4.81	5.47		
	NT2RP2000088	2.9	2.9	5.22	2.18	3.07	2.21		
	NT2RP2000091	5.84	5.84	6.54	6.62	8.28	6.72		
	NT2RP2000092	4.37	4.37	6.7	6.06	7.67	5.65		
40	NT2RP2000097	2.74	2.74	3.39	3.4	4.13	4.13	*	+
	NT2RP2000098	3.44	3.44	6.83	6.69	9.01	6.27		
	NT2RP2000108	1.93	1.93	7.24	4.8	6.31	6.68		
	NT2RP2000114	1.95	1.95	3.65	2.58	4.41	2.9		
	NT2RP2000116	3.17	3.17	7.36	5.35	3.85	9.42		
45	NT2RP2000119	3.14	3.14	7.16	4.58	7.96	5.6		
	NT2RP2000120	3.91	3.91	7.62	5.57	8.5	5.8		
	NT2RP2000126	2.86	2.86	4.86	3.88	5.1	3.44		
	NT2RP2000133	1.83	1.83	3.66	3.13	4.05	2.01		
50	NT2RP2000147	6.28	6.28	12.88	11.64	6.51	8.58		
	NT2RP2000153	4.61	4.61	9.55	10.57	6.49	12.05		
	NT2RP2000156	3.27	3.27	8.24	5.59	6.55	4.07		
	NT2RP2000157	3.7	3.7	6.33	6.57	5.02	4.15		
	NT2RP2000161	4.45	4.45	8.82	7.52	7.5	6.02		
55	NT2RP2000168	4.22	4.22	12.63	3.94	6.03	3.88		

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	NT2RP2000173	12.56	12.56	81.37	72.12	92.12	78.68	
	NT2RP2000175	1.9	1.9	3.78	2.03	3.33	4.43	
5	NT2RP2000178	2.06	2.06	6.06	3.23	3.01	3.81	
	NT2RP2000183	1.64	1.64	7.82	5.82	6.21	6.03	
	NT2RP2000195	3.1	3.1	6.65	6	6.71	3.22	
	NT2RP2000204	73.6	73.6	93.43	102.95	40.16	62.34	
	NT2RP2000205	4	4	6.56	3.91	5.74	4.5	
10	NT2RP2000208	3.06	3.06	9.42	4.23	6.77	3.36	
	NT2RP2000224	13.3	13.3	31.75	18.34	21.15	20.93	
	NT2RP2000230	9.96	9.96	18.99	12.16	16.4	11.95	
	NT2RP2000231	4.3	4.3	7.41	4.24	3.43	4.54	
	NT2RP2000232	1.08	1.08	2.75	1.53	2.45	0.74	
15	NT2RP2000233	8.04	8.04	60.44	47.2	64.72	52.31	
	NT2RP2000239	3	3	4.7	8.93	8.93	7.01	** +
	NT2RP2000240	2.01	2.01	5.25	2.49	3.41	1.45	
	NT2RP2000248	4.29	4.29	6.09	2.82	2.39	0.96	* -
	NT2RP2000256	5.7	5.7	8.25	5.62	6.22	5.44	
20	NT2RP2000257	3.47	3.47	6.92	4.86	6.52	4.34	
	NT2RP2000258	1.53	1.53	3.83	3.88	2.93	3.02	
	NT2RP2000261	2.95	2.95	3.94	4.47	3.59	2.91	
	NT2RP2000270	3.12	3.12	6.26	6.66	4.06	4.3	
	NT2RP2000274	1.78	1.78	3.87	3.48	5.16	2.56	
25	NT2RP2000277	2.18	2.18	6.13	3.19	4.02	2.98	
	NT2RP2000279	2.26	2.26	4.92	2.43	2.52	2.17	
	NT2RP2000283	5.75	5.75	27.65	21.53	27.32	24.78	
	NT2RP2000288	6.29	6.29	7.46	8.9	10.89	8.64	* +
	NT2RP2000289	1.12	1.12	2.79	3.09	2.77	1.93	
30	NT2RP2000297	2.57	2.57	5.7	4.8	4.53	6.09	
	NT2RP2000298	3.61	3.61	9.64	8.51	7.66	8.24	
	NT2RP2000310	1.43	1.43	2.3	2.46	3.41	1.7	
	NT2RP2000327	2.12	2.12	3.96	3.13	3.49	1.57	
	NT2RP2000328	6.95	6.95	11.56	13.43	16.7	14.68	* +
35	NT2RP2000329	10.73	10.73	10.17	17.55	23.92	18.52	** +
	NT2RP2000333	6.35	6.35	6.4	6.83	7.17	4.64	
	NT2RP2000337	2.05	2.05	5.16	4.43	5.32	5.31	
	NT2RP2000346	2.55	2.55	5.18	7.2	5.63	4.95	
	NT2RP2000357	1.57	1.57	6.87	5.48	5.14	5.35	
40	NT2RP2000358	2.09	2.09	4.52	5.03	4.9	4.01	
	NT2RP2000366	3.23	3.23	4.08	4.16	4.25	2.32	
	NT2RP2000369	7.22	7.22	9.94	44.13	45.2	44.34	** +
	NT2RP2000376	26.92	26.92	108.62	84.48	134.63	85.95	
	NT2RP2000394	6.49	6.49	5.92	5.08	8.52	4.21	
45	NT2RP2000396	2.71	2.71	6.55	7.52	6.8	5.02	
	NT2RP2000412	4.48	4.48	23.45	21.42	24.93	20.49	
	NT2RP2000414	8.03	8.03	18.69	23.83	18.98	23.37	
	NT2RP2000420	1.12	1.12	4.11	3.54	3.25	1.97	
	NT2RP2000422	6.41	6.41	13.18	17.56	17.88	18.67	* +
50	NT2RP2000426	21.59	21.59	80.94	87.94	110.97	74.98	
	NT2RP2000428	24.92	24.92	43.91	34.21	35.59	30.95	
	NT2RP2000438	5.06	5.06	5.17	5.62	6.94	5.11	
	NT2RP2000447	4.14	4.14	9.68	7.3	7.08	7.16	
55	NT2RP2000448	3.03	3.03	4.63	4.57	3.57	3.17	

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	NT2RP2000459	2.47	2.47	4.93	2.82	3.15	2.09		
	NT2RP2000479	3.3	3.3	7.51	5.33	5.71	5.06		
	NT2RP2000498	3.07	3.07	6.25	4.48	5.09	3.9		
5	NT2RP2000503	2.47	2.47	4.46	2.54	2.82	1.52		
	NT2RP2000510	4.01	4.01	6.19	5.08	6.45	3.7		
	NT2RP2000514	2.65	2.65	2.51	1.94	2.25	1.63	*	-
	NT2RP2000516	4.72	4.72	9.77	4.92	5.29	5.18		
10	NT2RP2000523	2.21	2.21	3.17	1.92	2.44	2.63		
	NT2RP2000533	17.82	17.82	29.05	22.57	27.56	30.78		
	NT2RP2000540	1.98	1.98	4.66	3.01	5.41	5.18		
	NT2RP2000547	3.1	3.1	5.26	4.38	5.27	3.71		
	NT2RP2000557	4.26	4.26	6.96	4.34	6.5	3.32		
15	NT2RP2000558	3.43	3.43	7.17	6.43	7.11	8.26		
	NT2RP2000564	3.04	3.04	7.2	3.49	8.03	4.77		
	NT2RP2000565	4.54	4.54	11.07	7.64	9.24	9.98		
	NT2RP2000583	14.8	14.8	44.9	49.6	34.93	49.08		
	NT2RP2000591	0.81	0.81	3.81	1.53	2.61	1.21		
20	NT2RP2000599	1.85	1.85	4.1	1.97	3.43	2.36		
	NT2RP2000601	1.78	1.78	4.67	1.28	2.48	1.3		
	NT2RP2000603	2.58	2.58	4.44	2.54	2.84	2.98		
	NT2RP2000610	3.77	3.77	7.23	6.32	7.62	5.53		
	NT2RP2000614	75.85	75.85	129.42	130.63	184.38	188.58	*	+
25	NT2RP2000616	1.81	1.81	4.89	3.9	5.1	3.83		
	NT2RP2000617	2.17	2.17	6.73	5.78	6.82	6.26		
	NT2RP2000623	3.1	3.1	5.36	3.46	5.1	3.49		
	NT2RP2000634	1.56	1.56	3.92	2.29	3.34	2.02		
	NT2RP2000636	3.78	3.78	8.64	6.27	7.6	6.62		
30	NT2RP2000638	4.37	4.37	8.91	4.57	7.41	5.69		
	NT2RP2000644	2.22	2.22	5.47	3.41	4.16	3.45		
	NT2RP2000649	8.96	8.96	15.76	13.65	17.22	13.07		
	NT2RP2000652	3.35	3.35	4.58	3.57	4.36	2.72		
	NT2RP2000656	3.73	3.73	6.93	4.83	3.91	4.08		
35	NT2RP2000658	1.08	1.08	2.64	1.51	3.18	1.43		
	NT2RP2000663	4.23	4.23	6.9	5.98	7.21	5.9		
	NT2RP2000664	4.24	4.24	10.24	12.72	12.54	16.44	*	+
	NT2RP2000668	7.49	7.49	26.84	16.92	20.41	17.17		
	NT2RP2000678	1.77	1.77	3.19	1.77	2.09	1.13		
40	NT2RP2000694	4.89	4.89	8.39	11.06	13	13.36	**	+
	NT2RP2000704	1.8	1.8	5.63	2.99	3.13	3.67		
	NT2RP2000710	4.51	4.51	9.96	6.72	8.08	7.23		
	NT2RP2000712	1.43	1.43	5.35	3.39	3.57	2.95		
	NT2RP2000715	3.42	3.42	7.43	6.04	7.56	4.49		
45	NT2RP2000720	4.92	4.92	11.76	7.24	8	7.11		
	NT2RP2000731	3.92	3.92	9.15	3.7	4.5	2.61		
	NT2RP2000739	3.23	3.23	5.67	2.62	3.32	5.65		
	NT2RP2000748	1.59	1.59	4.2	1.42	1.81	1.62		
50	NT2RP2000749	11.84	11.84	21.88	14.4	8.47	13.91		
	NT2RP2000758	1.6	1.6	3.17	2.65	6	1.17		
	NT2RP2000764	1.51	1.51	5.74	2.95	5.22	1.95		
	NT2RP2000766	9.08	9.08	52.24	46.37	59.37	52.89		
	NT2RP2000777	12.28	12.28	18.43	26.91	28.56	24.47	**	+
55	NT2RP2000786	21.32	21.32	73.91	55.85	67.59	58.16		

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	NT2RP2000793	5.32	5.32	6.9	4.32	3.57	4.38	*	-
	NT2RP2000796	5.32	5.32	7.41	7.38	9.17	6.66		
5	NT2RP2000809	3.25	3.25	8.3	6.46	4.69	5.45		
	NT2RP2000812	6.65	6.65	17.51	16.43	14.35	16.89		
	NT2RP2000814	4.16	4.16	4.97	3.75	4.6	3.29		
	NT2RP2000816	1.84	1.84	5.64	4.64	5.19	3.58		
	NT2RP2000818	3.28	3.28	5.19	3.18	3.66	1.95		
10	NT2RP2000819	2.76	2.76	5.79	3.03	3.05	1.94		
	NT2RP2000841	4.35	4.35	4.51	2.17	2.48	1.65	**	-
	NT2RP2000842	7.8	7.8	9.57	13.62	14.25	12.66	**	+
	NT2RP2000845	2.52	2.52	8.31	7.51	6.76	6.93		
	NT2RP2000863	2.45	2.45	3.48	3.82	3.37	2.47		
15	NT2RP2000880	5.96	5.96	11.61	9.5	11.13	10.25		
	NT2RP2000892	4.3	4.3	6.43	6.54	6.97	5.01		
	NT2RP2000894	5.59	5.59	11.88	5.41	5.59	2.16		
	NT2RP2000903	5.71	5.71	9.12	10.73	11.92	7.44		
20	NT2RP2000906	4.56	4.56	5.39	2.63	3.78	2.19	*	-
	NT2RP2000910	4.34	4.34	4.26	2.9	2.7	1.68	**	-
	NT2RP2000931	10.97	10.97	18.36	20.51	19.28	24.6		
	NT2RP2000932	2.86	2.86	5.43	4.8	4.72	4.21		
	NT2RP2000938	18.41	18.41	42.99	35.71	30.01	43.52		
25	NT2RP2000943	7.02	7.02	14.98	18.7	14.88	14.48		
	NT2RP2000957	3.19	3.19	4.11	4.26	3.66	2.71		
	NT2RP2000958	7	7	6.84	10.43	12.36	7.8		
	NT2RP2000959	9.88	9.88	14.99	13.92	17.38	10.69		
	NT2RP2000965	5.05	5.05	7.82	15.73	18.97	16.02	**	+
30	NT2RP2000970	2.31	2.31	6.72	5.14	5	4.62		
	NT2RP2000973	0.9	0.9	1.47	2.56	2.64	1.57	*	+
	NT2RP2000985	2.69	2.69	6	9.28	6.29	13.98		
	NT2RP2000987	1.89	1.89	3.31	4.54	3.17	1.66		
	NT2RP2000997	13.83	13.83	23.99	38.12	29.73	40.96	*	+
35	NT2RP2001024	2.86	2.86	5.34	3.61	3.12	2.36		
	NT2RP2001028	4.66	4.66	4.2	2.65	4.09	0.99		
	NT2RP2001036	5.14	5.14	8.86	6.16	6.44	4.91		
	NT2RP2001039	1.08	1.08	3.18	3.47	1.14	2.24		
	NT2RP2001044	1.13	1.13	2.5	2.53	1.89	2.8		
40	NT2RP2001056	4.97	4.97	28.32	20.16	26.9	18.16		
	NT2RP2001065	2.38	2.38	6.24	7.45	7.4	5.69		
	NT2RP2001067	2.98	2.98	5.38	4.12	5.29	2.41		
	NT2RP2001070	3.3	3.3	7.63	4.72	6.17	3.58		
	NT2RP2001081	2.91	2.91	8.19	4.8	6.68	3.9		
45	NT2RP2001087	3.93	3.93	2.36	2.06	2.92	1.61		
	NT2RP2001094	0.69	0.69	1.37	1.25	1.15	1.04		
	NT2RP2001119	2.02	2.02	6.11	5.86	4.44	4.35		
	NT2RP2001127	1.53	1.53	4.04	2.69	1.85	2.1		
	NT2RP2001133	2.45	2.45	4.73	4.06	3.61	3.6		
50	NT2RP2001137	2.68	2.68	4.07	2.3	2.82	2.9		
	NT2RP2001142	3.88	3.88	7.47	3.37	2.83	2.42		
	NT2RP2001149	2.7	2.7	2.98	2.11	3.39	1.32		
	NT2RP2001168	6	6	7.81	6.8	7.01	5.75		
	NT2RP2001173	4.15	4.15	7.88	3.98	3.09	5.44		
55	NT2RP2001174	9.23	9.23	14.98	14.12	15.45	18.01		

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	NT2RP2001184	2.78	2.78	5.46	4.21	7.18	4.64	
	NT2RP2001196	1.62	1.62	5.93	3.14	3.28	2.94	
5	NT2RP2001200	3.85	3.85	9.36	5.02	4.25	7.88	
	NT2RP2001218	2.29	2.29	5.69	2.55	3.89	3.6	
	NT2RP2001223	2.65	2.65	5.03	1.95	3.69	3.31	
	NT2RP2001226	4.34	4.34	10.19	6.95	5.72	7.35	
	NT2RP2001227	4.45	4.45	6.12	3.2	3.62	6.01	
10	NT2RP2001232	6.44	6.44	13.95	7.13	9.79	13.66	
	NT2RP2001233	4.02	4.02	10.57	7.04	7.77	8.01	
	NT2RP2001245	4.21	4.21	8.03	9.47	11.82	11.16	* +
	NT2RP2001246	6.3	6.3	9.84	9	11.28	11.57	
	NT2RP2001268	6.19	6.19	18.1	17.61	16.26	18.55	
15	NT2RP2001270	4.78	4.78	9.11	5.68	8.7	10.04	
	NT2RP2001276	4.92	4.92	13.29	12.73	10.92	12.73	
	NT2RP2001277	3.11	3.11	7.02	4.91	6.22	10.82	
	NT2RP2001290	2.71	2.71	6.46	4.42	5.61	6.01	
	NT2RP2001295	5.46	5.46	9.44	5.13	5.98	7.92	
20	NT2RP2001297	118.17	118.17	120.73	139.11	97.16	145.76	
	NT2RP2001301	9.12	9.12	18.56	15.89	19.62	14.24	
	NT2RP2001312	2.7	2.7	5.68	5.6	4.59	6.04	
	NT2RP2001327	4.73	4.73	5.69	6.39	8.53	11.86	
	NT2RP2001328	8.44	8.44	20.87	16.32	23.25	23.16	
25	NT2RP2001341	4.59	4.59	9.22	3.06	7.65	7.21	
	NT2RP2001347	3.09	3.09	8.54	5.54	9.55	6.9	
	NT2RP2001366	10.33	10.33	48.06	54.83	51.5	52.33	
	NT2RP2001378	2.33	2.33	3.77	3.74	4.64	5.02	
	NT2RP2001381	2.82	2.82	6.86	5.79	6.62	8.37	
30	NT2RP2001388	3.25	3.25	6.71	4.54	5.11	5.2	
	NT2RP2001391	443.52	443.52	734.13	742.83	990.71	747.95	
	NT2RP2001392	2.98	2.98	6.43	4.58	3.16	4.18	
	NT2RP2001394	3.3	3.3	8.55	8.35	6.09	10.15	
	NT2RP2001397	5.04	5.04	6.79	7.33	5.68	12.2	
35	NT2RP2001400	3.1	3.1	6.4	3.43	6.25	2.92	
	NT2RP2001408	3.31	3.31	6.13	4.02	5.97	5.62	
	NT2RP2001420	5.63	5.63	12.09	8.09	9.97	9.17	
	NT2RP2001423	4.71	4.71	9.71	6.21	8.29	7.19	
40	NT2RP2001427	2.68	2.68	5.32	3.69	4.61	5.49	
	NT2RP2001428	2.71	2.71	7.13	5.49	3.78	3.03	
	NT2RP2001436	4.27	4.27	8.85	5.84	2.85	4.84	
	NT2RP2001440	2.89	2.89	7.34	10.24	10.15	11.98	* +
	NT2RP2001445	2.43	2.43	6.75	5.86	5.55	5.89	
45	NT2RP2001449	4.37	4.37	6.41	5	4.74	5.02	
	NT2RP2001450	3.19	3.19	6.75	2.26	5.4	8.59	
	NT2RP2001467	4.53	4.53	10.28	5.32	4.72	6.5	
	NT2RP2001469	4.74	4.74	6.79	8.22	11.04	7.18	
	NT2RP2001480	6.54	6.54	26.68	14.98	12.63	15.42	
50	NT2RP2001495	5.86	5.86	11.96	3.16	9.04	10.39	
	NT2RP2001499	8.25	8.25	16.78	10.05	14.46	9.66	
	NT2RP2001506	2.79	2.79	7.24	5.32	8.19	5.33	
	NT2RP2001508	10.59	10.59	13.66	18.74	20.49	21.92	** +
	NT2RP2001511	6.41	6.41	9.74	6.08	8.63	6.53	
55	NT2RP2001514	7.04	7.04	7.02	7.24	6.44	6.38	

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	NT2RP2001520	2.93	2.93	4.84	2.6	3.19	2.87		
	NT2RP2001526	3.88	3.88	8.49	7.01	5.27	3.83		
5	NT2RP2001529	9.87	9.87	53.78	44.74	55.72	60.88		
	NT2RP2001536	1.63	1.63	4.17	3.81	4.52	4.71		
	NT2RP2001538	83.44	83.44	178.68	132.75	146.73	155.87		
	NT2RP2001547	4.96	4.96	14.87	16.77	19.21	17.77	*	+
	NT2RP2001560	6.28	6.28	21.64	25.41	28.19	27.75	*	+
10	NT2RP2001562	5.56	5.56	5.57	5.94	6.75	4.64		
	NT2RP2001566	7.96	7.96	9.24	8.22	7.91	8.56		
	NT2RP2001569	4.26	4.26	8.71	6.09	5.65	8.28		
	NT2RP2001576	3.95	3.95	11.58	13.42	9	12.82		
	NT2RP2001581	47.15	47.15	130.15	121.19	112.28	129.54		
15	NT2RP2001597	3.73	3.73	7.88	8.57	8.3	13.3		
	NT2RP2001601	2.37	2.37	4.81	3.67	4.81	3.34		
	NT2RP2001613	2.74	2.74	4.87	2.83	2.72	4.15		
	NT2RP2001628	3.42	3.42	3.97	3.14	3.04	7.84		
	NT2RP2001634	8.64	8.64	13.94	16.57	23.67	17.67	*	+
20	NT2RP2001635	2.51	2.51	5.92	5.63	5.53	4.72		
	NT2RP2001660	4.27	4.27	16.91	5.9	5.54	10.06		
	NT2RP2001662	1.49	1.49	4.07	4.5	4.44	3.47		
	NT2RP2001663	2.82	2.82	5.09	10.37	8.21	9.74	**	+
	NT2RP2001672	3.28	3.28	3.82	3.88	4.09	4	*	+
25	NT2RP2001675	4.1	4.1	5.01	5.23	4.73	5.06		
	NT2RP2001677	9.58	9.58	18.2	20.9	26.67	19.74	*	+
	NT2RP2001678	4.84	4.84	6.73	4.6	4.83	4.5		
	NT2RP2001683	1.89	1.89	3.12	4.6	4.72	2.78		
	NT2RP2001699	3.15	3.15	6.16	6.5	5.84	4.88		
30	NT2RP2001707	1.24	1.24	3.19	3.42	4.13	4.8	*	+
	NT2RP2001720	1.47	1.47	3.6	3.91	3	2.72		
	NT2RP2001721	2.26	2.26	4.57	5.53	3.96	3.66		
	NT2RP2001740	12	12	60.21	52.38	79.71	54.73		
35	NT2RP2001748	6.43	6.43	10.8	8.75	10.25	8.55		
	NT2RP2001755	5.51	5.51	4.96	3.71	4.62	2.69	*	-
	NT2RP2001762	1.25	1.25	2.01	3.87	2.56	3.52	*	+
	NT2RP2001768	1.91	1.91	4.7	6.7	5.55	4.55		
	NT2RP2001769	3.06	3.06	5.86	10.42	5.06	11.86		
	NT2RP2001784	3.62	3.62	6.23	7.06	6.02	6.91		
40	NT2RP2001805	2.33	2.33	5.61	6.02	4.93	6.6		
	NT2RP2001813	2.75	2.75	3.73	1.84	1.98	1.94	*	-
	NT2RP2001817	3.16	3.16	4.49	4.03	5.32	3.45		
	NT2RP2001818	2.72	2.72	2.45	2.35	3.62	2.66		
45	NT2RP2001837	5.13	5.13	13.43	10.29	10.16	12.33		
	NT2RP2001839	17.02	17.02	83.84	60.14	71.06	82.26		
	NT2RP2001861	2	2	6.37	3.16	3.52	3.87		
	NT2RP2001869	2.64	2.64	6.54	4.35	5.77	8.84		
	NT2RP2001876	12.15	12.15	27.71	24.54	24.93	23.67		
50	NT2RP2001878	2.32	2.32	3.96	2.95	3.32	4.95		
	NT2RP2001881	3.72	3.72	5.4	9.67	12.64	12.16	**	+
	NT2RP2001883	2.63	2.63	6.8	4.33	5.42	6.35		
	NT2RP2001884	13.59	13.59	23.56	15.33	10.54	23.6		
	NT2RP2001885	3.27	3.27	5.49	2.88	4.39	4.82		
55	NT2RP2001898	10.76	10.76	80.37	69.48	88.43	73.46		

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	NT2RP2001900	3.38	3.38	4.03	2.61	4.93	10.26	
	NT2RP2001903	3.73	3.73	7.71	5.57	5.7	8.2	
	NT2RP2001907	3.1	3.1	8.56	5.05	7.56	6.72	
5	NT2RP2001915	2.89	2.89	5.06	4.06	3.08	7.19	
	NT2RP2001921	4.04	4.04	10.3	13.02	12.45	19.33	* +
	NT2RP2001926	2.75	2.75	8.25	3.55	5.3	5.64	
	NT2RP2001933	5.65	5.65	52.55	43.62	43.55	48.58	
	NT2RP2001936	1.54	1.54	5.03	2.8	2.96	3.8	
10	NT2RP2001943	25.33	25.33	49.4	47.71	40.48	51.65	
	NT2RP2001946	3.05	3.05	4.3	3.41	4.51	6.1	
	NT2RP2001947	3.18	3.18	3.44	3.93	3.21	6.88	
	NT2RP2001948	3.59	3.59	10.79	5.71	7.29	19.72	
	NT2RP2001956	5.24	5.24	12.73	11.54	9.42	9.89	
15	NT2RP2001969	4.05	4.05	7.82	3.24	5.7	6	
	NT2RP2001976	2.9	2.9	6.39	5.68	6.95	6.41	
	NT2RP2001978	3.26	3.26	6.08	4.18	4.83	6.03	
	NT2RP2001985	2.14	2.14	3.8	2.56	4.63	2.51	
	NT2RP2001991	3.34	3.34	5.7	1.53	4.62	5.19	
20	NT2RP2001997	3.16	3.16	8.43	5.31	7.47	6.98	
	NT2RP2002015	136.21	136.21	265.98	266.8	340.89	272.43	
	NT2RP2002017	3.24	3.24	6.06	2.06	3.3	2.57	
	NT2RP2002025	6.08	6.08	51.73	31.83	26.94	37.84	
25	NT2RP2002030	6.06	6.06	11.95	9.77	8.07	8.76	
	NT2RP2002032	2.31	2.31	4.95	2.39	3.81	2.55	
	NT2RP2002033	3	3	6.71	3.53	7.57	8.05	
	NT2RP2002041	3.5	3.5	6.37	2.76	3.15	9	
	NT2RP2002046	3	3	6.88	2.99	7.4	6.01	
30	NT2RP2002047	2.71	2.71	3.86	2.06	3.87	3.83	
	NT2RP2002050	7.67	7.67	11.66	9.78	6.47	7.77	
	NT2RP2002052	3.77	3.77	8.39	6.6	3.99	6.28	
	NT2RP2002058	2.07	2.07	4.11	3.1	4.82	3.39	
	NT2RP2002060	1.48	1.48	3.44	2.1	5.9	3.18	
35	NT2RP2002063	3.61	3.61	5.83	3.3	5.2	6.65	
	NT2RP2002066	10.11	10.11	13.47	5.47	9.88	9.73	
	NT2RP2002070	3.74	3.74	6.3	2.15	3.1	3.83	
	NT2RP2002076	3.72	3.72	5.1	3.35	5.58	3.63	
	NT2RP2002078	13.09	13.09	105.74	73.87	88.51	76.08	
40	NT2RP2002079	5.76	5.76	36.34	31.87	32.66	36.54	
	NT2RP2002099	4.19	4.19	5.82	4.7	6.75	6.03	
	NT2RP2002105	2.66	2.66	12.25	11.41	14.04	11.23	
	NT2RP2002115	1.63	1.63	5.21	1.98	3.42	1.52	
	NT2RP2002124	3.66	3.66	6	4.56	5.38	3.88	
45	NT2RP2002137	3.99	3.99	4.83	2.21	2.1	1.76	** -
	NT2RP2002139	24.08	24.08	45.74	51.88	77.99	62.3	* +
	NT2RP2002154	1.37	1.37	4.13	3.56	2.36	3.2	
	NT2RP2002155	351.63	351.63	869.83	623.53	501.61	620.68	
	NT2RP2002172	1.5	1.5	3.33	2.78	3.53	5.13	
50	NT2RP2002185	3.29	3.29	7.65	7.3	8.56	8.12	
	NT2RP2002188	1.74	1.74	5.95	4.15	4.31	4.95	
	NT2RP2002192	2.9	2.9	7.6	6.65	6.42	5.83	
	NT2RP2002193	5.21	5.21	5.22	4.76	4.95	5.75	
55	NT2RP2002208	5.96	5.96	7.31	4.7	5.67	5.14	

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	NT2RP2002219	2.2	2.2	1.8	2.22	3.2	2.26		
	NT2RP2002231	1.72	1.72	3.1	4.11	2.76	5.76		
	NT2RP2002232	2.59	2.59	5.17	3.93	4.7	6.08		
5	NT2RP2002235	5.62	5.62	15.07	16.26	16.18	15.18		
	NT2RP2002239	37.02	37.02	67.99	72.09	67.21	63.77		
	NT2RP2002252	2.64	2.64	3.66	2.63	2.76	2.94		
	NT2RP2002256	4.62	4.62	15.3	11.37	16.99	12.91		
10	NT2RP2002257	7.01	7.01	22.77	18.65	25.09	20.6		
	NT2RP2002259	1.58	1.58	13.91	9.9	12.15	10.49		
	NT2RP2002264	0.6	0.6	3.14	3.2	3.12	3.92		
	NT2RP2002267	3.66	3.66	8.75	8.95	8.3	11.16		
	NT2RP2002270	4.26	4.26	8.23	16.09	10.47	14.71	*	+
15	NT2RP2002281	2.85	2.85	5.66	8.18	6.48	6.54	*	+
	NT2RP2002288	4.32	4.32	6.6	5.33	5.56	4.23		
	NT2RP2002292	5.42	5.42	8.4	6.64	8.08	6.95		
	NT2RP2002299	9.6	9.6	9.22	11.75	19.42	15.97	*	+
	NT2RP2002304	1.37	1.37	4.78	6.99	5.08	5.52		
20	NT2RP2002312	1.21	1.21	2.33	3.78	5.3	3.28	*	+
	NT2RP2002316	3.28	3.28	5.43	7.57	7.21	8.2	**	+
	NT2RP2002325	1.95	1.95	3.46	2.79	2.22	4.95		
	NT2RP2002333	2.13	2.13	3.03	3.53	4.86	5.69	*	+
	NT2RP2002371	5.43	5.43	9.14	9.72	12.07	11.65	*	+
25	NT2RP2002373	10.65	10.65	40.1	36.72	58.84	33.58		
	NT2RP2002381	4.68	4.68	2.35	2.66	3.19	3.71		
	NT2RP2002385	5.71	5.71	11.84	9.95	11.34	9.47		
	NT2RP2002394	0.94	0.94	1.52	1.24	0.96	1.26		
30	NT2RP2002408	2.7	2.7	5.08	3.89	3.12	4.29		
	NT2RP2002409	3.73	3.73	10.81	10.78	7.95	8.35		
	NT2RP2002424	2.98	2.98	4.22	5.84	6.22	7.85	*	+
	NT2RP2002426	6.44	6.44	11.38	7.59	8.46	8.93		
	NT2RP2002429	17.2	17.2	24.73	27.87	33.96	20.83		
35	NT2RP2002437	4.61	4.61	5.98	4.83	6.47	4.79		
	NT2RP2002439	3.83	3.83	6.69	2.68	3.22	4		
	NT2RP2002442	13.63	13.63	71.65	57.78	63.05	78.84		
	NT2RP2002457	3.27	3.27	5.31	4.35	4.87	5.82		
	NT2RP2002464	2.17	2.17	5.34	3.29	4.59	4.24		
40	NT2RP2002475	3.11	3.11	7.88	5.3	2.83	5.43		
	NT2RP2002479	3.09	3.09	4.25	1.95	2.99	1.93		
	NT2RP2002487	1.73	1.73	5.15	1.98	2.1	3.04		
	NT2RP2002498	1.52	1.52	2.2	2.62	2.82	4.47		
	NT2RP2002503	7.63	7.63	31.85	29.32	32.02	31.84		
45	NT2RP2002504	3.81	3.81	5.73	6	7.23	11.28		
	NT2RP2002510	2.65	2.65	8.92	4.68	6.59	6.85		
	NT2RP2002520	3.57	3.57	7.17	6.26	8.86	6.61		
	NT2RP2002527	5.18	5.18	6.02	9	12.37	11.22	**	+
	NT2RP2002533	3.34	3.34	6.27	4.83	6.94	5.88		
50	NT2RP2002537	3.22	3.22	4.02	4.09	5.91	10.08		
	NT2RP2002542	4.81	4.81	4.64	5.99	5.93	9.73		
	NT2RP2002546	4.31	4.31	5.85	6.5	4.91	5.24		
	NT2RP2002549	4.06	4.06	9.33	7.68	10.49	11.65		
	NT2RP2002564	4.11	4.11	11.18	10.67	9.21	9.29		
55	NT2RP2002591	2.45	2.45	7.03	3.31	4.79	5.79		

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	NT2RP2002595	9.67	9.67	12.41	12.06	13.39	14.79		
	NT2RP2002602	4.19	4.19	7.53	5.68	8.96	10.42		
	NT2RP2002606	1.27	1.27	2.93	2.26	2.97	3.95		
5	NT2RP2002609	6.12	6.12	9.95	4.79	5.48	7.74		
	NT2RP2002618	2.74	2.74	6.83	4.2	6.34	5.44		
	NT2RP2002621	4.24	4.24	10.22	6.58	7.52	9.79		
	NT2RP2002643	1.79	1.79	4.84	3.11	5.98	3.94		
	NT2RP2002672	4.48	4.48	9.23	8.03	9.37	9.87		
10	NT2RP2002673	4.13	4.13	5.01	8	12.88	17.73	*	+
	NT2RP2002674	2.4	2.4	4.06	2.78	2.37	1.84		
	NT2RP2002686	2.73	2.73	4.61	3.17	5.19	6.49		
	NT2RP2002688	10.73	10.73	28.07	22.34	33.34	28.71		
	NT2RP2002695	2.62	2.62	7.03	5.26	4.34	5.52		
15	NT2RP2002701	7.29	7.29	13.37	11.85	5.18	10.04		
	NT2RP2002706	3.02	3.02	5.58	6.47	8.14	6.19	*	+
	NT2RP2002710	11.2	11.2	36.97	39.43	33.9	42.75		
	NT2RP2002721	5.53	5.53	9.42	7.33	7.34	8.45		
20	NT2RP2002727	3.56	3.56	6.87	2.17	3.96	3.52		
	NT2RP2002734	3.59	3.59	6.65	5.71	7.65	7.54		
	NT2RP2002736	5.25	5.25	13.13	13.17	13.59	17.58		
	NT2RP2002740	2	2	5.11	3.18	2.81	3.13		
	NT2RP2002741	2.12	2.12	4.8	4.68	5.39	5.78		
25	NT2RP2002750	2.5	2.5	9.22	7.73	9.57	8.18		
	NT2RP2002752	4.59	4.59	10.39	7.93	7.66	8.03		
	NT2RP2002753	4.49	4.49	9.91	8.66	9.04	14.67		
	NT2RP2002760	4.79	4.79	10.31	3.56	4.5	4.13		
	NT2RP2002769	4.42	4.42	6.06	3.89	5.67	6.43		
30	NT2RP2002778	4.13	4.13	10.59	6.8	8.2	9.12		
	NT2RP2002791	8.89	8.89	54.27	48.75	53.08	50.19		
	NT2RP2002800	1.66	1.66	4.52	4	5.19	5.38		
	NT2RP2002805	3.38	3.38	5.46	4.75	6.44	3.81		
	NT2RP2002811	3.27	3.27	8.23	5.87	8.13	10.61		
35	NT2RP2002824	18.29	18.29	25.05	29.95	34.29	25.05		
	NT2RP2002839	13.26	13.26	31.21	16.09	23.42	16.27		
	NT2RP2002845	5.87	5.87	7.93	4.61	6.12	5.5		
	NT2RP2002857	2.95	2.95	3.6	2.35	4.23	2.99		
	NT2RP2002862	4.56	4.56	12.49	12.55	9.84	11.34		
40	NT2RP2002880	5.27	5.27	13.89	13.5	11.56	11.1		
	NT2RP2002885	8.6	8.6	17.12	7.56	10.07	10.02		
	NT2RP2002891	1.9	1.9	7.78	4.65	6.63	7.56		
	NT2RP2002907	2.95	2.95	6.91	5.95	5.5	4.9		
	NT2RP2002925	5.67	5.67	6.73	10.04	11.6	8.45	*	+
45	NT2RP2002927	10.08	10.08	10.63	19.05	21.85	15.48	**	+
	NT2RP2002928	4.32	4.32	4.56	2.65	2.34	2.51	**	-
	NT2RP2002929	3.96	3.96	9.74	8.09	7.86	9.87		
	NT2RP2002934	1.5	1.5	1.4	2.81	3.01	2.49	**	+
50	NT2RP2002939	2.96	2.96	5.09	5.15	6.71	4.91		
	NT2RP2002942	2.4	2.4	5.06	4.35	5.07	10.81		
	NT2RP2002954	5.41	5.41	11.46	7.21	9.1	8.65		
	NT2RP2002959	8.15	8.15	12.55	13.81	16.28	16.69	*	+
	NT2RP2002974	5.03	5.03	6.53	4.7	3.45	4.54		
55	NT2RP2002976	6.92	6.92	17.08	11.84	14.66	12.42		

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	NT2RP2002979	4.41	4.41	8.12	7.03	8.66	7.6		
	NT2RP2002980	6.44	6.44	15.09	15.56	11	17.45		
	NT2RP2002986	3.87	3.87	7.6	6.68	7.4	7.39		
5	NT2RP2002987	3.52	3.52	8.23	11.1	9.18	9.4	*	+
	NT2RP2002988	14.96	14.96	22.92	30.07	31.87	31.36	**	+
	NT2RP2002993	2.97	2.97	4.18	3.8	3.84	2.84		
	NT2RP2003000	4.88	4.88	8.34	6.97	9.62	9.97		
	NT2RP2003008	4.85	4.85	5.06	3.34	4.76	4.78		
10	NT2RP2003020	4.45	4.45	44.26	28.35	46.52	34.33		
	NT2RP2003032	1.91	1.91	4.02	5.82	6.48	6.59	**	+
	NT2RP2003034	4.21	4.21	13.47	13.16	11.15	16.31		
	NT2RP2003042	2.15	2.15	3.81	4.57	3.65	4.92		
15	NT2RP2003050	2.32	2.32	3.56	2.55	2.17	1.83		
	NT2RP2003060	7.27	7.27	15.51	21.53	18.91	17.46	*	+
	NT2RP2003073	5.61	5.61	8.73	7.06	10.51	8.17		
	NT2RP2003099	5.05	5.05	3.67	3.21	3.73	2.84		
	NT2RP2003108	3.6	3.6	4.23	5.29	3.91	6.62		
20	NT2RP2003115	1.68	1.68	5	7.75	4.69	4.84		
	NT2RP2003117	2.71	2.71	5.69	3.6	4.66	4.13		
	NT2RP2003121	1.83	1.83	3.47	4.03	2.69	3.33		
	NT2RP2003125	4.13	4.13	11.44	15.42	12.55	13.66	*	+
	NT2RP2003127	2.36	2.36	3.94	1.53	1.66	1.75		
25	NT2RP2003129	3.43	3.43	7.09	6.08	6.05	5.42		
	NT2RP2003137	4.49	4.49	6.14	7.58	8.4	6.46	*	+
	NT2RP2003138	4.66	4.66	20.24	16.55	17.45	16.92		
	NT2RP2003146	6.2	6.2	24.78	18.5	23.25	25.96		
	NT2RP2003148	3.09	3.09	6.73	3.06	4.6	4.04		
30	NT2RP2003150	1.45	1.45	5.71	3.98	5.2	4.3		
	NT2RP2003157	6.93	6.93	34.27	34.29	31.85	32.84		
	NT2RP2003158	6.3	6.3	25.32	26.87	28.69	59.31		
	NT2RP2003161	2.73	2.73	3.36	2.51	2.82	6.12		
35	NT2RP2003164	1.96	1.96	2.1	1.28	1.87	2.46		
	NT2RP2003165	2.18	2.18	5.94	3.1	3.69	4.84		
	NT2RP2003177	1.63	1.63	4.37	2.79	3.03	4.42		
	NT2RP2003179	1.23	1.23	4.98	4.08	3.63	7.96		
	NT2RP2003194	4.04	4.04	7.2	5.73	6.29	14.77		
40	NT2RP2003206	1.59	1.59	4.47	1.64	3.52	1.44		
	NT2RP2003210	5.06	5.06	15.15	16.14	12.93	15.9		
	NT2RP2003227	1.62	1.62	3.97	2.04	3.66	6.28		
	NT2RP2003228	6.57	6.57	29.53	29.56	43.94	44.24		
	NT2RP2003230	3.51	3.51	7.91	4.49	8.04	8.46		
45	NT2RP2003231	2.22	2.22	5.59	2.46	3.23	3.83		
	NT2RP2003237	2.52	2.52	4.59	4.59	6.4	6.46	*	+
	NT2RP2003239	2.3	2.3	4.46	2.97	4.46	4.05		
	NT2RP2003243	2.16	2.16	4.13	2.38	3.28	3.98		
	NT2RP2003265	3.93	3.93	5.33	4.22	4.88	4.92		
50	NT2RP2003267	2.73	2.73	3.15	3.24	4.17	7.42		
	NT2RP2003272	6.03	6.03	14.8	16.93	23.85	32.58	*	+
	NT2RP2003277	3.85	3.85	11.29	5.53	8.39	6.39		
	NT2RP2003280	3.47	3.47	9.38	7.67	7.25	6.09		
	NT2RP2003286	2.18	2.18	4.23	4.13	5	9.61		
55	NT2RP2003293	2.98	2.98	6.9	5.66	7.05	7.94		

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	NT2RP2003295	4.67	4.67	8.45	8.73	12.39	6.35		
	NT2RP2003297	3.43	3.43	7.57	4.32	6.89	5.28		
5	NT2RP2003300	20.38	20.38	32.04	45.7	53.51	48.07	**	+
	NT2RP2003302	2.88	2.88	4.52	3.46	3.81	7.26		
	NT2RP2003307	0.57	0.57	2.62	1.43	1.49	1.38		
	NT2RP2003308	1.44	1.44	4.5	2.77	4.44	5.44		
	NT2RP2003311	4.18	4.18	5.83	7.35	4.25	8.2		
10	NT2RP2003329	2.99	2.99	4.41	2.63	3.89	4.44		
	NT2RP2003339	3.06	3.06	7.01	3.76	4.92	3.64		
	NT2RP2003345	4.15	4.15	8.38	2.77	3.97	6.33		
	NT2RP2003347	2.55	2.55	4.23	2.08	1.98	3.46		
	NT2RP2003367	2.15	2.15	4.65	2.7	1.98	1.44		
15	NT2RP2003369	1.34	1.34	4.71	2.16	2.36	0.89		
	NT2RP2003383	4.05	4.05	6.75	7.66	7.17	6.99		
	NT2RP2003390	9.1	9.1	17.93	16.66	14.27	12.94		
	NT2RP2003391	9.39	9.39	12.9	11.96	9.91	12.84		
	NT2RP2003393	4.23	4.23	6.99	6.14	5.03	9.44		
20	NT2RP2003394	8.67	8.67	16.21	17.56	21.75	17.23		
	NT2RP2003401	4.39	4.39	5.97	3.52	3.72	2.9		
	NT2RP2003403	3.42	3.42	7.64	6.62	8.55	7.79		
	NT2RP2003433	3.02	3.02	15.54	13.62	13.5	13.08		
	NT2RP2003445	3.2	3.2	4.74	4.08	3.5	3.93		
25	NT2RP2003446	2.67	2.67	6.23	5.06	6.05	4.47		
	NT2RP2003456	2.04	2.04	6.57	4.26	5.89	3.81		
	NT2RP2003466	3.56	3.56	20.09	17.34	25.96	23.53		
	NT2RP2003469	6.2	6.2	5.65	6.19	7.53	6.33		
	NT2RP2003470	5.64	5.64	6.47	5.06	6.11	6.44		
30	NT2RP2003471	2.72	2.72	3.88	3.22	2.78	3.38		
	NT2RP2003480	7.15	7.15	20.74	19.77	19.89	21.14		
	NT2RP2003495	3.99	3.99	6.03	8.07	7.24	10.72	*	+
	NT2RP2003499	1.52	1.52	4.58	3.67	4.05	2.75		
	NT2RP2003505	0.98	0.98	3.21	2.62	3.88	1.4		
35	NT2RP2003506	2.54	2.54	6.53	5.65	5.36	4.78		
	NT2RP2003511	3.67	3.67	5.57	4.22	3.1	2.96		
	NT2RP2003513	3.79	3.79	6.01	5.49	5.57	5.71		
	NT2RP2003517	2.9	2.9	2.52	1.32	1.11	0.85	**	-
	NT2RP2003522	11.08	11.08	19.77	10.55	11.42	16.52		
40	NT2RP2003525	5.12	5.12	14.93	12.19	10.72	11.79		
	NT2RP2003533	3.36	3.36	10.44	12.12	10.72	12.94		
	NT2RP2003541	6.72	6.72	11.29	12.02	13.42	11.7		
	NT2RP2003543	2.48	2.48	5.96	4.17	3.55	6.54		
	NT2RP2003545	2.59	2.59	4.85	2.22	3.6	1.85		
45	NT2RP2003559	4.92	4.92	4.81	3.97	3.84	3.37	**	-
	NT2RP2003564	4.46	4.46	3.93	2.53	1.97	2.42	**	-
	NT2RP2003565	4.94	4.94	50.48	41.12	48.32	37.82		
	NT2RP2003567	3.51	3.51	16.65	16.25	19.43	16.05		
	NT2RP2003575	4.44	4.44	18.78	19.56	22.63	20.7		
50	NT2RP2003576	102.12	102.12	203.44	206.62	128.42	171.89		
	NT2RP2003579	11.45	11.45	26.58	38.62	39.51	39.88	*	+
	NT2RP2003581	3.85	3.85	6.1	4.33	4.38	3.96		
	NT2RP2003587	8.37	8.37	11.47	13.35	14.11	12.14	*	+
55	NT2RP2003590	7.15	7.15	9.08	11.06	13.15	14.91	*	+

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	NT2RP2003593	1.58	1.58	4.57	7.84	4.43	8.59		
	NT2RP2003596	4.86	4.86	10.86	14.43	13.12	17.96	*	+
	NT2RP2003599	6.49	6.49	12.46	14.29	10.17	11.98		
5	NT2RP2003600	1.88	1.88	2.95	3.02	3.64	6.36		
	NT2RP2003604	7.09	7.09	8.97	16.39	13.03	16.68	**	+
	NT2RP2003629	3.72	3.72	5.25	3.11	4.56	2.38		
	NT2RP2003630	4.09	4.09	6.66	4.79	6.78	3.84		
	NT2RP2003643	5.49	5.49	4.88	7.15	9.8	8.51	*	+
10	NT2RP2003655	4.27	4.27	11.12	7.52	6.38	7.59		
	NT2RP2003664	12.29	12.29	24.31	17.9	18.07	17.11		
	NT2RP2003668	2.52	2.52	5.01	3.3	3.18	3.62		
	NT2RP2003687	1.61	1.61	2.77	1.63	2.42	1.71		
15	NT2RP2003691	3.03	3.03	5.07	3.7	4.21	4.57		
	NT2RP2003702	3.99	3.99	6.14	2.89	3.02	2.89		
	NT2RP2003704	3.31	3.31	4.12	2.65	3.84	1.99		
	NT2RP2003706	2.44	2.44	1.24	1.72	1.42	1.6		
	NT2RP2003713	4.11	4.11	5.49	4.16	3.89	3.87		
20	NT2RP2003714	3.39	3.39	7.8	5.19	5.31	5.32		
	NT2RP2003727	3.96	3.96	11.63	4.81	6.08	10.46		
	NT2RP2003737	2.52	2.52	8.58	4.88	6.47	4.6		
	NT2RP2003751	1.66	1.66	4.84	1.24	1.67	1.37		
	NT2RP2003760	2.52	2.52	5.47	3.87	4.19	5.45		
25	NT2RP2003764	2.1	2.1	2.81	1.44	1.87	4.62		
	NT2RP2003769	5.52	5.52	11.45	7.41	8.17	10.64		
	NT2RP2003770	7.43	7.43	12.42	7.17	5.67	12.82		
	NT2RP2003777	3.44	3.44	6.78	5.01	5.6	9.57		
	NT2RP2003781	4.93	4.93	15.85	13.04	11.91	13.48		
30	NT2RP2003785	9.69	9.69	13.44	11.1	10.68	8.99		
	NT2RP2003793	9.32	9.32	9.5	8.29	13.22	10.51		
	NT2RP2003806	5.6	5.6	12.03	8.54	8.75	12.97		
	NT2RP2003825	10.73	10.73	62.01	57.88	71.84	82.78		
	NT2RP2003840	3.19	3.19	6.07	3.86	4.44	4.71		
35	NT2RP2003857	4.02	4.02	4.94	3.15	4.61	6.12		
	NT2RP2003859	1.82	1.82	6	3.35	4.16	4.21		
	NT2RP2003871	5.22	5.22	9.43	5.1	4.59	7.79		
	NT2RP2003876	3.82	3.82	8.8	5.92	5.87	7.92		
	NT2RP2003878	3.38	3.38	6.49	3.8	4.9	4.11		
40	NT2RP2003885	2.46	2.46	3.09	1.66	3.29	2.37		
	NT2RP2003898	5.39	5.39	8.91	12.3	12.73	18.25	*	+
	NT2RP2003902	5.09	5.09	10.78	8.24	8.23	10.42		
	NT2RP2003912	3.83	3.83	14.48	5.91	7.43	6.74		
	NT2RP2003931	1.81	1.81	6.03	3.95	6.86	4.42		
45	NT2RP2003940	2.31	2.31	9.51	7.1	6.2	7.3		
	NT2RP2003950	2.81	2.81	5.48	3.84	5.57	2.98		
	NT2RP2003952	1.86	1.86	5.63	2.58	4.23	2.98		
	NT2RP2003968	4.82	4.82	7.38	9.86	11.76	13.51	*	+
50	NT2RP2003976	5.35	5.35	9.56	12.56	12.6	13.2	*	+
	NT2RP2003981	3.27	3.27	7.41	4.62	2.03	4.07		
	NT2RP2003984	5.57	5.57	15.87	10.21	4.25	10.34		
	NT2RP2003986	2.79	2.79	6.22	6.29	6.32	5.17		
	NT2RP2003988	2.36	2.36	6.84	4.51	7.42	5		
55	NT2RP2004013	8.46	8.46	13.75	14.68	13.19	17		

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	NT2RP2004014	4.24	4.24	10.07	4.06	5.12	4.08		
	NT2RP2004036	6.88	6.88	14.85	14.08	19.02	16.03		
	NT2RP2004041	2.77	2.77	5.02	3.96	4.43	5.19		
5	NT2RP2004042	1.99	1.99	4.6	4.41	2.02	4.09		
	NT2RP2004049	4.68	4.68	19.13	14.24	15.5	16.3		
	NT2RP2004060	5.7	5.7	10.41	7.09	8.67	10.84		
	NT2RP2004066	2.17	2.17	4.31	3.05	4.83	3.65		
10	NT2RP2004069	3.99	3.99	7.24	3.54	6	4.26		
	NT2RP2004076	3.73	3.73	5.82	1.92	4.2	3.61		
	NT2RP2004080	4.21	4.21	9.26	4.45	6.47	6.15		
	NT2RP2004081	3.27	3.27	5.39	3.51	3.71	4.5		
	NT2RP2004098	2.32	2.32	6.48	5.4	3.1	5.75		
15	NT2RP2004108	3.82	3.82	9.56	7.18	5.89	7.56		
	NT2RP2004124	3.13	3.13	5.9	3.68	5.82	3.92		
	NT2RP2004130	3.67	3.67	9.32	5.51	9.12	8.4		
	NT2RP2004133	2.05	2.05	6.41	3.69	6.54	6.25		
	NT2RP2004141	5.72	5.72	7.15	5.14	7.05	7.05		
20	NT2RP2004142	5.33	5.33	8.1	4.18	5.45	3.93		
	NT2RP2004152	3.34	3.34	4.78	5.7	7.49	4.39		
	NT2RP2004165	3.71	3.71	8.3	5.87	5.92	6.54		
	NT2RP2004170	1.86	1.86	5.97	5.37	4.17	4.94		
	NT2RP2004172	2.93	2.93	5.24	4.69	5.58	4.26		
25	NT2RP2004176	3.45	3.45	8.4	7.77	10.21	8.98		
	NT2RP2004179	4.01	4.01	9.17	3.94	5.07	4.15		
	NT2RP2004187	3.16	3.16	6.36	3.87	3.88	4.59		
	NT2RP2004190	5.1	5.1	5.46	5.49	7.33	9.98		
30	NT2RP2004194	7.54	7.54	14.57	18.5	23.44	19.83	*	+
	NT2RP2004196	4.28	4.28	13.77	10.02	7.87	14.61		
	NT2RP2004205	2.67	2.67	8.14	8.64	6.62	7.81		
	NT2RP2004207	2.57	2.57	4.38	4.15	4.97	3.59		
	NT2RP2004226	2.09	2.09	4.95	4.11	6.15	5.33		
35	NT2RP2004232	2.79	2.79	6.52	6	6.59	5.33		
	NT2RP2004239	3.57	3.57	4.49	2.71	3.97	5.6		
	NT2RP2004240	7.07	7.07	12.57	13	15.8	8.95		
	NT2RP2004242	3.87	3.87	6.52	5.77	6.94	7.27		
	NT2RP2004245	1.74	1.74	3.47	2.42	3.29	3.15		
40	NT2RP2004270	9.77	9.77	33.78	28.39	27.43	29.48		
	NT2RP2004300	2	2	5.22	4.34	4.52	3.26		
	NT2RP2004304	6.46	6.46	15.37	17.41	12.33	13.9		
	NT2RP2004313	3.17	3.17	3.78	5.51	4.18	4.63	*	+
	NT2RP2004316	3.46	3.46	5.84	4.9	4.96	4.04		
45	NT2RP2004321	4.71	4.71	6.06	6.79	7.43	6.29	*	+
	NT2RP2004336	4.19	4.19	4.97	2.73	4.28	4.53		
	NT2RP2004339	5.3	5.3	20.89	17.11	18.07	15.39		
	NT2RP2004347	1.39	1.39	3.99	4.78	5	4.19		
	NT2RP2004364	2.26	2.26	6.52	5.08	6.72	4.76		
50	NT2RP2004365	3.18	3.18	6.58	6.68	6.34	7.7		
	NT2RP2004366	2.49	2.49	6.06	4.49	4.71	3.08		
	NT2RP2004373	8.17	8.17	14.38	7.1	7.22	5.91		
	NT2RP2004375	9.27	9.27	13.98	20.89	26.85	20.68	**	+
	NT2RP2004389	5.25	5.25	5.62	5.01	6.26	5.61		
55	NT2RP2004392	8.88	8.88	23.7	13.04	19.48	20.89		

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	NT2RP2004396	1.98	1.98	6.27	6.65	4.98	6.17		
	NT2RP2004399	5.24	5.24	8.12	12.56	7.74	9.52		
	NT2RP2004400	2.07	2.07	3.55	2.36	3.47	2		
5	NT2RP2004404	15.79	15.79	46	45.56	40.89	41.74		
	NT2RP2004410	16.64	16.64	24.04	27.99	33.46	32.69	*	+
	NT2RP2004412	5.84	5.84	6.74	7.37	9.71	7.37		
	NT2RP2004414	4.27	4.27	5.09	3.81	4.89	3.8		
10	NT2RP2004425	3.71	3.71	6.53	3.73	3.18	4.04		
	NT2RP2004447	1.93	1.93	5.68	2.75	5.22	3.56		
	NT2RP2004463	13.57	13.57	16.23	16.84	16.25	20.26		
	NT2RP2004476	9.11	9.11	12.69	11.89	12.66	15.87		
	NT2RP2004488	3.82	3.82	8.52	4.59	6.02	5.37		
15	NT2RP2004490	2.88	2.88	3.86	2.31	2.96	4.1		
	NT2RP2004495	35.59	35.59	88.76	96.31	109.31	123.5	*	+
	NT2RP2004512	4.25	4.25	7.62	5.84	6.41	7.12		
	NT2RP2004523	5.18	5.18	11.04	8.44	7.56	10.21		
	NT2RP2004524	2.19	2.19	6.33	4.97	5.32	5.56		
20	NT2RP2004536	8.99	8.99	16.96	14.1	14.51	17.51		
	NT2RP2004538	8.03	8.03	24.44	20.15	25.59	22.24		
	NT2RP2004548	4.45	4.45	9.92	7.39	9.1	10.51		
	NT2RP2004551	4.95	4.95	5.62	7.17	9.98	6.21		
25	NT2RP2004556	83.73	83.73	210.17	226.48	298.92	241.84		
	NT2RP2004568	5.19	5.19	11.18	6.52	9.16	9.99		
	NT2RP2004580	3.98	3.98	7.71	5.71	7.88	7.04		
	NT2RP2004585	11.28	11.28	49.82	36.69	46.91	64.56		
	NT2RP2004587	1.85	1.85	4.16	2.07	2.89	3		
30	NT2RP2004594	4.56	4.56	9.24	11.47	12.21	28.18		
	NT2RP2004600	3.49	3.49	5.76	2.22	3.22	3.09		
	NT2RP2004602	4.62	4.62	6.32	6	8.49	6.26		
	NT2RP2004606	392.21	392.21	581.19	612.4	897.5	764.63	*	+
	NT2RP2004614	2.92	2.92	4.73	2.69	3.63	3.81		
35	NT2RP2004648	2.52	2.52	4.96	3.24	5.01	4.12		
	NT2RP2004655	5.69	5.69	10.1	8.37	6.76	9.46		
	NT2RP2004664	3.64	3.64	5.35	3.59	4.62	5.97		
	NT2RP2004670	1.98	1.98	3.81	1.98	3.71	4.27		
	NT2RP2004675	3.37	3.37	9.29	4.08	5.87	5.33		
40	NT2RP2004681	3.46	3.46	7.56	5.72	8.92	7.55		
	NT2RP2004689	2.63	2.63	5.75	5.75	4.73	7.87		
	NT2RP2004709	3.93	3.93	7.79	4.46	2.89	5.25		
	NT2RP2004710	3.15	3.15	8.37	5.63	4.61	6.88		
	NT2RP2004721	1.79	1.79	5.99	3.39	4.41	2.78		
45	NT2RP2004736	3.26	3.26	5.81	6.11	4.79	4.63		
	NT2RP2004743	4.94	4.94	7.96	5.94	6.67	7.36		
	NT2RP2004750	6.21	6.21	17.46	11.9	15.49	11.01		
	NT2RP2004755	11.65	11.65	19.9	14.84	22.87	19.91		
	NT2RP2004767	3.54	3.54	9	4.05	5.8	4.81		
50	NT2RP2004768	3.48	3.48	29.51	18.48	18.73	19.6		
	NT2RP2004775	4.68	4.68	5.68	7.71	5.62	8.26		
	NT2RP2004791	7.23	7.23	16.58	9.33	10.24	11.68		
	NT2RP2004794	14.01	14.01	25.74	23.04	16.86	22.78		
	NT2RP2004795	5.15	5.15	7.97	6.96	5.67	11.2		
55	NT2RP2004799	6.74	6.74	10.99	5.35	8.58	6.3		

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	NT2RP2004802	6.35	6.35	11.79	6.1	7.62	6.24	
	NT2RP2004810	3.44	3.44	8.83	7.37	7.84	6.03	
	NT2RP2004816	5.58	5.58	12.1	11.22	8.76	11.15	
5	NT2RP2004837	4.13	4.13	9.89	10.43	7.23	12.98	
	NT2RP2004841	0.91	0.91	2.86	3.69	4.03	8.87	
	NT2RP2004847	3.25	3.25	13.75	13.82	13.87	17.16	
	NT2RP2004861	2.3	2.3	5.23	2.33	4.23	2.46	
10	NT2RP2004897	3.35	3.35	6.43	4.26	3.27	3.35	
	NT2RP2004932	6.64	6.64	10.16	7.96	8.53	6.91	
	NT2RP2004933	4.63	4.63	3.41	2.98	2.93	3.2	*
	NT2RP2004936	3.69	3.69	6.41	4.56	4.42	7.53	
	NT2RP2004951	2.98	2.98	10.48	5.09	5.22	19.28	
15	NT2RP2004959	3.13	3.13	6.61	6.43	6.26	6.5	
	NT2RP2004961	2.1	2.1	4.79	4.89	6.49	5.44	
	NT2RP2004962	2.27	2.27	7.28	4.5	5.57	4.47	
	NT2RP2004966	2.26	2.26	6.07	4.1	4.1	2.97	
	NT2RP2004967	3.87	3.87	6.16	4.07	4.82	3.26	
20	NT2RP2004974	5.27	5.27	5.43	3.59	3.47	3.89	**
	NT2RP2004978	2.68	2.68	5.26	4.17	6.39	5.09	
	NT2RP2004982	0.57	0.57	1.82	2.2	1.94	1.72	
	NT2RP2004985	16.03	16.03	45.34	44.65	46.12	54.4	
	NT2RP2004999	2.21	2.21	5.64	4.27	8.86	10.34	
25	NT2RP2005000	3.62	3.62	5.76	4.33	4.76	4.65	
	NT2RP2005001	5.41	5.41	7.91	8.26	9.15	8.32	
	NT2RP2005003	3.8	3.8	7.2	6.11	7.91	6.2	
	NT2RP2005012	6.61	6.61	20.14	18.41	20.96	17.87	
	NT2RP2005018	1.9	1.9	4.24	3.29	2.24	2.91	
30	NT2RP2005020	6.12	6.12	23.58	19.97	19.94	22.96	
	NT2RP2005022	1.65	1.65	5.01	5.09	7.24	4.77	
	NT2RP2005027	5.96	5.96	38.61	42.51	40.08	33.77	
	NT2RP2005031	1.54	1.54	4.99	3.94	4.53	3.92	
	NT2RP2005035	44.19	44.19	94.82	116.52	107.36	106.69	* +
35	NT2RP2005037	4.28	4.28	5.87	7.91	10.26	7.09	*
	NT2RP2005038	4.86	4.86	4.84	1.85	2.29	3.1	**
	NT2RP2005048	9.92	9.92	30.91	30.14	33.38	32.48	
	NT2RP2005069	16.01	16.01	34.88	21.99	20.63	27.64	
40	NT2RP2005073	7.36	7.36	30.35	29.36	28.24	30.33	
	NT2RP2005097	2.39	2.39	5.6	5.27	5.2	4.6	
	NT2RP2005108	1.76	1.76	3.95	2.84	4.21	7.12	
	NT2RP2005116	3.53	3.53	5.96	6.27	5.42	5.89	
	NT2RP2005126	5.88	5.88	8.31	8.9	14.96	8.51	
45	NT2RP2005135	5.08	5.08	5.22	4.65	6.59	5.47	
	NT2RP2005139	1.94	1.94	2.77	1.87	1.81	2.45	
	NT2RP2005140	3.82	3.82	4.86	12.39	6.72	8.55	* +
	NT2RP2005144	4.04	4.04	6.31	6.69	5.97	9.7	
	NT2RP2005147	2.23	2.23	5.49	5.61	6.15	6.25	
50	NT2RP2005148	2.86	2.86	5.63	3.83	6.65	4.83	
	NT2RP2005159	3.92	3.92	5.6	4.94	6.38	7.41	
	NT2RP2005162	3.23	3.23	5.56	4.57	5.4	4.21	
	NT2RP2005163	9.15	9.15	20.61	24.53	28.92	23.77	* +
	NT2RP2005168	2.87	2.87	6.14	5.24	4.79	4.88	
55	NT2RP2005181	2.64	2.64	5.42	3.4	2.11	1.98	

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	NT2RP2005204	5.4	5.4	7.81	9.08	11.94	11.81	*	+
	NT2RP2005219	4.61	4.61	9.64	7.09	10.28	8.7		
	NT2RP2005227	3.59	3.59	10.43	7.55	5.36	9.97		
5	NT2RP2005237	26.49	26.49	94.81	86.96	105.8	93.92		
	NT2RP2005239	2.24	2.24	6.07	2.62	4.27	4.34		
	NT2RP2005247	10.63	10.63	37.59	35.58	46.1	46.95		
	NT2RP2005254	4.35	4.35	9.14	5.7	6.44	6.93		
	NT2RP2005270	9.06	9.06	17.44	10.82	9.28	17.11		
10	NT2RP2005276	7.19	7.19	11.53	10.88	11.68	15.71		
	NT2RP2005287	7.98	7.98	11.97	8.37	7.7	13.36		
	NT2RP2005288	2.51	2.51	5.14	2.89	5.59	5.22		
	NT2RP2005289	4.26	4.26	8.48	6.68	9.08	7.49		
15	NT2RP2005293	5	5	6.93	13.68	14.37	15.66	**	+
	NT2RP2005315	5.79	5.79	10.64	8.04	12.95	16.68		
	NT2RP2005322	5.05	5.05	15.42	18.91	11.33	22.43		
	NT2RP2005325	8.45	8.45	18.4	15.57	13.63	20.01		
	NT2RP2005336	1.71	1.71	6.68	4.18	5.74	5.3		
20	NT2RP2005343	2.44	2.44	7.48	3.91	4.11	5.89		
	NT2RP2005344	3.39	3.39	4.83	2.37	2.67	3.32		
	NT2RP2005347	3.14	3.14	3.61	3.34	2.96	3.53		
	NT2RP2005354	6.49	6.49	11.79	10.37	13	11.38		
	NT2RP2005358	35.87	35.87	109.04	101.37	134.72	117.96		
25	NT2RP2005360	2.93	2.93	5	3.59	4.97	3.84		
	NT2RP2005378	5.27	5.27	13.12	7.54	8.7	13.93		
	NT2RP2005391	3.06	3.06	5.41	4.21	6.76	7.72		
	NT2RP2005393	1.61	1.61	6.34	4.86	6.16	4.07		
	NT2RP2005407	2.59	2.59	5.71	4.28	5.65	4.64		
30	NT2RP2005419	2.65	2.65	9.05	6.37	8.5	6.77		
	NT2RP2005425	5.63	5.63	18.38	15.27	18.89	15.46		
	NT2RP2005429	3.23	3.23	5.85	5.41	6.65	5.64		
	NT2RP2005436	4.65	4.65	10.5	7.02	4.28	4.97		
	NT2RP2005441	2.28	2.28	5.62	3.36	3.77	5.79		
35	NT2RP2005442	24.92	24.92	40.66	34.62	25.56	41.66		
	NT2RP2005444	10.72	10.72	19.24	21.92	21.07	25.56	*	+
	NT2RP2005453	2.79	2.79	7.44	2.63	4.09	3.15		
	NT2RP2005457	15.12	15.12	23.21	28.69	37.38	31.61	*	+
	NT2RP2005458	2.47	2.47	5.27	3.55	4.16	4.95		
40	NT2RP2005463	7.73	7.73	15.23	15.65	22.11	25.05	*	+
	NT2RP2005464	5.96	5.96	11.91	9.22	4.67	10.35		
	NT2RP2005465	1.81	1.81	6.69	3.86	3.75	3.74		
	NT2RP2005472	10.98	10.98	32.59	28.21	27.9	25.85		
	NT2RP2005476	5.01	5.01	8.99	7.01	6.98	6.08		
45	NT2RP2005490	7.51	7.51	21.09	18.18	25.55	23.45		
	NT2RP2005491	4.99	4.99	12.47	8.63	10.12	8.78		
	NT2RP2005495	3.56	3.56	5.77	3.38	4.55	4.3		
	NT2RP2005496	4.84	4.84	18.25	11.3	13.16	11.28		
	NT2RP2005498	2.92	2.92	7.45	5.18	5.03	4.98		
50	NT2RP2005501	2.04	2.04	5.54	3.12	4.34	2.46		
	NT2RP2005506	124.3	124.3	217.82	139.27	121.83	104.81		
	NT2RP2005509	6.97	6.97	10.45	11.4	9.61	15.73		
	NT2RP2005514	3.93	3.93	6	4.06	7.05	4.39		
55	NT2RP2005520	14.95	14.95	32.39	27.11	39.97	33.03		

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	NT2RP2005525	6.19	6.19	7.01	7.81	7.68	4.79		
	NT2RP2005531	2.18	2.18	3.33	1.67	2.12	1.9		
	NT2RP2005535	4.66	4.66	9.09	9.34	7.79	8.91		
5	NT2RP2005539	3.39	3.39	6.22	6.43	5.84	7.45		
	NT2RP2005540	3.2	3.2	7.15	4.79	5.58	6.59		
	NT2RP2005541	21.25	21.25	39.57	25.85	38.31	39.61		
	NT2RP2005549	2.69	2.69	7.66	6.72	4.85	7.11		
	NT2RP2005555	7.97	7.97	10.1	14.96	16.19	15.37	**	+
10	NT2RP2005557	4.89	4.89	8.47	4.03	6.52	6.26		
	NT2RP2005581	3.93	3.93	9.61	6.32	7.95	6.89		
	NT2RP2005586	1.56	1.56	3.18	3.21	2.92	4.74		
	NT2RP2005597	2.77	2.77	2.93	2.98	4.1	3.84		
15	NT2RP2005600	1.81	1.81	3.71	4.03	4.29	4.44	*	+
	NT2RP2005605	4.93	4.93	14.29	13.17	15.14	15.75		
	NT2RP2005614	3.06	3.06	5.62	3.68	4.11	2.45		
	NT2RP2005620	3.47	3.47	6.26	3.6	3.92	3.11		
	NT2RP2005622	6.14	6.14	5.07	6.21	7.43	4.61		
20	NT2RP2005632	5.72	5.72	10.95	11.57	10.42	14.89		
	NT2RP2005635	2.22	2.22	19.06	18.14	23.77	18.14		
	NT2RP2005637	1.53	1.53	8	3.73	3.71	4.14		
	NT2RP2005640	1.72	1.72	7.22	7.49	8.73	6.06		
	NT2RP2005645	4.68	4.68	11.8	10.61	11.47	9.67		
25	NT2RP2005651	3.45	3.45	7.88	7.64	6.78	10.15		
	NT2RP2005654	4.08	4.08	4.14	3.02	2.52	3.8		
	NT2RP2005666	4.91	4.91	5.27	4.34	7.7	4.74		
	NT2RP2005669	7.15	7.15	7.95	7.05	11.14	8.21		
	NT2RP2005670	2.35	2.35	6.91	7.77	5.04	5.2		
30	NT2RP2005671	3.12	3.12	7.83	10.77	8.9	9.78	*	+
	NT2RP2005675	7.32	7.32	37.84	34.46	40.94	40.02		
	NT2RP2005683	2.56	2.56	7.01	7.16	5.19	7.16		
	NT2RP2005690	2.84	2.84	4.48	2.82	3.74	3.4		
	NT2RP2005694	4.07	4.07	5.49	3.77	6.26	3.54		
35	NT2RP2005701	5.97	5.97	8.82	10.39	10.35	9.52	*	+
	NT2RP2005712	5.67	5.67	5.28	4.83	7.94	6.33		
	NT2RP2005719	1.86	1.86	3.26	4.42	3.8	3.76	*	+
	NT2RP2005722	4.16	4.16	11.13	13.39	15.7	15.94	*	+
	NT2RP2005723	2.71	2.71	4.2	3.65	4.58	3.67		
40	NT2RP2005726	2.55	2.55	4.13	2.86	4.01	3.22		
	NT2RP2005729	4.64	4.64	9.94	10.21	10.7	10.62		
	NT2RP2005731	3.05	3.05	3.39	2.51	2.16	1.27	*	-
	NT2RP2005732	9.41	9.41	57.73	48.37	75.21	41.64		
45	NT2RP2005737	10.75	10.75	22.28	27.16	25.02	17.59		
	NT2RP2005741	3.03	3.03	5.35	3.68	3.31	3.37		
	NT2RP2005748	1.86	1.86	5.94	3.8	3.72	2.95		
	NT2RP2005752	2.46	2.46	5.55	3.27	4.37	3.8		
	NT2RP2005753	8.45	8.45	14.76	11.12	11.69	14.45		
50	NT2RP2005763	3	3	8.03	4.22	4.77	5		
	NT2RP2005767	3.72	3.72	7.79	5.55	6.75	6.29		
	NT2RP2005773	8.11	8.11	10.02	10.6	11.59	13.37	*	+
	NT2RP2005774	4.25	4.25	12.72	6.86	12.24	14.61		
	NT2RP2005775	3.75	3.75	7.2	3.35	4.83	5.63		
55	NT2RP2005781	5.11	5.11	9.88	9.82	7.19	12.94		

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	NT2RP2005784	5.41	5.41	11.51	7.68	12.12	14.06		
	NT2RP2005789	3.98	3.98	11.24	7.89	9.52	8.86		
5	NT2RP2005799	2.45	2.45	6.35	2.64	4.67	3.7		
	NT2RP2005804	9.01	9.01	25	27.85	27.32	30.57		
	NT2RP2005812	2.63	2.63	4.83	2.9	3.89	5.21		
	NT2RP2005815	2.48	2.48	3.15	2.38	3.21	5.2		
	NT2RP2005835	5.99	5.99	11.26	7.13	13.74	11.69		
10	NT2RP2005841	2.32	2.32	10.04	4.89	7.43	11.23		
	NT2RP2005853	1.29	1.29	4.44	2.71	4.6	4.96		
	NT2RP2005857	7.37	7.37	9.87	13.46	7.93	20.27		
	NT2RP2005859	2.76	2.76	5	2.91	6.14	4.78		
	NT2RP2005860	1.41	1.41	3.54	1.45	1.89	2.22		
15	NT2RP2005863	3.03	3.03	6.55	10.76	18.29	15.94	*	+
	NT2RP2005868	3.86	3.86	5.85	5.1	6.3	7.77		
	NT2RP2005876	5.7	5.7	12.31	7.84	8.29	8.2		
	NT2RP2005878	2.26	2.26	8.44	5.25	4.95	6.32		
	NT2RP2005883	13.54	13.54	21.06	23.75	9.57	28.09		
20	NT2RP2005886	7.18	7.18	50.05	51.13	62.09	50.14		
	NT2RP2005887	3.76	3.76	6.51	4.74	8.05	4.81		
	NT2RP2005890	4.17	4.17	9.77	11.87	17.13	12.15	*	+
	NT2RP2005901	3.19	3.19	5.69	3.91	6.18	5.14		
	NT2RP2005902	3.17	3.17	4.33	4.78	4.77	6.25		
25	NT2RP2005908	3.09	3.09	7.86	4.89	3.7	6.34		
	NT2RP2005927	1.77	1.77	2.66	2.25	4.36	3.07		
	NT2RP2005933	2.5	2.5	5.59	6.4	4.77	6.42		
	NT2RP2005941	2.09	2.09	5.2	3.31	4.41	3.9		
	NT2RP2005942	4	4	6.86	3.08	4.59	4.64		
30	NT2RP2005946	4.63	4.63	9.49	5.33	7.06	6.24		
	NT2RP2005970	5.44	5.44	14	16.16	22.05	18.9	*	+
	NT2RP2005980	3.71	3.71	5.25	2.69	3.46	2.37		
	NT2RP2005994	2.99	2.99	6.76	4.28	3.28	5.14		
	NT2RP2006004	1.31	1.31	2.89	2.07	6.09	2.58		
35	NT2RP2006013	1.38	1.38	4.91	3.1	5.07	4.92		
	NT2RP2006023	8.37	8.37	17.77	20	21.43	21.14	*	+
	NT2RP2006028	5.03	5.03	10.23	7.47	9.89	9.71		
	NT2RP2006038	4.67	4.67	5.86	2.79	5.4	1.09		
40	NT2RP2006042	8.3	8.3	7.22	6.63	5.89	6.3	*	-
	NT2RP2006043	5.65	5.65	7.59	7.6	10.99	8.29		
	NT2RP2006052	1.48	1.48	4.48	4.13	3.12	4.54		
	NT2RP2006057	3.73	3.73	6.23	5.69	3.83	4.95		
	NT2RP2006064	4.16	4.16	7.73	5.86	6.81	9.08		
45	NT2RP2006068	2.76	2.76	6.75	6.8	7.81	5.81		
	NT2RP2006069	1.46	1.46	4.94	3.56	3.95	3.3		
	NT2RP2006071	8.37	8.37	7.8	9.28	10.48	9.11	*	+
	NT2RP2006090	6.62	6.62	5.78	3.27	3.55	3.64	**	-
	NT2RP2006092	3.78	3.78	8.3	6.18	8.04	7.07		
50	NT2RP2006097	14.05	14.05	40.38	31.2	25.81	40.02		
	NT2RP2006098	1.94	1.94	4.27	4.52	4.61	7.65		
	NT2RP2006099	3.84	3.84	11.02	10.65	10.99	13.34		
	NT2RP2006100	2.87	2.87	5.78	3.63	7.31	5.19		
	NT2RP2006103	2.39	2.39	5.54	2.6	3.93	1.71		
55	NT2RP2006106	6.48	6.48	21.51	18.05	24.81	22.3		

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	NT2RP2006127	3.17	3.17	4.92	1.62	1.26	1.21	*	-
	NT2RP2006134	4.25	4.25	4.41	6.08	6.7	5.47	**	+
	NT2RP2006141	3.91	3.91	7.94	7.45	6.04	9.08		
5	NT2RP2006166	3.1	3.1	10.65	9.01	8.94	7.85		
	NT2RP2006176	2.15	2.15	4.26	3.95	5.73	4.69		
	NT2RP2006181	1.68	1.68	2.84	3.21	3.14	2.45		
	NT2RP2006184	8.85	8.85	17.16	20.8	19.95	17.1		
10	NT2RP2006186	3.01	3.01	4.57	2.77	2.29	4.33		
	NT2RP2006196	5.24	5.24	7.21	5.25	5.23	4.16		
	NT2RP2006199	5.06	5.06	4.38	3.81	3.65	3.64	**	-
	NT2RP2006200	0.87	0.87	3.43	4.37	4.52	2.17		
	NT2RP2006210	20.08	20.08	59.85	75.37	70.55	96.59	*	+
15	NT2RP2006219	2.88	2.88	6.26	5.97	5.11	7.36		
	NT2RP2006224	3.7	3.7	7.55	9	7.7	8.93		
	NT2RP2006237	1.97	1.97	4.79	3.45	2.74	4.14		
	NT2RP2006238	3.9	3.9	6.33	4.2	4.69	3.93		
	NT2RP2006258	4.5	4.5	6.73	3.07	4.27	4.39		
20	NT2RP2006261	7.32	7.32	3.98	2.04	3.19	7.69		
	NT2RP2006269	4.11	4.11	7.96	9.52	5.46	9.06		
	NT2RP2006275	3.67	3.67	30.36	23.46	35.36	25.14		
	NT2RP2006282	3.16	3.16	8.89	8.85	8.4	7.05		
	NT2RP2006302	5.69	5.69	12.68	13.12	12.4	11.87		
25	NT2RP2006312	4.88	4.88	8.22	8.47	9.13	9.8		
	NT2RP2006320	4.27	4.27	9.87	6.42	9.32	9.69		
	NT2RP2006321	3.27	3.27	4.23	2.79	4.99	4.13		
	NT2RP2006323	4.1	4.1	2.59	2.39	3.6	1.83		
	NT2RP2006333	0.67	0.67	1.82	1.7	1.04	1.17		
30	NT2RP2006334	2.24	2.24	4.02	4.57	2.72	3.54		
	NT2RP2006338	2.4	2.4	5.26	4.73	5.11	4.04		
	NT2RP2006339	2.24	2.24	2.94	2.47	1.93	2.06		
	NT2RP2006355	3.61	3.61	4.59	3.14	3.39	2.22		
35	NT2RP2006365	3.3	3.3	4.44	2.42	2.6	1.3	*	-
	NT2RP2006374	16.34	16.34	111.62	108.73	174.7	73.65		
	NT2RP2006393	4.93	4.93	7.68	7.38	8	6.95		
	NT2RP2006394	8.59	8.59	17.91	11.3	11.18	15.38		
	NT2RP2006400	2.25	2.25	4.51	2.08	3.58	1.95		
40	NT2RP2006411	27.71	27.71	42.11	23.61	17.25	37.31		
	NT2RP2006429	2.22	2.22	7.3	2.82	5.3	2.21		
	NT2RP2006435	1.46	1.46	5.29	1.76	2.65	1.98		
	NT2RP2006436	2.33	2.33	6.43	4.33	5.28	3.75		
	NT2RP2006441	4.69	4.69	8.19	7.76	8.89	8.37		
45	NT2RP2006447	2.41	2.41	4.78	3.18	2.63	3.87		
	NT2RP2006454	2.58	2.58	5.38	4.39	3.37	4.03		
	NT2RP2006455	3.79	3.79	7.14	2.91	4.62	9.23		
	NT2RP2006456	1.96	1.96	5.99	2.51	4.49	3.17		
	NT2RP2006464	5.44	5.44	8.28	4.47	8.85	7.9		
50	NT2RP2006467	4.17	4.17	10	8.56	12.47	12.58		
	NT2RP2006472	5.05	5.05	6.84	7.24	6.92	7.37		
	NT2RP2006474	4.69	4.69	16.3	18.19	32.31	21.3		
	NT2RP2006475	2.5	2.5	9.54	6.14	6.86	7.66		
	NT2RP2006476	5.34	5.34	14.94	7.62	13.82	17.24		
55	NT2RP2006501	2.44	2.44	7.28	4.6	7.45	7.74		

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	NT2RP2006512	10.25	10.25	19.79	16.72	7.89	29.01	
	NT2RP2006526	2.09	2.09	5.19	2.24	2.78	2.31	
5	NT2RP2006527	3.61	3.61	7.05	4.56	6.14	6.46	
	NT2RP2006534	2.24	2.24	4.49	2.08	2.95	2.73	
	NT2RP2006537	6.08	6.08	15.7	11.72	17.73	12.82	
	NT2RP2006543	7.83	7.83	14.8	6.52	5.4	6.88	
	NT2RP2006554	1.33	1.33	3.71	1.79	3.76	2.2	
10	NT2RP2006565	3.78	3.78	8.91	5.79	8.42	7.55	
	NT2RP2006571	1.38	1.38	3.88	2.77	4.01	2.29	
	NT2RP2006573	2.1	2.1	4.02	3.05	3.6	2.41	
	NT2RP2006598	2.25	2.25	7.04	4.34	6.56	4.78	
	NT2RP2006601	24.92	24.92	35.13	38.45	45.47	31.69	
15	NT2RP3000002	5.04	5.04	6.09	4.7	5.04	8.18	
	NT2RP3000011	1.82	1.82	5.9	2.59	1.85	2.22	
	NT2RP3000014	3.29	3.29	7.66	4.22	3.06	4.95	
	NT2RP3000016	3.42	3.42	7	5.29	6.56	6.11	
	NT2RP3000022	1.71	1.71	3.93	1.72	4.68	0.59	
20	NT2RP3000024	3.74	3.74	7.03	4.31	4.92	4.06	
	NT2RP3000031	4.66	4.66	8.66	4	6.75	4.86	
	NT2RP3000034	3.76	3.76	6.24	4.44	7.13	3.23	
	NT2RP3000037	2.76	2.76	6.5	9.41	13.44	11.06	* +
	NT2RP3000040	2.04	2.04	5.96	3.21	3.46	3.56	
25	NT2RP3000041	2.15	2.15	7.35	3.71	3.01	3.16	
	NT2RP3000046	1.95	1.95	4.42	3.67	7.11	3.84	
	NT2RP3000047	3.25	3.25	5.55	5.85	6.2	5.94	
	NT2RP3000049	2.54	2.54	6.94	5.26	7.78	3.58	
	NT2RP3000050	4.99	4.99	9.03	3.76	8.5	6.22	
30	NT2RP3000051	5.99	5.99	10.69	8.51	11.19	9.72	
	NT2RP3000054	4.31	4.31	6.5	4.38	5.35	3.22	
	NT2RP3000055	1.98	1.98	4.76	3.81	2.67	3.96	
	NT2RP3000056	2.87	2.87	7.09	5.59	3.32	3.91	
	NT2RP3000059	2.54	2.54	5.1	1.89	4.07	1.6	
35	NT2RP3000063	2.18	2.18	5.51	3.34	5.19	2.27	
	NT2RP3000068	3.76	3.76	24.22	25.83	37.88	23.13	
	NT2RP3000069	17.44	17.44	20.58	22	28.87	18.2	
	NT2RP3000072	5.9	5.9	6.18	4.96	5.39	4.19	* -
	NT2RP3000080	4.38	4.38	6.72	3.78	5.28	3.93	
40	NT2RP3000085	1.9	1.9	4.84	5.13	4.66	5.5	
	NT2RP3000087	3.77	3.77	9.1	6.22	5.61	6	
	NT2RP3000092	1.92	1.92	3.6	2.72	3.2	2.52	
	NT2RP3000109	1.74	1.74	5.05	5.63	7.94	4.24	
	NT2RP3000119	4.66	4.66	14.27	11.29	13.7	14.28	
45	NT2RP3000125	3.02	3.02	5.56	3.42	4.53	2	
	NT2RP3000131	7.84	7.84	14.37	16.23	19.96	12.93	
	NT2RP3000134	5.96	5.96	9.01	6.61	7.25	6.46	
	NT2RP3000137	3.88	3.88	6.48	5.58	6.3	6.11	
	NT2RP3000142	2.87	2.87	7.77	7.28	5.03	5.31	
50	NT2RP3000148	1.84	1.84	6.28	4.9	5.04	5.34	
	NT2RP3000149	2.51	2.51	6.97	6.14	7.77	8.24	
	NT2RP3000163	2.16	2.16	6.17	3.27	3.9	2.5	
	NT2RP3000168	5.53	5.53	14.55	12.8	11.65	11.73	
55	NT2RP3000169	3.74	3.74	6.01	6.03	8.47	5.72	

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	NT2RP3000171	10.86	10.86	16.71	28.33	38.98	25.93	*	+
	NT2RP3000172	0.86	0.86	1.53	1.66	1.2	1.46		
	NT2RP3000186	4.32	4.32	10.6	19.18	15.43	15.82	*	+
5	NT2RP3000197	1.22	1.22	3.66	4.03	4.29	3.39		
	NT2RP3000201	2.4	2.4	7.2	10.49	8.4	7.88		
	NT2RP3000204	2.16	2.16	4.44	3.88	4.1	4.25		
	NT2RP3000207	2.87	2.87	4.71	3	2.6	2.45		
10	NT2RP3000216	5.38	5.38	10.1	5.87	9.5	5.73		
	NT2RP3000220	5.14	5.14	5.66	3.68	5.69	2.92		
	NT2RP3000221	2.18	2.18	5.45	6.26	6.63	5.93		
	NT2RP3000232	2.7	2.7	8.01	7.1	5.52	5.92		
	NT2RP3000233	1.55	1.55	6.01	6.9	5.91	4.06		
15	NT2RP3000234	3.23	3.23	9.09	12.89	10.4	11.41	*	+
	NT2RP3000235	1.57	1.57	3.3	2.35	2.92	1.38		
	NT2RP3000239	4.61	4.61	11.11	9.51	9.71	14.92		
	NT2RP3000247	3.25	3.25	5.82	2.92	4.04	1.96		
	NT2RP3000251	6.11	6.11	6.52	5.22	5.82	3.25		
20	NT2RP3000252	3.73	3.73	7.99	7.61	8.53	8.4		
	NT2RP3000255	2.18	2.18	2.96	3.26	3.13	1.97		
	NT2RP3000262	6.72	6.72	9.43	11.67	7.95	9.13		
	NT2RP3000266	6.47	6.47	15.5	13.38	10.83	12.64		
	NT2RP3000267	2.71	2.71	4.04	2.9	2.64	3.03		
25	NT2RP3000271	4.38	4.38	5.57	5.11	4.84	3.72		
	NT2RP3000278	7.84	7.84	56.85	48.55	82.07	42.57		
	NT2RP3000281	4.94	4.94	10.72	3.19	8.22	7.27		
	NT2RP3000292	5.63	5.63	14.1	9.17	6.77	6.93		
	NT2RP3000299	2.31	2.31	4.92	3.73	4.89	4.98		
30	NT2RP3000304	2.15	2.15	3.48	2.85	3.36	1.64		
	NT2RP3000310	7.24	7.24	24.22	18.94	23.07	19.88		
	NT2RP3000312	2.99	2.99	8.16	3.31	5.25	3.87		
	NT2RP3000320	7.06	7.06	6.17	5.25	4.74	4.74	**	-
35	NT2RP3000322	11.05	11.05	18.76	32.59	45.13	46.95	**	+
	NT2RP3000324	6.91	6.91	46.42	36.64	43.53	39.68		
	NT2RP3000326	1.95	1.95	6.17	4.02	5.75	3.53		
	NT2RP3000329	2.5	2.5	5.96	4.97	8.84	5.9		
	NT2RP3000330	4.1	4.1	6.18	4.62	5.53	6.12		
40	NT2RP3000333	3.23	3.23	7.45	4.36	5.28	4.52		
	NT2RP3000341	8.8	8.8	12.85	14.81	18.59	14.41	*	+
	NT2RP3000344	2.73	2.73	3.75	2.69	3.54	2.29		
	NT2RP3000345	3.09	3.09	3.57	1.65	1.97	2.66	*	-
	NT2RP3000348	444.59	444.59	802.63	824.62	1016.01	909.68		
45	NT2RP3000350	4.25	4.25	10.34	4.57	9.28	6.4		
	NT2RP3000359	9.53	9.53	24.44	8.54	11.36	16.62		
	NT2RP3000361	7.5	7.5	11.12	7.89	7.81	8.95		
	NT2RP3000366	7.38	7.38	14.27	9.52	11.84	16.13		
	NT2RP3000378	2.67	2.67	5.75	3.92	4.78	2.47		
50	NT2RP3000384	5.42	5.42	10.88	9.52	13.1	9.28		
	NT2RP3000389	12.54	12.54	21.49	23.95	35.02	27.32	*	+
	NT2RP3000393	3.74	3.74	6.16	5.03	4.53	4.77		
	NT2RP3000395	110.27	110.27	212	108.33	38.18	148.45		
	NT2RP3000397	2.83	2.83	5.28	2.51	5.26	3.31		
55	NT2RP3000398	3.39	3.39	10.12	11.46	11.18	12.26		

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	NT2RP3000403	3.22	3.22	9.39	10.1	8.2	8.44		
	NT2RP3000418	3.4	3.4	10.22	7.12	11.08	13.42		
5	NT2RP3000424	2.86	2.86	9.43	6.25	9.52	6.86		
	NT2RP3000427	4.65	4.65	9.05	11.55	13.43	12.35	*	+
	NT2RP3000431	2.05	2.05	4.93	3.43	3.26	3.93		
	NT2RP3000433	2.63	2.63	8.65	5.65	7.09	6.65		
	NT2RP3000436	11.39	11.39	20.93	18.76	9.35	18.86		
10	NT2RP3000439	1.4	1.4	3.61	2.54	3.56	2		
	NT2RP3000441	3.88	3.88	7.4	7.56	7.92	6.39		
	NT2RP3000444	3.31	3.31	7.29	2.36	3.25	2.2		
	NT2RP3000448	4.45	4.45	10.15	4.05	6.54	3.93		
	NT2RP3000449	2.84	2.84	4.59	3.1	3.94	2.93		
15	NT2RP3000451	1.76	1.76	5.12	3.7	5	2.96		
	NT2RP3000456	1.69	1.69	5.48	4.23	6.67	4.21		
	NT2RP3000460	18.87	18.87	36.67	24.52	25.24	26.25		
	NT2RP3000471	3.14	3.14	6.49	2.74	4.98	5.84		
	NT2RP3000477	19.96	19.96	23.67	28.98	17.78	32.78		
20	NT2RP3000478	5.86	5.86	8.95	5.21	8.98	2.6		
	NT2RP3000481	5.48	5.48	5.76	2.76	3.61	1.52	**	-
	NT2RP3000484	3.51	3.51	4.26	2.32	2.55	1.76	*	-
	NT2RP3000487	1.77	1.77	7.4	5.07	4.03	4.97		
25	NT2RP3000512	3.29	3.29	17.7	15.17	15.9	14.52		
	NT2RP3000523	13.05	13.05	30.74	31.75	27.83	34.4		
	NT2RP3000526	3.07	3.07	7.38	5.18	6.31	4.64		
	NT2RP3000527	2.83	2.83	6.5	3.76	7.25	5.03		
	NT2RP3000531	2.9	2.9	7.71	5.11	5.51	4.69		
30	NT2RP3000532	5.74	5.74	5.6	5.75	8.39	4.26		
	NT2RP3000542	6.23	6.23	8.1	7.21	7.3	6.39		
	NT2RP3000554	8.81	8.81	15.22	13.78	10.56	14.95		
	NT2RP3000561	1.21	1.21	3.51	3.11	2.76	2.25		
	NT2RP3000562	1.84	1.84	3.5	3.7	3.87	3.23		
35	NT2RP3000578	1.56	1.56	2.54	2.54	3.37	2.36		
	NT2RP3000582	1.26	1.26	4.66	2.24	2.52	0.41		
	NT2RP3000584	2.82	2.82	6.52	3.2	2.5	2.02		
	NT2RP3000586	4.08	4.08	4.59	3.28	3.9	2.87		
	NT2RP3000590	5.69	5.69	4.61	3.78	4.35	2.57		
40	NT2RP3000592	1.8	1.8	2.99	2.97	2.75	3.15		
	NT2RP3000596	2.27	2.27	4.89	4.5	3.33	3.03		
	NT2RP3000599	1.67	1.67	3.07	3.88	4.98	3.82	*	+
	NT2RP3000603	6.09	6.09	39.25	40.43	44.88	35.89		
45	NT2RP3000605	2.84	2.84	6.66	4.56	4.23	2.56		
	NT2RP3000607	5.35	5.35	7.59	5.74	8.46	7.55		
	NT2RP3000616	3.26	3.26	5.45	2.56	2.38	1.21		
	NT2RP3000621	5.18	5.18	8.48	10.28	10.29	6.01		
	NT2RP3000622	2.36	2.36	8.76	5.85	6.21	4.72		
	NT2RP3000624	1.53	1.53	3.19	3.97	3.06	2.78		
50	NT2RP3000628	2.44	2.44	8.04	10.27	7.85	5.58		
	NT2RP3000631	4.71	4.71	14.95	22.82	16.45	14.2		
	NT2RP3000632	2.35	2.35	5.5	7.78	8.91	5.91	*	+
	NT2RP3000638	6.95	6.95	17.93	11.8	11.6	9.97		
55	NT2RP3000644	25.72	25.72	48.41	57.98	72.01	52.49	*	+
	NT2RP3000645	5.85	5.85	10.48	9.84	12.55	8.43		

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	NT2RP3000652	3.39	3.39	5.34	6.22	5.9	7.74	*	+
	NT2RP3000658	2.26	2.26	5.01	6.16	4.24	4.86		
	NT2RP3000660	2.34	2.34	6.25	6.98	6.91	5.14		
5	NT2RP3000661	1.98	1.98	4.49	4.06	3.87	3.1		
	NT2RP3000665	4.79	4.79	12.26	11.83	11.92	7		
	NT2RP3000676	4.46	4.46	7.55	6.65	7.81	5.42		
	NT2RP3000677	2.87	2.87	4.13	2.44	3.07	1.54		
10	NT2RP3000681	19.85	19.85	30.12	32.94	41.51	34.34	*	+
	NT2RP3000683	2.68	2.68	9.67	6.69	7.09	6.69		
	NT2RP3000685	1.7	1.7	2.5	3.63	2.36	3.44		
	NT2RP3000690	2.77	2.77	3.29	3.82	3.75	2.72		
	NT2RP3000698	10	10	22.49	25.66	17.08	27.43		
15	NT2RP3000708	3.45	3.45	5.5	8.17	9.22	8.56	**	+
	NT2RP3000719	2.83	2.83	2.83	1.16	1.7	1.91	**	-
	NT2RP3000721	5.63	5.63	24.61	23.43	39.76	21.55		
	NT2RP3000728	3.33	3.33	2.57	1.4	1.64	1.05	**	-
	NT2RP3000730	2.06	2.06	5.04	2.76	4.23	1.86		
20	NT2RP3000733	2.87	2.87	6.32	3.48	4.47	4.25		
	NT2RP3000735	1.74	1.74	4.22	1.81	2.22	1.26		
	NT2RP3000736	2.71	2.71	6.35	3.29	5.05	3.65		
	NT2RP3000739	13.76	13.76	12.16	18.05	9.37	20.19		
	NT2RP3000742	3.89	3.89	10.06	4.54	4.97	4.43		
25	NT2RP3000753	2.29	2.29	3.9	2.17	2.65	6.3		
	NT2RP3000759	9.07	9.07	15.99	11.11	17.14	23.05		
	NT2RP3000789	1.58	1.58	5.76	4.89	4.23	3.69		
	NT2RP3000815	1.91	1.91	5.92	4.49	5.57	3.08		
	NT2RP3000818	4.35	4.35	11.29	6.64	10.49	8.27		
30	NT2RP3000820	9.01	9.01	18.49	18.58	20.1	16.9		
	NT2RP3000821	2.13	2.13	4.83	3.28	5.19	2.02		
	NT2RP3000825	1.87	1.87	4.94	1.92	1.47	2.27		
	NT2RP3000826	4.04	4.04	13.59	10.86	13.8	12.94		
	NT2RP3000836	5.33	5.33	11.61	11.55	14.11	13.3		
35	NT2RP3000838	319.2	319.2	741.74	710.2	743.55	1049.86		
	NT2RP3000839	2.35	2.35	6.67	4.53	6.38	4.36		
	NT2RP3000841	2.17	2.17	4.32	3.79	5.55	4.72		
	NT2RP3000845	3.96	3.96	8.89	5.76	6.71	7.85		
	NT2RP3000847	3.7	3.7	7.94	4.48	5.94	5.28		
40	NT2RP3000848	2.84	2.84	8.34	5.36	6.81	6.3		
	NT2RP3000850	5.67	5.67	7.04	6.58	11.29	7.47		
	NT2RP3000852	3.27	3.27	3.17	4.02	5.23	5.8	*	+
	NT2RP3000859	2.76	2.76	7.12	4.46	7.11	8.43		
	NT2RP3000861	2.58	2.58	10.51	6.13	10.36	6.43		
45	NT2RP3000862	15.29	15.29	24.16	16.36	9.81	23.13		
	NT2RP3000865	1.58	1.58	4.26	2.54	4.21	1.83		
	NT2RP3000866	2.08	2.08	5.03	2.37	3.59	5.22		
	NT2RP3000868	2.2	2.2	7.09	3.04	3.84	2.28		
50	NT2RP3000869	3.54	3.54	11.36	9.61	15.76	7.9		
	NT2RP3000871	1.75	1.75	3.79	1.81	3.24	1.94		
	NT2RP3000875	0.99	0.99	4.25	2.57	2.71	3.64		
	NT2RP3000895	2.54	2.54	5.56	2.84	3.55	4.93		
	NT2RP3000900	6.01	6.01	11.86	11.3	7.7	14.58		
55	NT2RP3000901	3.67	3.67	7.03	4.11	6.39	5.3		

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	NT2RP3000903	3.76	3.76	7.87	3.12	5.92	3.93		
	NT2RP3000904	3.83	3.83	8.67	3.05	4.87	3.16		
	NT2RP3000907	5.66	5.66	10.03	8.94	10.67	10.14		
5	NT2RP3000913	6.04	6.04	15.01	17.87	25.57	17.37	*	+
	NT2RP3000917	7.64	7.64	16.58	7.66	6.56	13.51		
	NT2RP3000919	1.99	1.99	5.15	3.5	4.3	2.68		
	NT2RP3000921	2.26	2.26	7.67	4.88	4.07	6.51		
10	NT2RP3000942	2.66	2.66	3.89	2.68	4.12	2.63		
	NT2RP3000968	70.24	70.24	87.55	105.89	110.05	115.38	**	+
	NT2RP3000974	5.36	5.36	9.06	3.21	4.48	2.64		
	NT2RP3000980	5.77	5.77	5.77	2.09	4.14	2.26	*	-
	NT2RP3000984	3.17	3.17	7.65	6.33	6.68	4.58		
15	NT2RP3000994	2.09	2.09	4.88	2.4	3.14	3.37		
	NT2RP3001001	1.46	1.46	3.45	3.75	4.14	1.31		
	NT2RP3001004	3.37	3.37	6.52	3.51	5.63	5.01		
	NT2RP3001007	4.46	4.46	9.87	10.02	10.62	6.81		
20	NT2RP3001012	2.78	2.78	5.4	4.99	6.83	3.65		
	NT2RP3001042	4.74	4.74	5.52	2.99	5.18	1.38		
	NT2RP3001044	6.26	6.26	7.12	7.16	6.76	4.92		
	NT2RP3001048	2.52	2.52	3.01	3.5	3.93	2.42		
	NT2RP3001050	1.79	1.79	4.99	4.68	5.94	4.7		
25	NT2RP3001055	6.55	6.55	15.6	16.48	12.44	20.49		
	NT2RP3001057	2.79	2.79	10.84	5.57	6.05	5.67		
	NT2RP3001061	3.18	3.18	6.57	5.03	7.85	5.42		
	NT2RP3001069	6.03	6.03	14.95	18.49	17.53	15.08		
	NT2RP3001074	4.2	4.2	7.22	8.72	10	6.64		
30	NT2RP3001078	5.11	5.11	7.29	7.51	8.72	5.18		
	NT2RP3001081	4	4	5.72	4.65	5.19	3.52		
	NT2RP3001084	2.7	2.7	7.92	6.85	6.71	6.23		
	NT2RP3001095	1.57	1.57	3.88	3.69	3.68	3.42		
	NT2RP3001096	2.52	2.52	7.33	16.78	8.08	18.7	*	+
35	NT2RP3001097	3.65	3.65	4.28	6.42	8.11	8.5	**	+
	NT2RP3001107	3.69	3.69	4.79	3.77	4.03	2.37		
	NT2RP3001109	3.2	3.2	5.5	6.01	9.56	7.26	*	+
	NT2RP3001111	4.58	4.58	4.19	3.41	3.51	2.29	*	-
40	NT2RP3001112	12.61	12.61	18.48	25.73	29.85	24.61	**	+
	NT2RP3001113	1.21	1.21	2.59	2.47	3.24	2.19		
	NT2RP3001115	1.51	1.51	3.32	2.57	3.77	2.19		
	NT2RP3001116	1.01	1.01	2.66	2.55	4.4	2.91		
	NT2RP3001119	3.69	3.69	6.75	9.07	6.67	5.44		
	NT2RP3001120	5.02	5.02	8.24	8.85	7.87	6.71		
45	NT2RP3001126	6.16	6.16	12.34	17.84	19.66	17.49	**	+
	NT2RP3001127	6.93	6.93	6.76	4.79	7.63	6.36		
	NT2RP3001133	3.95	3.95	4.95	3.95	4.16	3.62		
	NT2RP3001140	1.46	1.46	2.43	3.21	2.38	6.71		
	NT2RP3001147	3.16	3.16	6.96	16.08	14.49	13.84	**	+
50	NT2RP3001150	1.99	1.99	4.32	4.06	5.68	3.76		
	NT2RP3001152	1.7	1.7	3.29	3.15	3.62	2.51		
	NT2RP3001155	2.95	2.95	4.35	3.68	4.35	3.58		
	NT2RP3001156	4.38	4.38	6.57	2.91	5.72	5.67		
	NT2RP3001159	5.38	5.38	10.5	7.87	10.86	7.25		
55	NT2RP3001170	7.38	7.38	5.96	6.12	8.01	4.56		

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	NT2RP3001176	3.49	3.49	10.75	6.27	8.23	9.49		
	NT2RP3001195	2.35	2.35	4.81	6.79	5.79	6.22	*	+
	NT2RP3001209	3.47	3.47	5.98	5.96	4.64	5.22		
5	NT2RP3001214	1.63	1.63	4.91	3.44	3.87	3.81		
	NT2RP3001216	3.58	3.58	6.38	6.25	4.33	3.6		
	NT2RP3001221	3.33	3.33	4.27	3.07	3.06	1.79		
	NT2RP3001226	5.96	5.96	29.04	21.93	31.45	17.76		
10	NT2RP3001230	3.17	3.17	2.41	3.09	3.14	1.56		
	NT2RP3001232	1.8	1.8	4.72	2.36	3.7	2.85		
	NT2RP3001236	1.68	1.68	4.3	1.7	3.26	1.47		
	NT2RP3001239	1.58	1.58	5.21	2.81	4.31	2.01		
	NT2RP3001240	12.83	12.83	22.18	23.01	24.3	14.46		
15	NT2RP3001245	3.53	3.53	9.88	4.08	6.36	3.39		
	NT2RP3001253	2.79	2.79	4.87	3.34	4.53	5.21		
	NT2RP3001259	6.62	6.62	11.97	12.33	15.62	11.83		
	NT2RP3001260	3.74	3.74	5.15	3.45	5.44	3.97		
	NT2RP3001264	2.2	2.2	10.29	5.99	6.92	6.38		
20	NT2RP3001268	2.25	2.25	7.18	4.93	4.72	4.35		
	NT2RP3001271	7.06	7.06	16.29	13.07	12.27	14.24		
	NT2RP3001272	3.73	3.73	12.45	9.43	11.09	10.15		
	NT2RP3001274	6.08	6.08	8.09	6.72	6.35	5.11		
	NT2RP3001275	9.78	9.78	11.58	21.56	26.84	22.59	**	+
25	NT2RP3001280	3.39	3.39	5.5	3.58	5.24	4.18		
	NT2RP3001281	3.15	3.15	3.89	3.08	4.48	5.14		
	NT2RP3001288	49.31	49.31	103.24	124.07	142.92	164.41	*	+
	NT2RP3001297	6.39	6.39	42.01	37.04	42.75	41.14		
	NT2RP3001300	5.23	5.23	15.92	16.78	17.41	17.76		
30	NT2RP3001301	2.91	2.91	6.59	3.96	4.58	3.9		
	NT2RP3001307	1.76	1.76	7.67	2.07	2.81	2.06		
	NT2RP3001310	11.55	11.55	17.04	25.54	26.07	28.13	**	+
	NT2RP3001318	2.11	2.11	3.4	2.49	3.37	2.37		
	NT2RP3001322	3.58	3.58	5.23	2.62	3.84	5.48		
35	NT2RP3001325	2.7	2.7	8.39	5.82	6.82	5.58		
	NT2RP3001338	2.67	2.67	6.19	4.1	4.21	3.5		
	NT2RP3001339	2.53	2.53	5.64	3.08	4.89	2.91		
	NT2RP3001340	2.9	2.9	8.42	6.36	7.07	5.79		
40	NT2RP3001341	2.26	2.26	6.97	5.1	5.62	4.73		
	NT2RP3001354	3.22	3.22	9.77	4.28	6.93	9.35		
	NT2RP3001355	1.9	1.9	5.41	2.65	3.82	2.74		
	NT2RP3001356	2	2	5.34	2.59	3.2	3.55		
	NT2RP3001359	1.09	1.09	4.05	1.63	2.5	1.75		
45	NT2RP3001364	2.34	2.34	5.31	3.26	6.67	2.67		
	NT2RP3001373	1.12	1.12	3.22	2.1	3.74	1.71		
	NT2RP3001374	1.9	1.9	4.17	3.18	3.92	3.1		
	NT2RP3001383	3.84	3.84	8.96	3.92	6.65	3.85		
	NT2RP3001384	4.11	4.11	9.47	3.54	4.46	2.41		
50	NT2RP3001388	3.98	3.98	8.79	9.48	10.99	9.4		
	NT2RP3001392	4.61	4.61	6.19	3.91	6.14	3.23		
	NT2RP3001396	1.7	1.7	6.39	4.04	4.66	4.53		
	NT2RP3001398	2.51	2.51	6.55	3.85	7.05	2.94		
	NT2RP3001399	4.91	4.91	20.67	15.86	16.12	12.44		
55	NT2RP3001402	6.46	6.46	36.36	33.37	41.61	39.66		

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	NT2RP3001407	6.96	6.96	19.16	13.69	17.65	12.35	
	NT2RP3001416	7.92	7.92	15.88	13.02	18.3	14.72	
5	NT2RP3001420	5.33	5.33	6.4	3.27	3.64	1.8 *	-
	NT2RP3001425	3.73	3.73	4.92	4.74	5.67	3.15	
	NT2RP3001426	2.39	2.39	6.08	5.45	4.45	5.11	
	NT2RP3001427	1.82	1.82	5.61	3.46	2.89	3.59	
	NT2RP3001428	2.42	2.42	6.29	5.69	4.81	3.77	
10	NT2RP3001429	3.08	3.08	5.91	4.15	7.37	4.73	
	NT2RP3001432	2.14	2.14	6.61	3.72	4.44	3.58	
	NT2RP3001439	4.14	4.14	6.39	5.87	7.27	4.41	
	NT2RP3001441	6.45	6.45	12.63	11.13	14.61	11.2	
	NT2RP3001446	4.99	4.99	4.99	4.64	5.22	4.39	
15	NT2RP3001447	2.72	2.72	5.21	6.64	5.14	6.33	
	NT2RP3001449	3.95	3.95	11.85	16.9	14.57	13.16 *	+
	NT2RP3001453	1.84	1.84	3.66	3.5	4.4	2.81	
	NT2RP3001457	3.86	3.86	7.71	6.06	6.93	5.5	
	NT2RP3001459	2.39	2.39	6.03	2.64	2.78	1.17	
20	NT2RP3001463	2.77	2.77	6.74	5.93	5.94	3.98	
	NT2RP3001466	2.87	2.87	3.56	1.19	1.43	0.78 **	-
	NT2RP3001472	5.74	5.74	4.02	3.7	4.85	4.32	
	NT2RP3001475	3.54	3.54	7.61	6.91	6.65	7.39	
	NT2RP3001479	2.54	2.54	6.66	4.37	5.69	5.16	
25	NT2RP3001490	3.18	3.18	9.26	4.4	6.02	5.21	
	NT2RP3001492	4.36	4.36	7.84	7.59	7.08	5.72	
	NT2RP3001495	4.14	4.14	3.85	2.75	2.92	1.76 *	-
	NT2RP3001497	5.8	5.8	6.32	7.47	9.96	6.8	
30	NT2RP3001501	5.36	5.36	5.52	3.12	4.49	3.43 *	-
	NT2RP3001527	4.89	4.89	6.71	4.9	5.14	3.52	
	NT2RP3001529	1.51	1.51	3.5	4.12	3.95	4.18 *	+
	NT2RP3001538	1.78	1.78	6.2	6.93	7.81	6.23	
	NT2RP3001539	5.81	5.81	14.5	15.19	14.15	16.47	
35	NT2RP3001542	1.52	1.52	5.26	4.23	4.38	2.13	
	NT2RP3001549	4.75	4.75	11.12	14.57	11.37	13.44	
	NT2RP3001554	3.06	3.06	6.16	6.37	7.5	5.05	
	NT2RP3001560	4.96	4.96	5.73	4.67	6.35	2.36	
	NT2RP3001561	8.85	8.85	20.77	20.38	27.2	17.15	
40	NT2RP3001564	1.54	1.54	8.24	6.43	4.53	5.96	
	NT2RP3001568	2.1	2.1	7.68	11.84	10.29	8.49 *	+
	NT2RP3001575	3.94	3.94	7.24	6.39	6.97	6.16	
	NT2RP3001580	1.78	1.78	4.49	4.35	3.8	3.11	
	NT2RP3001587	4.38	4.38	8.74	10.75	10.04	7.77	
45	NT2RP3001589	3.17	3.17	8.21	5.6	7.79	4.36	
	NT2RP3001592	4.52	4.52	21.6	19	32.62	14.54	
	NT2RP3001607	3.42	3.42	1.86	1.59	2.8	1	
	NT2RP3001608	1.05	1.05	3.59	2.41	1.73	2.31	
	NT2RP3001613	3.08	3.08	2.77	3.89	2.91	3.99	
50	NT2RP3001619	4.31	4.31	8.15	7.69	6.45	7.62	
	NT2RP3001621	1.18	1.18	2.69	2.39	2.28	2.02	
	NT2RP3001629	2.58	2.58	3.28	2.68	2.41	1.7	
	NT2RP3001630	3.39	3.39	4.56	1.67	2.02	1.17 **	-
	NT2RP3001631	9.01	9.01	14.34	18.65	21.16	15.24 *	+
55	NT2RP3001634	4	4	5.29	4.51	6.89	5.11	

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	NT2RP3001642	3.71	3.71	7.45	5.77	4.41	5.09	
	NT2RP3001646	1.56	1.56	3.7	0.89	2.79	0.95	
	NT2RP3001650	2.06	2.06	5.81	4.86	7.03	2.08	
5	NT2RP3001667	4.66	4.66	11.91	6.93	9.95	5.13	
	NT2RP3001671	2.28	2.28	7.98	7.7	4.69	5.99	
	NT2RP3001672	1.33	1.33	4.55	1.66	1.47	1.72	
	NT2RP3001676	2.18	2.18	5.02	2.35	3.14	2.24	
	NT2RP3001678	2.86	2.86	9.24	5.12	5.14	6.03	
10	NT2RP3001679	6.12	6.12	9.19	6.74	4.73	6.91	
	NT2RP3001682	1.82	1.82	5.09	4.45	6.18	3.35	
	NT2RP3001685	3.02	3.02	6.74	3.52	6.53	3.01	
	NT2RP3001688	3.01	3.01	9.42	5.46	8.21	6.43	
	NT2RP3001690	3.21	3.21	4.87	2.91	3.54	2.99	
15	NT2RP3001693	5.69	5.69	10.93	16.59	18.34	16.12	** +
	NT2RP3001696	2.28	2.28	3.63	1.77	3.68	3.39	
	NT2RP3001698	35.35	35.35	79.65	85.09	91.88	105.32	
	NT2RP3001708	4.82	4.82	8.78	6.34	6.95	9.01	
20	NT2RP3001712	8.69	8.69	16.06	10.22	14.19	13	
	NT2RP3001716	1.44	1.44	5.45	2.14	3.42	2.31	
	NT2RP3001724	2.75	2.75	6	4.08	4.54	2.63	
	NT2RP3001727	11.73	11.73	38.73	39.17	49.36	31.26	
	NT2RP3001729	3.36	3.36	4.7	5.69	6.55	3.06	
25	NT2RP3001730	12.54	12.54	26.52	12.53	19.94	16.4	
	NT2RP3001733	1.46	1.46	3.04	2.09	3.7	1.62	
	NT2RP3001737	3.02	3.02	7.12	4.62	5.49	2.78	
	NT2RP3001738	1.59	1.59	8.22	3.38	6.01	3.03	
	NT2RP3001739	3.26	3.26	5.25	5.63	6.1	2.51	
30	NT2RP3001742	2.54	2.54	5.36	3.86	4.55	4.03	
	NT2RP3001751	3.61	3.61	11.54	9.94	12.82	8.76	
	NT2RP3001752	2.58	2.58	7.01	2.1	3.59	2.76	
	NT2RP3001753	5.73	5.73	9.48	10.83	15.3	13.69	* +
	NT2RP3001754	4.63	4.63	9.08	5.86	3.73	5.33	
35	NT2RP3001756	4.66	4.66	7.36	9.37	5.75	8.03	
	NT2RP3001764	2.1	2.1	3.76	2.54	4.25	2.49	
	NT2RP3001771	2.63	2.63	3.2	1.52	4.14	1.22	
	NT2RP3001777	2.59	2.59	5.99	3.25	5.19	3.26	
	NT2RP3001782	3.52	3.52	14.68	6.47	6.63	6.47	
40	NT2RP3001792	2.27	2.27	4.35	2.91	4.09	1.35	
	NT2RP3001799	1.76	1.76	5.18	5.71	6.36	5.68	
	NT2RP3001819	1.36	1.36	4.54	1.7	1.52	2.06	
	NT2RP3001829	21.63	21.63	43.14	35.64	17.14	24.87	
45	NT2RP3001836	7.31	7.31	10.67	15.24	7.26	11.37	
	NT2RP3001839	18.86	18.86	31.77	31.97	19.23	17.53	
	NT2RP3001844	4.15	4.15	11.37	8.33	9.59	8.54	
	NT2RP3001848	9.61	9.61	52.04	44.52	74.75	43.87	
	NT2RP3001854	6.41	6.41	11.29	12.86	16.75	13.26	* +
50	NT2RP3001855	2.27	2.27	3.94	1.87	1	1.74	
	NT2RP3001857	3.1	3.1	5.22	5.13	5.6	3.33	
	NT2RP3001858	1.53	1.53	4.45	4.41	6.04	2.97	
	NT2RP3001861	7.35	7.35	16.34	11.85	14.46	10.42	
	NT2RP3001866	4.35	4.35	9.63	5.52	10.42	7.93	
55	NT2RP3001871	4.82	4.82	6.34	5.55	6.38	4.55	

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	NT2RP3001874	6.8	6.8	9.73	7.72	11.19	6.14		
	NT2RP3001878	5.98	5.98	6.35	4.59	6.89	5.02		
	NT2RP3001885	3.21	3.21	5.3	5.65	5.25	4.42		
5	NT2RP3001896	1.64	1.64	3.49	3.37	2.13	2.02		
	NT2RP3001898	9.03	9.03	17.69	14.71	8.69	11.94		
	NT2RP3001899	3.21	3.21	7.33	4.52	6.9	5.81		
	NT2RP3001901	4.58	4.58	9.18	8.19	9.44	9.21		
10	NT2RP3001915	4.84	4.84	11.12	14.09	15.67	14.04	*	+
	NT2RP3001926	2.8	2.8	4.88	2.47	2.45	1.65		
	NT2RP3001929	3.74	3.74	4.06	2.56	3.38	0.86		
	NT2RP3001931	4.63	4.63	5.26	3.9	5.62	2.98		
	NT2RP3001938	2.27	2.27	5.53	4.93	3.93	4.75		
15	NT2RP3001943	3.27	3.27	5.36	5.77	6.5	5.56		
	NT2RP3001944	1.77	1.77	3.72	4.08	5.91	4.34		
	NT2RP3001945	4.25	4.25	12.2	11.86	11.78	6.11		
	NT2RP3001947	2.94	2.94	5.89	4.06	5.41	3.4		
	NT2RP3001949	4.21	4.21	8.9	10.49	11.08	8.08		
20	NT2RP3001952	23.54	23.54	43.64	48.59	88.56	41.86		
	NT2RP3001954	5.06	5.06	3.68	4.34	4.79	1.85		
	NT2RP3001956	4.97	4.97	9.44	7.76	8.22	6.29		
	NT2RP3001967	3.78	3.78	7.74	6.7	5.37	5.66		
	NT2RP3001969	1.71	1.71	2.91	4.05	4.39	3.62	*	+
25	NT2RP3001976	2.25	2.25	4.67	6.22	6.25	4.84	*	+
	NT2RP3001986	3.55	3.55	3.88	3.43	2.82	2.19		
	NT2RP3001989	3.76	3.76	5.23	2.86	3.58	2.54		
	NT2RP3002002	6.68	6.68	9.47	6.25	8.85	3.86		
	NT2RP3002004	5.02	5.02	6.23	3.79	5.74	3.55		
30	NT2RP3002007	1.29	1.29	2.3	3.46	4.05	1.69		
	NT2RP3002014	1.38	1.38	6.23	6.04	6.24	4.21		
	NT2RP3002015	3.61	3.61	10.33	14.17	9.94	8.85		
	NT2RP3002033	1.54	1.54	5.03	7.29	5.03	3.65		
35	NT2RP3002045	1.89	1.89	5.29	4.67	4.36	2.5		
	NT2RP3002054	5.26	5.26	8.12	6.27	9.17	5.42		
	NT2RP3002056	5.67	5.67	5.52	4.24	4.24	2.7	*	-
	NT2RP3002057	4.35	4.35	3.5	2.87	2.41	0.81	*	-
	NT2RP3002061	4.71	4.71	13.94	8.64	8.9	10.74		
40	NT2RP3002062	0.8	0.8	2.42	3.58	3.26	1.11		
	NT2RP3002063	5.61	5.61	10.31	9.29	9.3	7.31		
	NT2RP3002064	2.6	2.6	3.37	2.72	3.74	2.52		
	NT2RP3002071	1.6	1.6	3.91	1.99	3.29	1.45		
	NT2RP3002073	6.47	6.47	9.55	10.45	11.13	8.64		
45	NT2RP3002074	4.2	4.2	7.25	6.33	7.82	4.24		
	NT2RP3002075	7.58	7.58	11.93	21.64	30.17	18.15	*	+
	NT2RP3002077	3.81	3.81	5.95	2.48	3.05	2.78		
	NT2RP3002081	4.25	4.25	7.55	13.22	12.62	11.13	**	+
	NT2RP3002086	3.86	3.86	9.77	5.59	8.66	6.95		
50	NT2RP3002094	7.34	7.34	10.28	13.84	14.79	11.67	*	+
	NT2RP3002096	1.98	1.98	4.53	1.28	3.12	1.73		
	NT2RP3002097	3.77	3.77	6.16	6.1	8.34	6.88		
	NT2RP3002098	1.61	1.61	4.3	1.04	1.8	1.46		
	NT2RP3002102	2	2	4.86	3.11	3.4	3.16		
55	NT2RP3002106	2.74	2.74	4.98	2.83	4.9	2.51		

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	NT2RP3002108	3.69	3.69	7.8	3.11	3.39	3.15	
	NT2RP3002109	12.49	12.49	32.04	31.61	27.15	25.12	
	NT2RP3002110	36.38	36.38	54.93	55.24	58.94	46.55	
5	NT2RP3002113	11.15	11.15	13.99	10.66	15.22	11.44	
	NT2RP3002120	2.22	2.22	4.42	2.31	4.13	2.7	
	NT2RP3002121	5.93	5.93	14.39	13.38	14.39	15.06	
	NT2RP3002126	34.03	34.03	108.96	121.18	130.55	142.49	* +
	NT2RP3002128	4.06	4.06	8.23	3.36	6.87	3.92	
10	NT2RP3002130	8.29	8.29	18.59	11.69	10.7	14.03	
	NT2RP3002133	14.24	14.24	18.31	10.06	8.3	19.51	
	NT2RP3002136	10.32	10.32	15.42	12.49	17.64	17.49	
	NT2RP3002140	3.13	3.13	6.35	6.15	3.9	4.16	
	NT2RP3002142	16.86	16.86	50.85	56.54	81.25	62.65	* +
15	NT2RP3002146	4	4	7.22	5.14	9.31	6.56	
	NT2RP3002147	3.8	3.8	10.45	6.06	7.4	6.2	
	NT2RP3002151	5.62	5.62	10.64	6.27	4.43	7.33	
	NT2RP3002155	1.62	1.62	3.27	2.01	4.98	0.8	
20	NT2RP3002156	3.15	3.15	4.82	2.55	4.08	2.42	
	NT2RP3002160	1.57	1.57	3.43	1.36	3.43	1.56	
	NT2RP3002163	20.86	20.86	55.1	35.13	44.03	32.6	
	NT2RP3002165	4.17	4.17	3.67	6.21	8.31	4.86	
	NT2RP3002166	4.04	4.04	10.53	7.76	8.79	5.58	
25	NT2RP3002173	2.24	2.24	5.75	2.95	3.34	3.53	
	NT2RP3002174	8.41	8.41	15.8	13.21	7.82	14.77	
	NT2RP3002181	1.1	1.1	3.46	1.87	3.51	1.61	
	NT2RP3002185	2.69	2.69	4.51	2.94	4.35	2.61	
	NT2RP3002193	5.51	5.51	13.38	16.39	15.35	11.36	
30	NT2RP3002204	5.66	5.66	12.49	17.04	24.14	18.95	* +
	NT2RP3002244	4.03	4.03	8.29	5.28	6.11	4.8	
	NT2RP3002248	5.42	5.42	11.1	3.19	11.78	6.52	
	NT2RP3002253	2.61	2.61	9.3	9.66	11.26	6.18	
	NT2RP3002255	11.07	11.07	26.56	22.78	11.53	20.93	
35	NT2RP3002264	3.06	3.06	5.54	5.88	7.37	4.07	
	NT2RP3002267	1.26	1.26	4.33	3.1	4.65	1.82	
	NT2RP3002273	7.51	7.51	12.98	10.15	13.8	12.11	
	NT2RP3002276	5.22	5.22	7.89	3.08	7.68	3.48	
	NT2RP3002281	6.37	6.37	6.83	7.45	8.46	3.44	
40	NT2RP3002286	3	3	4.79	3.54	4.34	3.88	
	NT2RP3002297	10.62	10.62	29.36	22.26	20.57	23.93	
	NT2RP3002301	5.73	5.73	13.24	9.47	7.55	6.21	
	NT2RP3002303	3.01	3.01	6.39	5.29	6.65	4.58	
	NT2RP3002304	2.66	2.66	7.17	6.3	7.3	4.91	
45	NT2RP3002309	2.3	2.3	7.18	9.26	13	4.39	
	NT2RP3002311	4.54	4.54	6.67	3.17	4.02	1.83	
	NT2RP3002315	15.27	15.27	20.91	25.82	33.13	21.82	
	NT2RP3002319	2.37	2.37	5.06	3.07	3.51	2.38	
	NT2RP3002324	8.97	8.97	61.42	49.85	51.23	55.4	
50	NT2RP3002330	4.74	4.74	8.33	10.31	8.24	8.15	
	NT2RP3002333	5.13	5.13	14.32	13.14	13.65	8.12	
	NT2RP3002337	2.61	2.61	5.14	4.8	5.57	4.87	
	NT2RP3002342	5.16	5.16	11.56	5.52	7.51	6.43	
55	NT2RP3002343	3.38	3.38	7.29	5.8	7.03	4.13	

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	NT2RP3002351	4.32	4.32	4.55	4.38	3.9	2.55		
	NT2RP3002352	6.3	6.3	8.01	4.4	6.76	4.31		
	NT2RP3002353	3	3	4.85	4.87	6.18	5.9		
5	NT2RP3002362	5	5	11.74	15.86	11.03	10.49		
	NT2RP3002363	2.41	2.41	3.67	5.53	6.17	2.32		
	NT2RP3002377	2.61	2.61	5.47	6.8	7.31	4.73		
	NT2RP3002377	4.47	4.47	7.73	11.4	5.31	7.09		
	NT2RP3002394	5.58	5.58	7.35	7.82	10.17	4.46		
10	NT2RP3002397	3.77	3.77	4.81	2.7	3.12	1.68	*	-
	NT2RP3002399	4.61	4.61	7.69	14.65	13.02	16.16	**	+
	NT2RP3002402	2.84	2.84	6.99	8.94	8.7	6.99		
	NT2RP3002404	2.88	2.88	5.6	3.12	3.73	1.83		
15	NT2RP3002410	4.85	4.85	15.65	17.05	14.13	10.65		
	NT2RP3002411	2.98	2.98	5.68	3.7	5.29	2.85		
	NT2RP3002414	5.62	5.62	9.35	10.28	6.81	7.92		
	NT2RP3002430	5.11	5.11	14.63	18.24	19.29	14.51		
	NT2RP3002448	5.4	5.4	4.6	4.35	5.25	3.62		
20	NT2RP3002454	7.3	7.3	15.31	12.9	12.71	9.32		
	NT2RP3002455	4.62	4.62	12.11	14.31	9.11	13.25		
	NT2RP3002456	3.21	3.21	7.75	7.09	6.57	5.9		
	NT2RP3002462	2.79	2.79	4.16	4.94	6.17	4.79	*	+
	NT2RP3002469	3.84	3.84	6.38	9.24	6.78	8.07	*	+
25	NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48		
	NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59		
	NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46	**	-
	NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2		
	NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37		
30	NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07	**	+
	NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69		
	NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57		
	NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85		
	NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18		
35	NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85		
	NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65	*	-
	NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31		
	NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8	*	-
40	NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54		
	NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06		
	NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27		
	NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52		
	NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65		
45	NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74		
	NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21		
	NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06		
	NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9		
	NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16		
50	NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45	*	+
	NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97		
	NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06	**	+
	NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77		
	NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26	*	+
55	NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85		

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	NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67		
	NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64		
	NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21		
5	NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	*	+
	NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69		
	NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6		
	NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23		
	NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88		
10	NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25		
	NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2		
	NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87		
	NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47		
	NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52		
15	NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84		
	NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13		
	NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35		
	NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11		
	NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7		
20	NT2RP3002684	4	4	6.34	3.32	6.16	3.18		
	NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41		
	NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61		
	NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38		
25	NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6		
	NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72		
	NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9		
	NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69		
	NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	**	+
30	NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	*	-
	NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96		
	NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62		
	NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76		
	NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37		
35	NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54		
	NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	*	+
	NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71		
	NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	**	-
	NT2RP3002757	12	12	17.79	19.76	24.24	19.75	*	+
40	NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38		
	NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76		
	NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18		
	NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93		
	NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4		
45	NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66		
	NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	*	-
	NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	*	-
	NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49		
	NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4		
50	NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	*	+
	NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47		
	NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02		
	NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87		
55	NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12		

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	NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8	
	NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19	
	NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66	
5	NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*
	NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21	
	NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63	
	NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*
	NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*
10	NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*
	NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53	
	NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91	
	NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3	
15	NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06	
	NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93	
	NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24	
	NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07	
	NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*
20	NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*
	NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64	
	NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33	
	NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29	
25	NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49	
	NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37	
	NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12	
	NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13	
	NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51	
30	NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96	
	NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79	
	NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54	
	NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59	
	NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01	
35	NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*
	NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94	
	NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69	
	NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57	
	NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06	
40	NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42	
	NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72	
	NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06	
	NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16	
	NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04	
45	NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39	
	NT2RP3003076	2.67	2.67	9.49	5.57	6.57	4.01	
	NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43	
	NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97	
	NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25	
50	NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93	
	NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73	
	NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18	
	NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91	
	NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44	
55	NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96	

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	NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29	
	NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74	
	NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7	
5	NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72	
	NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97	
	NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94	
	NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62	
10	NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65	
	NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2	
	NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27	
	NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79	
	NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66	
15	NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36	
	NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44	
	NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64	
	NT2RP3003226	3.25	3.25	5.68	5.57	5.94	3.63	
	NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72	
20	NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89	
	NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25	
	NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08	
	NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42	
	NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47	** +
25	NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68	
	NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86	
	NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72	
	NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63	
	NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19	
30	NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48	** -
	NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78	* -
	NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23	
	NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91	
	NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55	** +
35	NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41	
	NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87	
	NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34	
	NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78	** +
	NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6	
40	NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24	
	NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65	** +
	NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45	
	NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5	
	NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63	
45	NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62	
	NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65	
	NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56	** -
	NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47	* -
	NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32	
50	NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92	
	NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03	
	NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96	
	NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85	
55	NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49	

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	NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45	
	NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03	
5	NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87	
	NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77	
	NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63	
	NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44	
	NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08	
10	NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2	
	NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07	
	NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46	** +
	NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52	
	NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28	
15	NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12	
	NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26	
	NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45	
	NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65	
	NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72	
20	NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13	
	NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19	
	NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97	
	NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83	
25	NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55	
	NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58	
	NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23	
	NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49	
	NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25	
30	NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32	
	NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22	
	NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75	
	NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58	
	NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74	
35	NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49	
	NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09	
	NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96	
	NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96	
	NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71	
40	NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4	
	NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83	
	NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53	
	NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13	
45	NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04	
	NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09	
	NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3	
	NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88	
	NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64	
50	NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55	
	NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96	
	NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29	
	NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35	* +
	NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12	
55	NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88	
	NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88	

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	NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25	
	NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27	
	NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74	
5	NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57	
	NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96	
	NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14	
	NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24	
10	NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18	
	NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45	
	NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32	
	NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6	
	NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45	
15	NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94	
	NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59	
	NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73	
	NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81	
	NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43	
20	NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06	
	NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79	*
	NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97	
	NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27	
25	NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52	
	NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76	
	NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37	
	NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96	* +
	NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24	
30	NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75	
	NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91	
	NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89	
	NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82	
	NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35	
35	NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32	* +
	NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75	
	NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55	
	NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23	
40	NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96	
	NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31	
	NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09	
	NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2	
	NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32	
45	NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05	
	NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68	
	NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88	
	NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05	** -
	NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44	* +
50	NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81	
	NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73	
	NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53	
	NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37	
	NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39	
55	NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6	
	NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42	

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	NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96	
	NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91	
5	NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85	
	NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09	
	NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06	
	NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88	
	NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49	
10	NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52	
	NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22	** +
	NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48	
	NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96	
	NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84	
15	NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92	
	NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61	
	NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05	
	NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8	
20	NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62	
	NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11	
	NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84	
	NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57	
	NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88	
25	NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01	
	NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66	* +
	NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81	
	NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67	
	NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22	
30	NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69	
	NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78	
	NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17	
	NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47	
	NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11	
35	NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33	
	NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47	
	NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47	
	NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3	
	NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79	
40	NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37	
	NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32	
	NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03	
	NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61	** +
45	NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47	
	NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55	
	NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21	
	NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97	
	NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73	
50	NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38	
	NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08	
	NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05	
	NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81	
	NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59	
55	NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5	
	NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59	

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	NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18		
	NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3	*	-
	NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95	**	-
5	NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7		
	NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28		
	NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26		
	NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09	*	+
10	NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3		
	NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28		
	NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9		
	NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77	**	-
	NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08	*	+
15	NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55		
	NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65		
	NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56		
	NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8		
20	NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8		
	NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39		
	NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01	*	-
	NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34	*	-
	NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57		
25	NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99		
	NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24	*	+
	NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83		
	NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31		
	NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34		
30	NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56		
	NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72		
	NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06		
	NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63		
	NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47		
35	NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13		
	NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48		
	NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54		
	NT2RP3004349	5	5	7.5	4.89	7.75	5.76		
40	NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18		
	NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56		
	NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85		
	NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87	*	+
	NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75		
45	NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81	*	+
	NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06		
	NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93		
	NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12		
	NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51		
50	NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83		
	NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09		
	NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38		
	NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99		
	NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63		
55	NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48		
	NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5		

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	NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61	
	NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72	
5	NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88	
	NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9	
	NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82	
	NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39	
	NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25	
10	NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08	
	NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92	
	NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88	
	NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52	
	NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82	
15	NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68	
	NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75	
	NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62	
	NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08	*
	NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38	
20	NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12	
	NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25	
	NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48	
	NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98	
	NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98	
25	NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16	* +
	NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1	
	NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79	
	NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91	
30	NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07	
	NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24	
	NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29	
	NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28	
	NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94	
35	NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27	
	NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34	
	NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39	
	NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9	
	NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1	
40	NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47	
	NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32	
	NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12	
	NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	* +
	NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34	
45	NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46	
	NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23	
	NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77	
	NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87	
50	NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98	
	NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	* +
	NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01	
	NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68	
	NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3	
55	NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05	
	NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96	

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	NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		
	NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+
	NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
5	NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
	NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
	NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
	NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
10	NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
	NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
	NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
	NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
	NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
15	NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
	NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
	NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
	NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
	NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
20	NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		
	NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
	NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
	NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
	NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
25	NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
	NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
	NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
	NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
	NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
30	NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
	NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
	NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
	NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		
35	NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
	NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
	NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
	NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
	NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
40	NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
	NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
	NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
	NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		
	NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39		
45	NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67		
	NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19		
	NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08		
	NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48		
	NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64		
50	NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78		
	NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23		
	NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94		
	NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5		
	NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61		
55	NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	*	+

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	NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92	
	NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75	
5	NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12	
	NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08	
	NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24	
	NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38	
	NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2	
10	NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48	
	NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04	
	NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13	
	NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73	
	NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83	
15	NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99	
	NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95	
	NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5	
	NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59	
20	NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03	
	NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02	
	NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79	
	NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61	
	NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08	
25	NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13	
	NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12	
	NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68	
	NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19	
	NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46	
30	NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27	
	NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48	
	NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27	
	NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67	
	NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12	** +
35	NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4	
	NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58	
	NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98	
	NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6	
40	NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37	
	NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36	
	NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98	
	NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66	** -
	NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35	* +
45	NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66	
	NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33	
	NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26	
	NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91	
	NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65	
50	NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9	* +
	NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49	
	NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39	* -
	NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51	* +
	NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12	
55	NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82	
	NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79	

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	NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82	
	NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77	
	NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3 **	-
5	NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01	
	NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52	
	NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09 *	+
	NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75	
10	NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78	
	NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03	
	NT2RP4000549	23.81	23.81	56.43	41.6	51.57	38.82	
	NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07	
	NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27	
15	NT2RP4000558	30.12	30.12	94.23	68.16	57.01	73.2	
	NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12	
	NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46 *	+
	NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56	
	NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24	
20	NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55 *	+
	NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65	
	NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59	
	NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12	
25	NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35	
	NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19	
	NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31	
	NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73	
	NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19	
30	NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49	
	NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73	
	NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12	
	NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14	
	NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71	
35	NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52	
	NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83	
	NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33 **	-
	NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83	
	NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28	
40	NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84	
	NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68	
	NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2	
	NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27	
	NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55	
45	NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67	
	NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54 *	-
	NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73	
	NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45	
50	NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62	
	NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82	
	NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22	
	NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6	
	NT2RP4000823	697.74	697.74	1127.48	923.16	1026.8	947.85	
55	NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69	
	NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91	

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	NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29		
	NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06		
5	NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65		
	NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07		
	NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43		
	NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78		
	NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24		
10	NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33		
	NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03		
	NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19		
	NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04		
	NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62		
15	NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8		
	NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	*	+
	NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97		
	NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64		
	NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95		
20	NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81		
	NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87		
	NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	*	+
	NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35		
25	NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86		
	NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	**	-
	NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18		
	NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84		
	NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47		
30	NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79		
	NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38		
	NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	*	-
	NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	*	+
35	NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53		
	NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03		
	NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62		
	NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1		
	NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85		
	NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52		
40	NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63		
	NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	**	-
	NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	**	-
	NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	*	+
	NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
45	NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
	NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
	NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
	NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
50	NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
	NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
	NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
	NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		
	NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
55	NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
	NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		

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	NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
	NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
	NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
5	NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
	NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
	NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
	NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
10	NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
	NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
	NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
	NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
	NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
15	NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
	NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
	NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
	NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
	NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
20	NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
	NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
	NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
	NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
	NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
25	NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
	NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
	NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
	NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
	NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		
30	NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
	NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
	NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
	NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
35	NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
	NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
	NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
	NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
	NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
40	NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
	NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
	NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
	NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
	NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
45	NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+
	NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
	NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
	NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
	NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
50	NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
	NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
	NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
	NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
	NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
55	NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		

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	NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97	
	NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74	
5	NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24	
	NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89	
	NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11	
	NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76	
	NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06	
10	NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62	
	NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87	
	NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42	
	NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86	
	NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08	
15	NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16	
	NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07	
	NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48	
	NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94	
	NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38	
20	NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27	
	NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32	
	NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09	
	NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12	*
25	NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76	
	NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84	
	NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8	
	NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8	
	NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41	
30	NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38	
	NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76	* +
	NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64	* -
	NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41	
	NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57	
35	NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8	
	NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97	
	NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98	
	NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19	
	NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42	
40	NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91	
	NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13	
	NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83	
	NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37	
	NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18	** +
45	NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02	
	NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27	* -
	NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05	
	NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19	
	NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98	
50	NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29	
	NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81	
	NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45	
	NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81	
55	NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02	
	NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74	

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	NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68	
	NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97	
	NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18	
5	NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13	
	NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29	
	NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24	
	NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92	
10	NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68	
	NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04	
	NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66	
	NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75	
	NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78	
15	NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7	
	NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86	
	NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02	
	NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44	** +
	NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26	
20	NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87	** -
	NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99	
	NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21	
	NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07	
	NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02	
25	NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31	
	NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53	
	NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78	
	NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87	
30	NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72	
	NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42	
	NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15	
	NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28	
	NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43	
35	NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98	
	NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3	
	NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98	
	NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97	
	NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64	
40	NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96	
	NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22	
	NT2RP4001790	2	2	5.29	3.42	2.97	2.58	
	NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34	
	NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67	
45	NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95	
	NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33	
	NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71	
	NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33	
	NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24	
50	NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5	* +
	NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3	
	NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78	
	NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71	
	NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46	
55	NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58	

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	NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39	
	NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	* +
5	NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73	
	NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91	
	NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72	
	NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92	
	NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15	
10	NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69	
	NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93	
	NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12	
	NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52	
	NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82	
15	NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89	
	NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22	
	NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55	
	NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71	
	NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77	
20	NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66	
	NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16	
	NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	* -
	NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36	
25	NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52	
	NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88	
	NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02	
	NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	* +
	NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42	
30	NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	** +
	NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36	
	NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54	
	NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5	
	NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11	
35	NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	* +
	NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37	
	NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75	
	NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41	
	NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22	
40	NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	* -
	NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27	
	NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27	
	NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97	
	NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42	
45	NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88	
	NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51	
	NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55	
	NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72	
	NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22	
50	NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65	
	NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	** +
	NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42	
	NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21	
	NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69	
55	NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88	

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	NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19
	NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58
	NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78
5	NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17
	NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41
	NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78
	NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29
10	NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98
	NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16
	NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19
	NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13
	NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56
15	NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75
	NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68
	NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97
	NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87
	NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18
20	NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64
	NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1
	NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63
	NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49
	NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48
25	NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77
	NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16
	NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93
	NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11
	NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23
30	NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82
	NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59
	NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83
	NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04
	NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87
35	NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18
	NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41
	NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42
	NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02
40	NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08
	NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58
	NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3
	NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54
	NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16 * +
45	NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28
	NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1
	NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83
	NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68
	NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62
50	NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3
	NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33
	NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06
	NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33
	NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43
55	NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46

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	NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54		
	NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06		
5	NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96		
	NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87		
	NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08	*	-
	NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91		
	NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4		
10	NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78		
	NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28		
	NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41		
	NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37	*	+
	NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8		
15	NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14		
	NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9		
	NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93		
	NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91	*	+
	NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59		
20	NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04		
	NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15		
	NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34		
	NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84	**	-
25	NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59		
	NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11		
	NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55		
	NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29		
	NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44		
30	NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88		
	NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56		
	NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17	**	-
	NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91		
	NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3		
35	NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22	*	+
	NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74		
	NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48		
	NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71		
	NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01		
40	NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88		
	OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35		
	OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05		
	OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44		
	OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73		
45	OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33		
	OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17		
	OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72		
	OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53	*	+
	OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36		
50	OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9		
	OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6		
	OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13		
	OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42		
55	OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42		
	OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04		

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	OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
	OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
	OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
5	OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+
	OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
	OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
	OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
10	OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
	OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
	OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
	OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
	OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
15	OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
	OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
	OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
	OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
	OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
20	OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
	OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
	OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+
	OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
	OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
25	OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
	OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
	OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
	OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
	OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		
30	OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
	OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
	OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
	OVARC1000209	7.99	13.69	22.32	23.42	27.81	29.16		
	OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
35	OVARC1000216	1.72	4.96	4.35	15.43	11.3	12.54	**	+
	OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
	OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
	OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
40	OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
	OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
	OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
	OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
	OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
45	OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
	OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
	OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
	OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
	OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
50	OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
	OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
	OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		
	OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
	OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
55	OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		

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	OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58		
	OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75		
5	OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44		
	OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05		
	OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83		
	OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45		
	OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03		
10	OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04		
	OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64		
	OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63	*	+
	OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16		
	OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25		
15	OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01		
	OVARC1000411	0.91	1.5	2.6	3.49	3	2.22		
	OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71		
	OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1		
	OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99	*	+
20	OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19		
	OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78	*	+
	OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36		
	OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52	**	+
	OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08	*	+
25	OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12		
	OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62		
	OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14		
	OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95		
30	OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76		
	OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78		
	OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78		
	OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39		
	OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88		
35	OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87		
	OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28		
	OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62		
	OVARC1000520	0.84	5.89	1.18	1.32	2.27	2		
	OVARC1000522	4.1	7.19	12	13.85	14.03	10.34		
40	OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69		
	OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08		
	OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83		
	OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72		
	OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34		
45	OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95		
	OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96		
	OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88		
	OVARC1000561	3.48	7.38	9.26	13	17.66	15.09	*	+
	OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69	*	+
50	OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83		
	OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58		
	OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93		
	OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23		
	OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93		
55	OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05		

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	OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+
	OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
	OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		
5	OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
	OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
	OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
	OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
10	OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
	OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
	OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
	OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
	OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
15	OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
	OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
	OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
	OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		
	OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
20	OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
	OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
	OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
	OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
	OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
25	OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
	OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
	OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
	OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
	OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
30	OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
	OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
	OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
	OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
35	OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		
	OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
	OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
	OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
	OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
40	OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
	OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
	OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
	OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		
	OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
45	OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
	OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
	OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
	OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		
	OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
50	OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
	OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
	OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
	OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
	OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
55	OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+

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	OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18	
	OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76	
	OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88	
5	OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48	
	OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35	
	OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49	
	OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24	
	OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28	
10	OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99	
	OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51	
	OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9	
	OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	* +
15	OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14	
	OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	* +
	OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22	
	OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5	
	OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53	
20	OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54	
	OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16	
	OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72	
	OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56	
	OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29	
25	OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86	
	OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47	
	OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54	
	OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45	
	OVARC1001030	96.19	101.41	143.98	119.24	154.26	133	
30	OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92	
	OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77	
	OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	* +
	OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25	
	OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4	
35	OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84	
	OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26	
	OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49	
	OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93	
	OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	* +
40	OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57	
	OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97	
	OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52	
	OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07	
45	OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79	
	OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04	
	OVARC1001078	2	5.12	2.79	3.57	3.08	2.83	
	OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	** +
	OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13	
50	OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99	
	OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05	
	OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03	
	OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22	
	OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39	
55	OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67	

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	OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28	
	OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	** +
	OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	** +
5	OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66	
	OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	** +
	OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84	
	OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64	
	OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89	
10	OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26	
	OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54	
	OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	* +
	OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06	
	OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99	
15	OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51	
	OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49	
	OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7	
	OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56	
20	OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16	
	OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96	
	OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	* +
	OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9	
	OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27	
25	OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62	
	OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63	
	OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65	
	OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4	
	OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86	
30	OVARC1001244	9.07	12.05	18	21.61	18.57	26.62	
	OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	** +
	OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49	
	OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85	
	OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94	
35	OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16	
	OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	* -
	OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26	
	OVARC1001282	0.88	3.02	3.09	1.37	1.59	2	
	OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41	
40	OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82	
	OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32	
	OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36	
	OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22	
45	OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42	
	OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02	
	OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07	
	OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	** +
	OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3	
50	OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69	
	OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78	
	OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2	
	OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69	
	OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6	
55	OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62	

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	OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1		
	OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95		
	OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18		
5	OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21		
	OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26		
	OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79	*	+
	OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1		
10	OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81		
	OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16		
	OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07	*	+
	OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18		
	OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69		
15	OVARC1001451	3.09	2	3.89	5.18	5.98	4.75	*	+
	OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13		
	OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57		
	OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09		
	OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21		
20	OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09		
	OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48	*	+
	OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03		
	OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84		
	OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48		
25	OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07		
	OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86		
	OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39		
	OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81		
30	OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23		
	OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22		
	OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23	*	+
	OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22		
	OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39		
35	OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34		
	OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1		
	OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55		
	OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2		
	OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15		
40	OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15		
	OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67		
	OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45	*	+
	OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7		
	OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79		
45	OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74		
	OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15		
	OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48		
	OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25		
	OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65		
50	OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55		
	OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4		
	OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79		
	OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01		
	OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18		
55	OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14		

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	OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
	OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
	OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
5	OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
	OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
	OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
	OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
10	OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
	OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
	OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
	OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		
	OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
15	OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
	OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
	OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
	OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
	OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
20	OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
	OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
	OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
	OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
	OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
25	OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
	OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
	OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
	OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
30	OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		
	OVARC1001873	3.09	3.78	4.68	5.47	4.42	4.73		
	OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
	OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
	OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
35	OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
	OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
	OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
	OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
	OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
40	OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
	OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
	OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
	OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		
	OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
45	OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
	OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
	OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
	OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
50	OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
	OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
	OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
	OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
	OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
	OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
55	OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+

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	OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53		
	OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43		
5	OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63		
	OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49		
	OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64		
	OVARC1002092	1.38	2.72	2.2	4	3.97	1.88		
	OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88		
10	OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35	**	+
	OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6		
	OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92		
	OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79		
	OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52		
15	OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75	*	+
	OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09		
	OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65		
	OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51		
	OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87		
20	OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64		
	OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25		
	OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12		
	OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56		
25	PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05	*	+
	PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83	*	+
	PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67		
	PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56		
	PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55		
30	PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79		
	PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56		
	PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37		
	PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74		
	PLACE1000050	2.12	5.36	9.1	9	6.55	8.25		
35	PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37		
	PLACE1000066	14.23	15	19.46	15.86	15.62	18.52		
	PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11		
	PLACE1000078	2.1	5.75	5	6.07	6.93	5.19		
	PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27		
40	PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75		
	PLACE1000094	0.7	4.18	1.72	1	3.44	2.96		
	PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65	*	+
	PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39		
45	PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71		
	PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24		
	PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82		
	PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78		
	PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29		
50	PLACE1000181	1.06	3	2.98	2.63	3.75	2.86		
	PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27		
	PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03		
	PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93		
	PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09		
55	PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22		
	PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1		

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	PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		
	PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
5	PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
	PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
	PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
	PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
	PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
10	PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
	PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
	PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		
	PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
	PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
15	PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
	PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
	PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
	PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
	PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
20	PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
	PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
	PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
	PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
	PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
25	PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		
	PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
	PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
	PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
30	PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
	PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
	PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
	PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
	PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
35	PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
	PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
	PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
	PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
	PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
40	PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
	PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
	PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		
	PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		
	PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
45	PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
	PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
	PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
	PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
	PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
50	PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
	PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
	PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
	PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
	PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
55	PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		

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	PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
	PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
	PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
5	PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
	PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
	PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
	PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
10	PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
	PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
	PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
	PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
	PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
15	PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
	PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
	PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
	PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+
	PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
20	PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
	PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
	PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
	PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
	PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
25	PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
	PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
	PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
	PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
30	PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+
	PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
	PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		
	PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
	PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
35	PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
	PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
	PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
	PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
	PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
40	PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
	PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
	PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
	PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
45	PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
	PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
	PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
	PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
	PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		
	PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
50	PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
	PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
	PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
	PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
	PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
55	PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		

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	PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
	PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
5	PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
	PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
	PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
	PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		
	PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
10	PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
	PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
	PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
	PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
	PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
15	PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
	PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		
	PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
	PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
20	PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
	PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
	PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
	PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
	PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
25	PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		
	PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
	PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
	PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
	PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
30	PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
	PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
	PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
	PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
	PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
35	PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
	PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
	PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
	PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		
40	PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
	PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
	PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
	PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
	PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
45	PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
	PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
	PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
	PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
	PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
50	PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
	PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
	PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
	PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
	PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
55	PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		
	PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		

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	PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		
	PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
5	PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
	PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
	PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
	PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
	PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
10	PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
	PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
	PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
	PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
	PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		
15	PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
	PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
	PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
	PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
20	PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
	PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
	PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
	PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
	PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
25	PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
	PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
	PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
	PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
	PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
30	PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
	PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		
	PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9		
	PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08		
35	PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71		
	PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7		
	PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32		
	PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81		
	PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28		
40	PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71		
	PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56		
	PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7		
	PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85		
	PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88		
45	PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52		
	PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37		
	PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38		
	PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1		
	PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49		
50	PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02		
	PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09		
	PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85		
	PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13		
	PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83		
55	PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13		
	PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32		

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	PLACE1001716	1.68	3	2.61	2.24	3.79	3.58		
	PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71		
	PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51		
5	PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36		
	PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16		
	PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69		
	PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31		
10	PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82		
	PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96		
	PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	*	+
	PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99		
	PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	*	+
15	PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39		
	PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54		
	PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79		
	PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69		
20	PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3		
	PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54		
	PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6		
	PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32		
	PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42		
25	PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97		
	PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73		
	PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38		
	PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99		
	PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63		
30	PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09		
	PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
	PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
	PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
	PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
35	PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
	PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
	PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		
	PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
	PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
40	PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
	PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
	PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
	PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
	PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
45	PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
	PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
	PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
	PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
50	PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
	PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+
	PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
	PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
	PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
55	PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
	PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		

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	PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
	PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
5	PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
	PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
	PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
	PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
	PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
10	PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
	PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
	PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
	PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		
	PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
15	PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
	PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+
	PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
	PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
	PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
20	PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
	PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
	PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
	PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
	PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
25	PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
	PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		
	PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
	PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
30	PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
	PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
	PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
	PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
	PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
35	PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
	PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
	PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
	PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
	PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
40	PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
	PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
	PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
	PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		
	PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
45	PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
	PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
	PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
	PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
	PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
50	PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
	PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
	PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
	PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
	PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
55	PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		

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	PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		
	PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
	PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
5	PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
	PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
	PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
	PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
	PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
10	PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
	PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
	PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
	PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
15	PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
	PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
	PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
	PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
	PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		
20	PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
	PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
	PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
	PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
	PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
25	PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
	PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
	PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
	PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
	PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
30	PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
	PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
	PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		
	PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
	PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
35	PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
	PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
	PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
	PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
40	PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
	PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
	PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
	PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		
	PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
45	PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
	PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
	PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
	PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
	PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		
50	PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
	PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
	PLACE1002822	0.58	2.51	2.06	2.2	2.87	1.94		
	PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
	PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
55	PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		

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	PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81		
	PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7		
	PLACE1002853	4.18	6.23	9.15	6.26	5.6	7		
5	PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26		
	PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	*	+
	PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09		
	PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4		
10	PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81		
	PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75		
	PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31		
	PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51		
	PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64		
15	PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02		
	PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67		
	PLACE1002967	1.34	4.83	3.19	4.37	3.52	2.81		
	PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81		
	PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05		
20	PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6		
	PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56		
	PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01		
	PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32		
25	PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	*	+
	PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76		
	PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74		
	PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01		
	PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99		
30	PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25		
	PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33		
	PLACE1003092	3.94	4.87	6.25	7	5.6	6.17		
	PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63		
	PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29		
35	PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39		
	PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	*	+
	PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19		
	PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08		
	PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34		
40	PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8		
	PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	*	+
	PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28		
	PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82		
	PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26		
45	PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52		
	PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68		
	PLACE1003176	0.47	2	1.89	2.88	1.27	1.46		
	PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36		
	PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06		
50	PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34		
	PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16		
	PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2		
	PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89		
55	PLACE1003214	0.83	1.3	2	2.15	2.44	1.81		
	PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48		

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	PLACE1003238	0.46	2.34	1.24	1.35	2	0.75		
	PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89		
	PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08		
5	PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87		
	PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58	*	+
	PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64		
	PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4		
10	PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3		
	PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47		
	PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09		
	PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76		
	PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97		
15	PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12		
	PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98		
	PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26		
	PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6	*	+
	PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97		
20	PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62		
	PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39		
	PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89		
	PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21		
	PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08		
25	PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57		
	PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27		
	PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04		
	PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04		
30	PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02		
	PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7		
	PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96		
	PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42		
	PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99		
35	PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84		
	PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61		
	PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17		
	PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79		
	PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86		
40	PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24		
	PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2		
	PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08		
	PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81		
	PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87		
45	PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39		
	PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75		
	PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19		
	PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4		
	PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88		
50	PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22		
	PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83		
	PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3		
	PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93		
	PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23		
55	PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58		

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	PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04		
	PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48		
5	PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15		
	PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23		
	PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65		
	PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53		
	PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55		
10	PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36		
	PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25		
	PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95		
	PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68		
	PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55	**	+
15	PLACE1003611	2.34	5.18	6.07	5.65	7.14	6		
	PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32		
	PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8		
	PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19		
20	PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86		
	PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44		
	PLACE1003638	1.3	2.58	3	5.21	4.19	3.13		
	PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76	*	+
	PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4		
25	PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77		
	PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11		
	PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08		
	PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76		
	PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57		
30	PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42		
	PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97	*	+
	PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44		
	PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39		
	PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16		
35	PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49		
	PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29		
	PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41		
	PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85		
	PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13	*	+
40	PLACE1003758	0.85	4.55	0.96	2	1.46	1.16		
	PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79		
	PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49		
	PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11		
	PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07		
45	PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43		
	PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43		
	PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61	**	+
	PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68		
50	PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32		
	PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54		
	PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92		
	PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31		
	PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86		
55	PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6		
	PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39		

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	PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05		
	PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92		
	PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73		
5	PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69		
	PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03		
	PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38	*	+
	PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3		
10	PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68		
	PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87		
	PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6		
	PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29		
	PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59		
15	PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84		
	PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75		
	PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32		
	PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09		
	PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78		
20	PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21		
	PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57		
	PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62		
	PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15		
	PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91		
25	PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04	*	+
	PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44	*	+
	PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45		
	PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14		
30	PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71		
	PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29		
	PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93		
	PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5		
	PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01		
35	PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73		
	PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12		
	PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31		
	PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53		
	PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48		
40	PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2		
	PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79		
	PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76		
	PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36		
	PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84		
45	PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65		
	PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35		
	PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83		
	PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64		
50	PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22	*	+
	PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93		
	PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37		
	PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64		
	PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11		
	PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65		
55	PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15		

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	PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82		
	PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74		
5	PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04		
	PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02		
	PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49		
	PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15		
	PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1		
10	PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83		
	PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12		
	PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78		
	PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52		
	PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75	*	+
15	PLACE1004325	2.43	6.38	3.84	3.85	3.66	4		
	PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01		
	PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71		
	PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69		
	PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03		
20	PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46		
	PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1		
	PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67		
	PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04		
	PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74	**	+
25	PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85		
	PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58		
	PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44		
	PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24		
30	PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62		
	PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05	*	+
	PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15		
	PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37		
	PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41		
35	PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39		
	PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7		
	PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88		
	PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18		
	PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24	**	+
40	PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75		
	PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48		
	PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14		
	PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21		
	PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17		
45	PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15		
	PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3		
	PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82		
	PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03		
	PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18		
50	PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16		
	PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22		
	PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83		
	PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51	*	+
	PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52		
55	PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09		

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	PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65	
	PLACE1004547	5	7.61	7.82	8.66	11.2	10.28	
	PLACE1004548	1.69	6.73	4.43	6.93	8.48	6.5	
5	PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15	
	PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95	
	PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82	
	PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34	
	PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49	
10	PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97	
	PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99	
	PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	* +
	PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17	
15	PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29	
	PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59	
	PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28	
	PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22	
	PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01	
20	PLACE1004658	2.4	7.34	6.31	6.64	8.37	6	
	PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89	
	PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14	
	PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25	
	PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39	
25	PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	* +
	PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72	
	PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75	
	PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97	
	PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1	
30	PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47	
	PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98	
	PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26	
	PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51	
35	PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63	
	PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78	
	PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2	
	PLACE1004743	1.31	4.04	3.1	1.97	4	3.55	
	PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06	
40	PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22	
	PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72	
	PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72	
	PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07	
	PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4	
45	PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25	
	PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88	
	PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22	
	PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45	
	PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1	
50	PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44	
	PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84	
	PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85	
	PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3	
	PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49	
55	PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68	

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	PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37		
	PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33		
5	PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36		
	PLACE1004868	0.81	2.97	2.04	1.62	2.23	2		
	PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77		
	PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93		
	PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33		
10	PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03		
	PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44		
	PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6		
	PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03		
	PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	**	+
15	PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79		
	PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64		
	PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	*	+
	PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5		
	PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36		
20	PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04		
	PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4		
	PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01		
	PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76		
25	PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62		
	PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24		
	PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75		
	PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65		
	PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2		
30	PLACE1005003	2.85	4.22	6	6.05	6.37	5.78		
	PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85		
	PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17		
	PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62		
	PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16		
35	PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68		
	PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	*	+
	PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	*	+
	PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	*	+
	PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33		
40	PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1		
	PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1		
	PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62		
	PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	**	+
	PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	*	+
45	PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45		
	PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79		
	PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46		
	PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14		
	PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39		
50	PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8		
	PLACE1005108	2	6.08	5.87	6.58	6.19	5.09		
	PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15		
	PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54		
	PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98		
55	PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44		

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	PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
	PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
5	PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
	PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
	PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
	PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
	PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		
10	PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
	PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
	PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
	PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
	PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
15	PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
	PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+
	PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
	PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
	PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
20	PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
	PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
	PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		
	PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
	PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
25	PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
	PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
	PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
	PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
30	PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
	PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
	PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
	PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
	PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
35	PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
	PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
	PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
	PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
	PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		
40	PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
	PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
	PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
	PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
	PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
45	PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
	PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
	PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
	PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
	PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
50	PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
	PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
	PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		
	PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28		
	PLACE1005467	3.09	11.87	7	5.57	11.63	7.28		
55	PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28		

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	PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46	
	PLACE1005477	1.58	2.26	2.51	3	2.93	2.74	
5	PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53	
	PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44	
	PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06	
	PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62	
	PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91	
10	PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49	
	PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49	
	PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98	
	PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78	
	PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83	
15	PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71	
	PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33	
	PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67	
	PLACE1005536	1.74	1	2.74	3.12	2.43	2.88	
	PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22	
20	PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57	
	PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27	
	PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86	
	PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17	
	PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7	
25	PLACE1005563	0.51	4	1.89	1.45	2.07	1.06	
	PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09	
	PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22	
	PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03	
30	PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02	
	PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89	
	PLACE1005601	2	5.66	4.22	3.77	4	4.02	
	PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94	
	PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46	
35	PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89	
	PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26	
	PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61	
	PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	** +
	PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18	
40	PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55	
	PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25	
	PLACE1005648	3	8.11	9.21	8.34	10.59	8.22	
	PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67	
	PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58	
45	PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32	
	PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34	
	PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19	
	PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97	
50	PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6	
	PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47	
	PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38	
	PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76	
	PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29	
55	PLACE1005727	2.97	4.54	4.15	3.9	3.49	4	
	PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28	

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	PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
	PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
	PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
5	PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
	PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
	PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
	PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
10	PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
	PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
	PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
	PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
	PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
15	PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
	PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
	PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
	PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
	PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
20	PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
	PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
	PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
	PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
	PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
25	PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
	PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
	PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
	PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
	PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		
30	PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
	PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
	PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
	PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
	PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
35	PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
	PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
	PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
	PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
40	PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
	PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
	PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
	PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
	PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
45	PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
	PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
	PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
	PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
	PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
50	PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
	PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
	PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
	PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
	PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
55	PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		

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	PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91		
	PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58		
5	PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29		
	PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77		
	PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25		
	PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47		
	PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93		
10	PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69		
	PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75		
	PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11		
	PLACE1006093	0.49	3.76	1	3.56	3.85	1.83		
	PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91		
15	PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03		
	PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65		
	PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58		
	PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	*	+
	PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44		
20	PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04		
	PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21		
	PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13		
	PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68		
	PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22		
25	PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48		
	PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87		
	PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19		
	PLACE1006197	2.12	5.6	5.24	4	3.47	3.39		
30	PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5		
	PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28		
	PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5		
	PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35		
	PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	*	+
35	PLACE1006223	1.55	1.46	3.19	1.39	3	1.64		
	PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99		
	PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29		
	PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41		
	PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28		
40	PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33		
	PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82		
	PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4		
	PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33		
	PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53		
45	PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88		
	PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21		
	PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13		
	PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55		
	PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	**	+
50	PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01		
	PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	**	+
	PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56		
	PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92		
	PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2		
55	PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62		

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	PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		
	PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
	PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
5	PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
	PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
	PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
	PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
10	PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
	PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
	PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
	PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
	PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
15	PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
	PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
	PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
	PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
	PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
20	PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
	PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
	PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
	PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
	PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
25	PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
	PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
	PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
	PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
	PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
30	PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
	PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
	PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
	PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
	PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
35	PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
	PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
	PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
	PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
40	PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
	PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
	PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
	PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		
	PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
45	PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
	PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
	PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
	PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
	PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
50	PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
	PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
	PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
	PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
	PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
55	PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		

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	PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
	PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
	PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
5	PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
	PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
	PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
	PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
	PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
10	PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
	PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
	PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
	PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
15	PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
	PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
	PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
	PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
	PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
20	PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
	PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
	PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
	PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
	PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
25	PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
	PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
	PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
	PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
	PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		
30	PLACE1006860	1	4.29	1.62	1.61	2.1	1		
	PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
	PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
	PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
35	PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
	PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
	PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
	PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
	PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
40	PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		
	PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
	PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
	PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
	PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
45	PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
	PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
	PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
	PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
	PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
50	PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
	PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
	PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
	PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		
55	PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
	PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		

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	PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45		
	PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74		
	PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43		
5	PLACE1007053	4.9	6.69	10	3.59	4.91	4.71		
	PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69		
	PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3		
	PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	*	+
10	PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43		
	PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37		
	PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99		
	PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34		
	PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97		
15	PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04		
	PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72		
	PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
	PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
20	PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
	PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
	PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
	PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
	PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
25	PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
	PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
	PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
	PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
	PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
30	PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		
	PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
	PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
	PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
	PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
35	PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
	PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
	PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
	PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
	PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
40	PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
	PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
	PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
	PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
45	PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
	PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
	PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+
	PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
	PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
50	PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
	PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
	PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
	PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
	PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
55	PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
	PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		

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	PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51	
	PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8	
	PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02	
5	PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52	
	PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	* +
	PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91	
	PLACE1007450	0.79	1.22	2.65	3	2.99	2.39	
10	PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45	
	PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61	
	PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58	
	PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92	
	PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69	
15	PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46	
	PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11	
	PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42	
	PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9	
20	PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96	
	PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24	
	PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1	
	PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61	
	PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4	
25	PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41	
	PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59	
	PLACE1007565	0.37	2.27	1	1	1.16	0.91	
	PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	** +
30	PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09	
	PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07	
	PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71	
	PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5	
	PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41	
35	PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38	
	PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53	
	PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63	
	PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37	
	PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95	
40	PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13	
	PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9	
	PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4	
	PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91	
	PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98	
45	PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61	
	PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8	
	PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08	
	PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75	
	PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49	
50	PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39	
	PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99	
	PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32	
	PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17	
55	PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03	
	PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97	
	PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94	

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	PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58	
	PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17	
	PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87	
5	PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29	
	PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27	
	PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3	
	PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44	
10	PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06	
	PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39	
	PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39	
	PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86	
	PLACE1007845	1.76	3	4.11	3.45	3.42	2.36	
15	PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5	
	PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25	
	PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24	
	PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	** +
	PLACE1007866	19.42	25.98	40.48	43	80.39	56.73	
20	PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08	
	PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53	
	PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9	
	PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93	
25	PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01	
	PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41	
	PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24	
	PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54	
	PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94	
30	PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63	
	PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51	
	PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05	
	PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22	
	PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8	
35	PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17	
	PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21	
	PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92	
	PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88	
	PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66	
40	PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51	
	PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02	
	PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16	
	PLACE1008045	0.4	4.07	1.54	1.75	2	1.65	
45	PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78	
	PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86	
	PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23	
	PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74	
	PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68	
50	PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04	
	PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	* +
	PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5	
	PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91	
	PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63	
55	PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8	
	PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46	

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	PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
	PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
5	PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
	PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
	PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
	PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
	PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
10	PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
	PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
	PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
	PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
	PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
15	PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
	PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		
	PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
	PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		
	PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38		
20	PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21		
	PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65		
	PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29		
	PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83		
	PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49		
25	PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96		
	PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91		
	PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1		
	PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35		
30	PLACE1008359	1.57	4.11	2.89	2	2.97	2.94		
	PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95		
	PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68		
	PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24		
	PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76		
35	PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33		
	PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33		
	PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26		
	PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4		
	PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65		
40	PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27	*	+
	PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71		
	PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32		
	PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84		
	PLACE1008430	1.63	4.85	3.04	2.93	3.52	3		
45	PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57		
	PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17		
	PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92		
	PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87		
50	PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47		
	PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48		
	PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1		
	PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8		
	PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51		
55	PLACE1008524	1.04	11.09	1.72	2	3.22	2.02		
	PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72		

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	PLACE1008532	2.12	3	5.51	5.66	4.72	4.19		
	PLACE1008533	2.01	4	4.07	5.53	5.18	3.77		
	PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72		
5	PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53		
	PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47		
	PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38		
	PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21		
10	PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6		
	PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31		
	PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57		
	PLACE1008603	5.9	7.25	31	30.55	43.67	29.76		
	PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16		
15	PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03		
	PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95		
	PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7		
	PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41		
	PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51		
20	PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94		
	PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24		
	PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91		
	PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13		
25	PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2		
	PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47		
	PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65		
	PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	*	+
	PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45		
30	PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8		
	PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41		
	PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74		
	PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61		
	PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17		
35	PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06		
	PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	*	+
	PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96		
	PLACE1008798	1.71	3.82	4.45	6	5.93	3.32		
40	PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8		
	PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04		
	PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3		
	PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1		
	PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54		
45	PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6		
	PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49		
	PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82		
	PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24		
	PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28		
50	PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06		
	PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66		
	PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71		
	PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44		
	PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84		
55	PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17		
	PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7		

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	PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
	PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
5	PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
	PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
	PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
	PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
	PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
10	PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49		
	PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
	PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
	PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
	PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
15	PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
	PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
	PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		
	PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
	PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
20	PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
	PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
	PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
	PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
25	PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
	PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
	PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
	PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
	PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
30	PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		
	PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38		
	PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06		
	PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91		
	PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65		
35	PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99		
	PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91		
	PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23		
	PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46		
	PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13		
40	PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05		
	PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17		
	PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63		
	PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55		
	PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34		
45	PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5		
	PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17		
	PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01		
	PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57		
50	PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84		
	PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	*	+
	PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19		
	PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53		
	PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72		
55	PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96		
	PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94		

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	PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
	PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
	PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
5	PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
	PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		
	PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
	PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
10	PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
	PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
	PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
	PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
	PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
15	PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
	PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		
	PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
	PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
	PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
20	PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
	PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
	PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
	PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
	PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
25	PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
	PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
	PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
	PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
30	PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
	PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
	PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
	PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
	PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
35	PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
	PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
	PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
	PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
	PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
40	PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
	PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
	PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
	PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
	PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
45	PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
	PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
	PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
	PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
50	PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
	PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
	PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
	PLACE1009731	1.36	3.59	3	3.58	6.53	5		
	PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
55	PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
	PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		

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	PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68	
	PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39	
5	PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75	
	PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89	
	PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74	
	PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03	
	PLACE1009798	1.59	5.37	4	6.26	5.57	5.67	
10	PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92	
	PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59	
	PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56	
	PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11	
	PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73	
15	PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32	
	PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34	
	PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72	
	PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94	
	PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9	
20	PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15	
	PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47	
	PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57	
	PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04	
	PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5	
25	PLACE1009931	2.78	5.21	9	8.71	6.93	8.09	
	PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5	
	PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03	
	PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9	
	PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45	
30	PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96	
	PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68	
	PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23	
	PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64	
35	PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46	
	PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68	
	PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68	
	PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06	
	PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14	
40	PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82	
	PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19	
	PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64	
	PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37	
	PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05	
45	PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3	
	PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09	
	PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22	
	PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82	
	PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85	
50	PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59	*
	PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26	
	PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48	
	PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2	
	PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57	
55	PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82	

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	PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
	PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
	PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
5	PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
	PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
	PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
	PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
10	PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
	PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
	PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
	PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
	PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
15	PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
	PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
	PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
	PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
	PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
20	PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
	PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
	PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
	PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
	PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
25	PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
	PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
	PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
	PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
	PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		
30	PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
	PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
	PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
	PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
	PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
35	PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
	PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
	PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
	PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
40	PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
	PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
	PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
	PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
	PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
45	PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
	PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
	PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
	PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
	PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
50	PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
	PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
	PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
	PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
	PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
55	PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		

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	PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24		
	PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64		
	PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2		
5	PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45		
	PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51		
	PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63		
	PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26		
10	PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52		
	PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13		
	PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51		
	PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81		
	PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*	+
15	PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22		
	PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22		
	PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5		
	PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29		
	PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67		
20	PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	*	+
	PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22		
	PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61		
	PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75		
25	PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2		
	PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25		
	PLACE1010713	7	10.81	14.7	9.14	8.16	15.14		
	PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47		
	PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93		
30	PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61		
	PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49		
	PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93		
	PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21		
	PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53		
35	PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08		
	PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42		
	PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34		
	PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21		
	PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17		
40	PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93		
	PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3		
	PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18		
	PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7		
	PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81		
45	PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09		
	PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13		
	PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59		
	PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56		
	PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94		
50	PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62		
	PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51		
	PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95		
	PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47		
55	PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85		
	PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2		

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	PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56		
	PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
5	PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
	PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
	PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
	PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
	PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
10	PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
	PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
	PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
	PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
	PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
15	PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
	PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
	PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
	PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		
20	PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
	PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
	PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
	PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
	PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
25	PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
	PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
	PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
	PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
	PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
30	PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
	PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
	PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		
	PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
	PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
35	PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
	PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
	PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
	PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
	PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
40	PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
	PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
	PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
	PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		
	PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
45	PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
	PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
	PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
	PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		
50	PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
	PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
	PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
	PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
	PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
55	PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
	PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		

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	PLACE1011278	2.42	5	6.12	3.98	4.84	4.31		
	PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08		
5	PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95		
	PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05		
	PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48		
	PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73		
	PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33		
10	PLACE1011325	0.63	4.2	1.84	2	2.74	1.59		
	PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04	*	+
	PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47		
	PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43		
15	PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41		
	PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57		
	PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06		
	PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33		
	PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62		
20	PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93		
	PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77		
	PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38		
	PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02		
	PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72		
25	PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99		
	PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27		
	PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68		
	PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85		
	PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59		
30	PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67		
	PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01		
	PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27		
	PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15		
	PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5		
35	PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35		
	PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74		
	PLACE1011514	5.86	11.61	11.98	13	17.7	13.17		
	PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63		
40	PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01		
	PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9		
	PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48		
	PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08		
	PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87		
45	PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77		
	PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28		
	PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03		
	PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94		
	PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71	**	+
50	PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19		
	PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09		
	PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14		
	PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76	*	+
	PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46		
55	PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75		
	PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46		

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	PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
	PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
5	PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
	PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
	PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
	PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
	PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
10	PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
	PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
	PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
	PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
	PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		
15	PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
	PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		
	PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22		
	PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47		
	PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75		
20	PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07		
	PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23		
	PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95		
	PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84		
	PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49		
25	PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35		
	PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65		
	PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64		
	PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97	*	+
	PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26		
30	PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32		
	PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76		
	PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98		
	PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28		
35	PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64		
	PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88	**	+
	PLACE1011940	6.13	7.58	12.68	5.73	7	7.23		
	PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01		
	PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46		
40	PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14		
	PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35		
	PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99		
	PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57		
	PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86		
45	PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91		
	PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8		
	PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03		
	PLACE20000003	1.18	3.64	6.86	7.38	8.12	8.92		
	PLACE20000005	1.16	2.41	2.16	2.76	2.03	1.89		
50	PLACE20000006	2.52	4.13	15.6	11.34	16.58	13.4		
	PLACE20000007	0.96	4.85	4.24	3.94	5.13	3.33		
	PLACE20000011	1.72	3.27	3.34	4.3	5.06	3.62		
	PLACE20000014	4.04	5.93	23.94	27.19	30.87	30.97	*	+
	PLACE20000015	1.27	4.79	3.52	2.77	3.31	2.69		
55	PLACE20000017	0.48	4.78	2.15	2.65	2.56	2.45		

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	PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61
	PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71
5	PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97
	PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32
	PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37
	PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
	PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
10	PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
	PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
	PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
	PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
	PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
15	PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
	PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
	PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
	PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
	PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
20	PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
	PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
	PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
	PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
25	PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
	PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
	PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
	PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
	PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
30	PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
	PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
	PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
	PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
	PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
35	PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
	PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
	PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05
	PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42
	PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19
40	PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68
	PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3
	PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56
	PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48
	PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47
45	PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97
	PLACE2000246	1.93	2	6.06	4.58	5.09	3.93
	PLACE2000264	0.67	1.39	1.85	2.45	3.74	3 * +
	PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1
	PLACE2000287	0.81	4.44	1.49	2	2.59	1.34
50	PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69
	PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45
	PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02
	PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4
	PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3
55	PLACE2000334	3.52	5	6.6	7.33	8.12	5.88

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	PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76		
	PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65		
	PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16		
5	PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49		
	PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55		
	PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	*	+
	PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37		
10	PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61		
	PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17		
	PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32		
	PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19		
	PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49		
15	PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04		
	PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56		
	PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49		
	PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24		
	PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	*	+
20	PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35		
	PLACE2000399	3.7	6.82	7.01	7.15	7	6.79		
	PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9		
	PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47		
	PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68		
25	PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37		
	PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	*	+
	PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2		
	PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47		
	PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46		
30	PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5		
	PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15		
	PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63		
	PLACE2000455	0.24	2.62	1.24	1.65	2	1.82		
	PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24		
35	PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	*	+
	PLACE2000465	1.43	6.72	6	6.51	8.27	6.31		
	PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74		
	PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97		
	PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2		
40	PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95		
	PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82		
	PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04		
	PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05		
45	PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94		
	PLACE3000059	0.57	5	2.42	0.75	2.8	1.27		
	PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75		
	PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55		
	PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57		
50	PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37		
	PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95		
	PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64		
	PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18		
	PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59		
55	PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01		

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	PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13		
	PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96		
	PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34		
5	PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38		
	PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44		
	PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04		
	PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81		
10	PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72		
	PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77		
	PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+
	PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12		
	PLACE3000181	1.06	2.14	3.94	3.22	2.62	3		
15	PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42		
	PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21		
	PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43		
	PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63		
	PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23		
20	PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84		
	PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05		
	PLACE3000215	1.88	5.02	5.71	4.74	5	3.03		
	PLACE3000218	0	1.63	1.18	0.97	0.62	0.31		
25	PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+
	PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99		
	PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28		
	PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68		
	PLACE3000230	0.83	3.46	1.36	2	2.8	1.73		
30	PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+
	PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39		
	PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29		
	PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64		
	PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27		
35	PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+
	PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+
	PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78		
	PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5		
	PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+
40	PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4		
	PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32		
	PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09		
	PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17		
	PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31		
45	PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11		
	PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+
	PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+
	PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+
	PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71		
50	PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+
	PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39		
	PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07		
	PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12		
55	PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3		
	PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15		

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	PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29	
	PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22	
	PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05	
5	PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82	
	PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4	* +
	PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79	
	PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01	
10	PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42	
	PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52	
	PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72	
	PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92	
	PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14	
15	PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91	
	PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21	
	PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42	
	PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31	
20	PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84	
	PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82	
	PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19	
	PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25	
	PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91	
	PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86	
25	PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02	
	PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71	
	PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73	
	PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84	
	PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98	
30	PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94	
	PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9	
	PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21	
	PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4	
	PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78	
35	PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22	
	PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61	
	PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07	
	PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84	
40	PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76	
	PLACE4000192	1.3	2.27	3.6	2.36	2	1.25	
	PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02	
	PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44	
	PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69	
45	PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5	
	PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38	
	PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48	
	PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15	
	PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51	
50	PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35	
	PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35	
	PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8	
	PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64	
	PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02	
55	PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12	

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	PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51	
	PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85	
5	PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59	
	PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87	
	PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58	* +
	PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21	
	PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82	
10	PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59	
	PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18	
	PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36	* +
	PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79	
	PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38	
15	PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82	
	PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07	
	PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12	
	PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63	
20	PLACE4000399	10.99	17.08	75.17	59.11	80.22	58	
	PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4	
	PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87	
	PLACE4000411	2.22	2.28	4	2.27	2.6	1.82	
	PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78	
25	PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83	
	PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51	
	PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79	
	PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14	
	PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27	
30	PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04	
	PLACE4000455	5.18	7.39	9.55	8	7.21	4.63	
	PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34	
	PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31	
	PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22	
35	PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05	
	PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69	
	PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08	
	PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37	
	PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2	
40	PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11	
	PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22	
	PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32	
	PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15	
	PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44	
45	PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25	
	PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83	
	PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74	
	PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58	
	PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16	
50	PLACE4000651	2.42	6.4	7.48	5	7.01	6.07	
	PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47	
	PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67	
	PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77	
	PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12	
55	PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07	

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	PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76	
	PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79	
	PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32	
5	PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09	
	PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	* +
	PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84	
	PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87	
10	PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54	
	PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64	
	PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73	
	PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57	
	PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8	
15	PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87	
	PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82	
	SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96	
	SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77	
	SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44	
20	SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96	
	SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44	
	SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56	
	SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55	
	SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12	
25	SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73	
	SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92	
	SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39	
	SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	** +
	SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18	
30	SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43	
	SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89	
	SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67	
	SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1	
35	SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11	
	SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02	
	SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3	
	SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88	
	SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26	
40	SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52	
	SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99	
	SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84	
	SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99	
	SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68	
45	SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47	
	SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64	
	SPLEN1000072	1	8.5	4.7	2.82	3	2.21	
	SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63	
	SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76	
50	SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04	
	SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32	
	SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99	
	SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52	
	SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8	
55	SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51	

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	SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61
	SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68
5	SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15
	SPLEN1000182	0.98	2.66	0.23	0.83	0.6	0.67
	SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95
	THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6
	THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1
10	THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8 * +
	THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38
	THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6
	THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14
	THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31
15	THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45
	THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28
	THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23
	THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11
20	THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55
	THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04
	THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74
	THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94
	THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05 * +
25	THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74
	THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27
	THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93
	THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97
	THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66
30	THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11
	THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36
	THYRO1000034	0.49	4.16	1.59	1.99	2	1.82
	THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11
	THYRO1000036	0.93	8.32	4	3.08	4.36	5.59
35	THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93
	THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61
	THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3
	THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45
	THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06
40	THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42
	THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85
	THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15
	THYRO1000087	0.72	3.86	1.01	0	0.58	0.17
	THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5
45	THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95
	THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39
	THYRO1000107	0.5	2.95	2.7	2.86	3.22	2
	THYRO1000111	0.85	4.58	1.78	1.4	2.06	2.36
	THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95
50	THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64
	THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92
	THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39
	THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26
55	THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73
	THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33

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	THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23		
	THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58		
	THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
5	THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
	THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
	THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
	THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
	THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
10	THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
	THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
	THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
	THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
15	THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
	THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
	THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
	THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
	THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
20	THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		
	THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
	THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
	THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
	THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
25	THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
	THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
	THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
	THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
	THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		
30	THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
	THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
	THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
	THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		
35	THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
	THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
	THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
	THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
	THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
40	THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
	THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
	THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
	THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
	THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
45	THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
	THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
	THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
	THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
	THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
50	THYRO1000501	1.12	4.01	2.73	3	1.92	1.82		
	THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
	THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
	THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
	THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
55	THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		

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	THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88
	THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49
5	THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42
	THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78
	THYRO1000577	1.06	5	1.34	0.96	1.22	0.71
	THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79
	THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58
10	THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52
	THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21
	THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97
	THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56
	THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29
15	THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78
	THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67
	THYRO1000637	0.91	3.96	1.71	1.18	2.03	1.54
	THYRO1000641	0.38	4.19	2.49	1.36	1.67	1.64
20	THYRO1000657	2.99	3.69	5.42	7.67	12.28	3.86
	THYRO1000658	2.68	3.62	5.39	5.4	5.55	6.09
	THYRO1000662	1.1	3.19	2.09	2.42	2.69	1.66
	THYRO1000666	0.57	3.19	2.28	1.63	1.48	1.43
	THYRO1000676	1.37	4.53	2.01	1.75	1.83	1.56
25	THYRO1000678	0.52	5.86	0.99	1.29	1.4	0.53
	THYRO1000684	0.95	4.98	2.94	1.92	2.65	1.47
	THYRO1000694	2.08	6.64	4.65	2.8	2.48	3.59
	THYRO1000699	2.98	2.14	5.55	4.86	7.08	7.12
	THYRO1000712	1.88	4.25	5.9	6.25	6.75	7.78
30	THYRO1000715	5.74	5.67	27.37	21.74	28.63	16.99
	THYRO1000716	0.92	3.26	3.2	1.88	1.78	1.35
	THYRO1000717	1.58	5	4.36	2.98	4.63	1.91
	THYRO1000723	0.6	4.54	1.6	0.55	1.06	0.85
	THYRO1000734	-0.01	4.81	1.89	1.49	1.73	1.07
35	THYRO1000748	0.98	5.51	5.23	2.35	3.85	3.18
	THYRO1000755	1.74	3.26	4.32	4.33	3.47	4.38
	THYRO1000756	2.79	4.24	3.24	3.46	4.2	3.41
	THYRO1000776	0.48	2.17	3.02	3.36	3.99	3.34
	THYRO1000777	1.81	3.39	4.54	4.99	2.05	2.37
40	THYRO1000779	1.45	3.55	0.88	0.18	1.01	-0.26
	THYRO1000782	3.92	10.13	12.52	10.76	15.05	14.05
	THYRO1000783	0.12	5.51	1.2	1.11	1.41	0.92
	THYRO1000786	6.65	9.54	19.71	15.74	7.92	13.7
	THYRO1000787	0.23	1.88	1.67	1.31	1.54	0.78
45	THYRO1000792	1.51	3.13	2.29	3.09	3.13	2.11
	THYRO1000793	0.11	3.13	0.84	1.51	1.86	1.16
	THYRO1000795	1.23	6.03	3.54	2.76	3.1	3.05
	THYRO1000796	0.6	7.73	2.44	2.26	2.95	1.66
	THYRO1000798	1.89	5.82	2.51	2.59	3.57	3.53
50	THYRO1000800	9.26	17.2	24.74	17.74	20.68	21.06
	THYRO1000805	0.49	3.04	1.08	0.72	2.66	1.38
	THYRO1000815	2.54	3.49	9.48	7.61	5.47	7.87
	THYRO1000829	5.55	7.83	10.57	3.78	8.32	10.01
55	THYRO1000835	0.96	3.2	1.93	1.07	2.36	1.8
	THYRO1000843	1.09	11.48	3.56	3.69	4.41	3.62

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	THYRO1000846	0.76	5.71	1.32	2.67	1.62	1.26	
	THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32	
	THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	* +
5	THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95	
	THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01	
	THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	* +
	THYRO1000894	0.33	3.95	1.36	1.75	1.48	1	
	THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82	
10	THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29	
	THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89	
	THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82	
	THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46	
15	THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9	
	THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24	
	THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87	
	THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48	
	THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64	
20	THYRO1000964	0.42	11.59	0.76	1	1.27	1.06	
	THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19	
	THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71	
	THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68	
	THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12	
25	THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26	
	THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67	
	THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2	
	THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26	
	THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56	
30	THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66	
	THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24	
	THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41	
	THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16	
	THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02	
35	THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62	
	THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84	
	THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76	
	THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78	
	THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5	
40	THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78	
	THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93	
	THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18	
	THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99	
45	THYRO1001113	11.41	17.42	32	21.81	26.65	18.72	
	THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72	
	THYRO1001121	1.57	4.28	4.19	3.92	2.72	3	
	THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09	
	THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12	
50	THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38	
	THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22	
	THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62	
	THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52	
	THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97	
55	THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94	

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	THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31	
	THYRO1001204	2.17	3.58	4.27	4.03	4.74	4	
	THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9	
5	THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33	
	THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55	* +
	THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46	
	THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46	
10	THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66	
	THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69	
	THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66	
	THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97	
	THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2	
15	THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36	
	THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5	
	THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18	
	THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5	
	THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48	
20	THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83	
	THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23	
	THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01	
	THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49	
	THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18	
25	THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65	
	THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1	
	THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28	
	THYRO1001365	0.86	3	1.6	2.19	2.6	1.96	
30	THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21	
	THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29	
	THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94	
	THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63	
	THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36	
35	THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12	
	THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87	
	THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18	
	THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81	
	THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73	
40	THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4	
	THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67	
	THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23	
	THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21	
	THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64	
45	THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75	
	THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57	
	THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13	
	THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48	
50	THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55	
	THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6	
	THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35	
	THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54	
	THYRO1001519	5.92	7.77	11.05	8.91	5.75	10.38	
55	THYRO1001522	2.02	4.7	5.79	4.15	4.69	5.51	
	THYRO1001523	1.83	4.92	3.73	4.38	4.07	4.26	

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	THYRO1001526	26.21	28.22	44.73	34.28	47.64	46.52	
	THYRO1001529	1.64	5.27	2.8	2.32	2.42	2.98	
	THYRO1001534	1.41	4.01	4.96	5.1	5.9	4.54	
5	THYRO1001537	7.4	5.17	12.33	5.97	7.42	7.23	
	THYRO1001541	2.14	3.88	8.27	7.76	8.7	6.73	
	THYRO1001545	1.26	3.84	2.9	4.95	3.57	3.16	
	THYRO1001559	4.52	6.34	8.04	9.06	10.5	10.54	* +
10	THYRO1001563	9.49	14.06	15.89	10	15.49	22.09	
	THYRO1001570	2.01	8.2	3.85	4.25	5.17	3.41	
	THYRO1001573	1.15	5.77	2.22	1.47	2.87	2.67	
	THYRO1001584	2.47	8.54	8.38	5.14	7.81	7.29	
	THYRO1001593	4.27	5.67	11.17	9.5	10.93	9.52	
15	THYRO1001595	3.14	4.53	7.06	5.97	6.35	7.29	
	THYRO1001596	4.71	5.48	7.44	6.45	5.86	2.51	
	THYRO1001602	1.49	3.26	3.52	4.95	5.22	3.41	
	THYRO1001605	1.58	4.48	3.22	3.2	3.43	2.42	
	THYRO1001608	1.87	9.45	5.1	5.04	8.23	4.7	
20	THYRO1001617	6.06	13.68	11.47	9.75	10.87	9.61	
	THYRO1001634	1.87	9.08	3.46	2.93	5.59	2.05	
	THYRO1001637	3.51	3.13	9.65	8.72	7.94	9.07	
	THYRO1001641	2.57	3.73	5.09	4.03	3.08	2.94	
	THYRO1001656	1.59	2.94	4.16	2.82	5.36	2.33	
25	THYRO1001658	22.34	29.19	40.11	34.98	33.16	42.01	
	THYRO1001661	1.4	5.83	2.31	2.93	3.31	2.05	
	THYRO1001671	0.67	7.36	2.68	1.89	1.34	1.8	
	THYRO1001672	1.1	9.24	2.1	1.14	1.52	1.66	
30	THYRO1001673	1.59	7.6	3.49	2.86	4.74	2.16	
	THYRO1001677	1.6	2.27	3.87	3.03	3.54	3.36	
	THYRO1001683	12.71	17.66	29.06	24.4	15.4	16.72	
	THYRO1001700	1.39	2.52	2.67	2.09	1.58	1.37	
	THYRO1001702	11.83	15.98	16.19	15.63	14.35	14.29	
35	THYRO1001703	1.63	6.74	4.25	4.72	3.27	4.21	
	THYRO1001706	1.7	6.47	3.01	2.96	5.6	3.53	
	THYRO1001721	1.84	5.66	3.2	2.73	6.37	2.77	
	THYRO1001725	5.3	6.55	9.69	8.97	8.65	8.29	
	THYRO1001730	17.72	20.4	40.1	30.61	26.56	34.8	
40	THYRO1001738	1.35	3.18	4.65	3.52	2.82	1.78	
	THYRO1001743	0.19	2.13	1.85	1.8	1.64	1.06	
	THYRO1001745	0.47	2.88	1.55	1.05	1.2	1.27	
	THYRO1001746	1.9	6.25	4.04	6.12	4.01	3.88	
	THYRO1001770	15.49	20.38	35.39	41.65	44.42	40.17	* +
45	THYRO1001772	1.12	4.88	3.64	4.78	4.24	3.06	
	THYRO1001778	3.89	6.68	9.89	14.67	13.47	14.25	* +
	THYRO1001793	3.85	3.77	9.43	10.3	10.42	4.92	
	THYRO1001796	1.35	2.28	2.28	3.45	4.22	3.24	* +
50	THYRO1001800	1.82	2.99	2.75	4.17	5.12	2.09	
	THYRO1001803	3.42	6.03	5.21	4.31	4.14	3.42	
	THYRO1001809	1.6	4.26	3.4	5.9	4.23	3.39	
	THYRO1001817	8.69	18.33	24.88	22.11	22.77	25.27	
	THYRO1001819	4.68	8.46	9.01	7.84	10.46	6.77	
55	THYRO1001828	21.89	24.53	104.32	106.68	121.95	68.55	
	THYRO1001854	6.67	6.12	12.45	13.43	15.86	13.31	

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	THYRO1001895	0.85	1.31	2.52	3.54	4.31	1.28	
	THYRO1001907	2.16	3.08	3.37	3.9	4.53	2.74	
	TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22	
5	TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65	
	TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77	
	TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11	
	TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65	
	TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09	
10	TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54	
	TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75	
	TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72	
	TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69	
15	VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02	
	VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94	
	VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88	
	VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	* +
	VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27	
20	VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59	
	VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48	
	VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79	
	VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5	
25	VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65	
	VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27	
	VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87	
	VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	* +
	VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59	
30	VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7	
	VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36	
	VESEN1000410	1.11	5	1.78	2.36	2.71	3.69	
	VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	* +
	VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29	
35	VESEN1000440	7	5.53	7.81	3.79	9.4	12.22	
	VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11	
	VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	* +
	VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58	
	VESEN1000557	4.22	7.94	7.73	6.55	9.07	10	
40	VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8	
	VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08	
	VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46	
	VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91	
45	VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51	
	VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21	
	VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96	
	VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	* +
	VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1	
50	VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61	
	VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66	
	VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59	
	VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47	
	VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12	
55	VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6	
	VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33	

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	VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
	VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
	VESEN2000272	2.29	4	8.92	7	8.31	5.88		
5	VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
	VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
	VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
	VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
10	VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
	VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
	VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
	VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
	VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
15	VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
	VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
	VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
	VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
	VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
20	VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
	VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
	VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
	VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
	VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
25	VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
	VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
	VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
	VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
30	Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		
	Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
	Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
	Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
	Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
35	Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
	Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
	Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
	Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
	Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
40	Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
	Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
	Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
	Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
	Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
45	Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
	Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
	Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
	Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
	Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
50	Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
	Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
	Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
	Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
	Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
55	Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		

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	Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
	Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		
5	Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
	Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
	Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
	Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
	Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
10	Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
	Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
	Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
	Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
	Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
15	Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
	Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		
	Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		
	Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
20	Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
	Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
	Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
	Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
	Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
25	Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
	Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
	Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
	Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
	Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
30	Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
	Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
	Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
	Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
35	Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		
	Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
	Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
	Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
	Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
40	Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
	Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
	Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
	Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
	Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
45	Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
	Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
	Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
	Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+
	Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
50	Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
	Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
	Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
	Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
	Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
55	Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
	Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		

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	Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45	
	Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22	
	Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17	
5	Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31	
	Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97	
	Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	** +
	Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18	
10	Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45	
	Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7	
	Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	** +
	Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95	
	Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71	
15	Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94	
	Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56	
	Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62	
	Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38	
	Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21	
20	Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11	
	Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01	
	Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44	
	Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96	
	Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	** +
25	Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23	
	Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39	
	Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1	
	Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6	
30	Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	* +
	Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56	
	Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79	
	Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14	
	Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	** +
35	Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	* +
	Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21	
	Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51	
	Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59	
	Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	** +
40	Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48	
	Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68	
	Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	* +
	Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07	
	Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79	
45	Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13	
	Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1	
	Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3	
	Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	* +
50	Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41	
	Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43	
	Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56	
	Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89	
	Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	* +
55	Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23	
	Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	* +

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	Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
	Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
5	Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
	Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
	Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
	Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
	Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
10	Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
	Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
	Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
	Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
	Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
15	Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
	Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
	Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
	Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
	Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
20	Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
	Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
	Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
	Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
	Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
25	Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
	Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
	Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
	Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
	Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		
30	Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
	Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
	Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
	Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
	Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
35	Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
	Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
	Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
	Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
40	Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
	Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
	Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
	Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
	Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
45	Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
	Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
	Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
	Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
	Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
50	Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
	Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
	Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
	Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
	Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
55	Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		

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	Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94	
	Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2	
	Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94	
5	Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14	
	Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25	
	Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	* +
	Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82	
	Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53	
10	Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	** +
	Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	* +
	Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57	
	Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46	
15	Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47	
	Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1	
	Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	** +
	Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	* +
	Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19	
20	Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34	
	Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1	
	Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	* +
	Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83	
	Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54	
25	Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05	
	Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02	
	Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73	
	Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66	
	Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66	
30	Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67	
	Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65	
	Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73	
	Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75	
	Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35	
35	Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51	
	Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55	
	Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85	
	Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21	
	Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14	
40	Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43	
	Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77	
	Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33	
	Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24	
	Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28	
45	Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42	
	Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15	
	Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35	
	Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8	
50	Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	* +
	Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9	
	Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33	
	Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17	
	Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15	
55	Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79	

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	Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52		
	Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07		
5	Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14		
	Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63		
	Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85		
	Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46		
	Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51		
10	Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63		
	Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86		
	Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31		
	Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35		
	Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	*	+
15	Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21		
	Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57		
	Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	*	+
	Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41		
	Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27		
20	Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	*	+
	Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47		
	Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83		
	Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93		
25	Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85		
	Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87		
	Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82		
	Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01		
	Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09		
30	Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11		
	Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33		
	Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23		
	Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51		
	Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81		
35	Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13		
	Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66		
	Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	*	+
	Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96		
	Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91		
40	Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06		
	Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98		
	Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43		
	Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08		
	Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26		
45	Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17		
	Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6		
	Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7		
	Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95		
50	Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31		
	Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6		
	Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93		
	Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15		
	Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34		
55	Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17		
	Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73		

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	Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
	Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
5	Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
	Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
	Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
	Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
	Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
10	Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
	Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
	Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
	Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
	Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
15	Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
	Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
	Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
	Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
	Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
20	Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
	Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
	Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
	Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
25	Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
	Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
	Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
	Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
	Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
30	Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		
	Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
	Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
	Y79AA1002376	110.81	135.82	249.8	205.99	213.25	191.69		
	Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
35	Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		
	Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
	Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
	Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
	Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
40	Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
	Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
	Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
	Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
45	Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
	Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
	Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
	Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
	Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		
50	Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13		
	Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69		
	Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56		
	Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86		
	Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1		
55	ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11		

Table 367

Difference in the expression level of each clone in response to TNF. stimulation or IL-1. stimulation

Before stimulation, IL1 1h, and IL1 7h represent relative levels of expression in the absence of the stimulation, 1 hour after the IL-1. stimulation, and 7 hours after the stimulation, respectively. TNF 1h, TNF 3h, and TNF 7h represent relative levels of expression 1 hour after the TNF. stimulation, 3 hours after the stimulation, and 7 hours after the stimulation, respectively. Correlation coefficients 1 and 2 indicate the correlation coefficients in the calibration curves prepared based on the data for the internal standard in reaction systems A and B, respectively.

Clone	IL1		TNF			Correlation coefficients			
	before stimulation	1h	7h	1h	3h	7h	1	2	
NT2RM1000858	5.6	7.6	3.8	4.7	2.1	1.7	0.98	0.94	
NT2RM1000462	0.9	0.9	0.5	0.7	0.1	0	1	1	
NT2RM1000855	1	1.3	1	1.1	0.4	0.4	1	1	
NT2RM1000789	1	0.9	0.4	1	0.4	0.6	0.96	0.98	
NT2RM2000306	0.7	1.1	0.3	1.1	0.3	0.1	1	0.98	
NT2RM2000514	0.2	0.2	0.6	0.2	0.1	0.2	0.98	0.96	
NT2RM2001126	0.5	0	0.4	0.3	0.3	1.2	0.99	0.99	
NT2RM2001902	1.3	1.6	0.6	1.3	0.8	0.8	1	1	
NT2RM2001738	1.6	1.8	1.5	1.7	0.8	0.9	0.98	1	
NT2RM2000582	0.2	0.1	0	0.7	0.1	0.1	0.99	0.99	
NT2RM2000773	1.1	1.2	1.4	2	1	0.8	0.95	1	
NT2RM2001626	0.4	0.2	0.6	0.7	0.1	0.7	1	1	
NT2RM2001643	1.6	3.1	1.2	2.4	0.7	0.8	1	1	
NT2RM2001792	0.2	0	0	0.3	0.1	0.1	0.98	0.97	
NT2RM2000589	0.2	0.1	0	0.1	0	0	1	0.99	
NT2RM2000588	0.6	0.7	0.1	0.8	0.2	0.2	1	1	
NT2RM2002109	0	0	0	0.2	0.1	0	0.99	0.99	
NT2RM4000284	6.5	9.1	4.8	10.1	3.4	3	1	1	
NT2RM4001735	3.8	4.6	2.1	5	1.6	1.4	1	1	
NT2RM4000100	0.5	0.6	0.2	0.5	0.3	0.3	0.95	0.95	
NT2RM4000417	0.2	0	0	0.2	0.1	0	0.99	0.98	
NT2RM4000761	3.2	3.2	2.2	2.6	0.7	0.7	0.95	1	
NT2RM4001843	1.5	1.8	1.7	2.8	1.2	0.6	0.98	1	
NT2RP1000239	2.1	3.2	1.2	2.1	0.5	0.6	1	0.99	
NT2RP1000465	0.9	0.3	0.3	0.9	0.2	0.1	0.97	0.96	
NT2RP1000679	0.3	0.3	0.4	0.9	0.2	0.3	0.97	1	
NT2RP1001031	1.4	1.4	0.4	1.2	0.1	0.3	1	0.98	
NT2RP2001200	2	1.5	0.8	2.2	0.7	0.7	0.99	1	
NT2RP2001562	2.7	2.4	0.7	3.6	0.4	1.1	1	0.94	
NT2RP2001948	1.1	1.5	0.7	1.3	0.6	0.7	0.97	0.99	
NT2RP2002015	1.3	1.7	0.7	1.8	0.6	0.5	0.99	1	
NT2RP2003390	2	1.7	1.3	2.3	0.6	0.5	0.99	0.99	
NT2RP2003664	0.4	0.1	0.1	0.8	0.1	0	0.99	0.99	
NT2RP2005597	1.2	1.4	0.5	2.7	2.2	2.2	0.96	0.99	
NT2RP2001469	1.7	1.4	1.2	2	0.6	0.6	1	1	
NT2RP2000240	0.9	0.9	0.3	1.4	0.7	0.3	1	1	
NT2RP2000610	2.4	2.2	2.1	2.7	1.5	1.6	0.93	0.96	

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	NT2RP2001276	1	0.4	0.4	0.8	0.2	0.7	0.95	1
	NT2RP2001817	1.2	0.8	0.5	1.9	0.7	0.7	1	1
5	NT2RP2004069	0.6	0.6	0.4	0.8	0.5	0.3	0.93	0.97
	NT2RP2004108	0.3	0.2	0.6	1.1	0.4	0.5	0.96	1
	NT2RP2005391	0.7	0.5	0.1	1.2	0.3	0.3	1	0.99
	NT2RP2006092	1.6	1.2	0.9	2.1	0.6	0.7	0.97	1
	NT2RP2006134	1.2	1.5	0.7	1.9	1	0	0.91	1
10	NT2RP2000818	0.9	0.3	0.3	1.6	0.3	0.3	0.95	1
	NT2RP2000092	1.8	1.8	0.8	2	1	1	0.99	0.98
	NT2RP2000092	1.1	1.1	0.5	1.4	0.6	0.6	0.99	0.97
	NT2RP2001538	2.1	1.9	1.8	2.5	0.6	0.8	0.98	1
	NT2RP2006476	2.1	2.2	1.4	3.2	1.6	2	0.97	0.98
15	NT2RP3000616	0.1	0.1	0	0	0	0	1	1
	NT2RP3000721	2.2	2.8	0.7	2.4	0.4	0.4	1	0.98
	NT2RP3001044	1.5	1.9	0.6	2	0.7	0.4	1	1
	NT2RP3001240	0.8	1	0.8	1.5	0.6	0.7	0.97	0.99
	NT2RP3001592	0.3	0.8	0.8	1.1	0	0	0.94	0.93
20	NT2RP3002448	4.6	4.2	2.5	4.5	0.8	1.2	1	0.98
	NT2RP3002721	1.3	1.6	0.5	1.4	0.3	0.3	1	0.99
	NT2RP3002738	0.1	0	0.1	1.9	0.1	0.1	0.99	1
	NT2RP3002790	1.6	2	0.6	1.7	0.6	0.5	0.98	1
	NT2RP3002836	1.7	3	0.9	2.4	1.6	0.7	1	1
25	NT2RP3003354	0.9	0.7	0.5	0.6	0.4	0.5	0.99	0.92
	NT2RP3003614	0.5	0.4	0	0.3	0.3	0.2	0.99	0.99
	NT2RP3004075	0.8	1.4	0.7	1	0.4	0.4	1	1
	NT2RP3004130	0.3	0.4	0	0.2	0.1	0	0.93	0.96
	NT2RP3004133	1.9	3.5	0.6	3.8	1	1.3	0.99	1
30	NT2RP3004321	0.2	0.2	0	1.4	0.4	0.2	1	0.99
	NT2RP3004406	1.3	0.2	0.2	0.7	0.1	0	1	1
	NT2RP3004552	0.1	0.1	0.1	0.1	0	0	1	1
	NT2RP3004557	1.3	1.1	2.2	2.6	1.5	1.4	0.98	0.94
	NT2RP3004647	1.2	2.1	0.6	1.2	1	0.5	1	1
35	NT2RP3000201	2.3	2.9	0.4	1	1.3	0.5	1	0.98
	NT2RP3000820	1.2	1.6	0.9	1.2	0.6	0.5	1	1
	NT2RP3000818	1.4	1.5	0.7	1.8	0.5	0.7	1	0.99
	NT2RP3001159	1.2	2.5	1.2	1.4	0.6	0.7	0.99	0.99
	NT2RP3002281	1.6	2	1.2	1.8	1	1.2	0.99	1
40	NT2RP3002571	3.9	1.8	1.2	5.2	1.4	0.8	0.99	0.97
	NT2RP3002983	1.4	1.7	0.5	1.4	0.4	0.3	1	1
	NT2RP3003473	0.8	0.9	1	0.7	0.4	0.5	1	0.99
	NT2RP3001976	0.6	1.1	0.1	0.7	0.4	0.1	1	0.99
	NT2RP3002286	1.4	1.8	1	1.6	0.6	0.5	1	0.99
45	NT2RP3002353	7.7	6.4	2.2	8.7	1.1	1.3	0.94	0.99
	NT2RP3004025	1.9	2	1	2.1	1	1	0.96	0.98
	NT2RP3004119	0.8	1.1	0.4	0	0	0.2	1	0.99
	NT2RP3000171	0.7	1.3	0.6	1	0.4	0.3	0.99	1
	NT2RP3000676	1.2	1.9	0.7	1.1	1.3	0.5	0.99	1
50	NT2RP3000921	0.2	0.1	0	0.2	0.1	0	1	0.99
	NT2RP3002015	0.8	0.6	0.4	0.7	0.1	0.1	0.99	0.99
	NT2RP3004294	0	0	0	0.1	0.1	0	1	1
	NT2RP3004345	0.6	0.4	0.2	0.9	0.2	0.5	1	1
55	NT2RP3000148	1.7	2.5	0.8	2	0.8	0.8	1	1

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	NT2RP3000232	0.6	0.8	0.4	0.3	0	0	1	0.99
	NT2RP3001650	2.3	1.5	1.6	1.7	1	1.3	1	1
5	NT2RP3002411	0.5	0.4	0.1	0.5	0.2	0.1	1	1
	NT2RP4001001	0.8	1.3	0.7	1	0.7	0.4	0.97	0.97
	NT2RP4001877	1.5	0.9	1.1	1.2	0.5	0.7	1	0.99
	NT2RP4002451	0.7	1	0.6	0.7	0.2	0.3	0.91	0.95
	NT2RP4000634	1	1	0.3	0.9	0.3	0.4	0.99	1
10	NT2RP4002187	0.4	0.4	0.1	0.7	0.3	0.2	1	0.99
	NT2RP4002715	1.5	1.6	0.7	1.5	0.4	0.3	1	0.99
	MAMMA1000986	3.9	4.1	1.9	4.2	1.8	1.4	0.99	1
	MAMMA1001237	0	0	1.6	0.2	0	0	0.99	0.98
	MAMMA1001978	3.5	3.4	2.3	6	3.4	2.5	0.97	0.98
15	MAMMA1002080	0.4	0	0	0.4	0.1	0	1	0.99
	MAMMA1002234	4	4.4	3	7.7	1.9	3	0.97	1
	MAMMA1000614	4.8	1	15.5	5.6	3.9	4.8	0.95	0.93
	MAMMA1000141	7.1	11.5	3.5	14.8	6.5	3.7	1	0.98
	MAMMA1000706	7.2	9.3	3.9	3.7	2.3	2.6	0.98	0.99
20	MAMMA1000788	3	3.8	2.8	8.9	4.8	4.2	0.92	0.98
	MAMMA1000994	0.3	0	0	0.4	0	0	1	1
	MAMMA1001310	4.1	6.1	3.8	8	2.5	3.6	0.99	0.95
	MAMMA1001344	2.7	4.4	2.2	3.2	2.6	2.1	1	0.99
	MAMMA1001957	2.3	2.7	1.9	1.7	1	1.8	0.99	1
25	MAMMA1002070	0.1	0.1	0	0.8	0.4	0.2	1	0.99
	MAMMA1002586	1.7	1.6	1.2	1.3	0.4	0.3	0.94	1
	MAMMA1000102	2.1	2.3	1.4	3.3	1.6	1.6	1	1
	MAMMA1001066	2.8	2.6	1.8	5.3	0.7	1.2	1	0.98
	MAMMA1001094	2.3	2.9	2	3.3	2.1	2.5	0.96	0.9
30	MAMMA1001609	2	3	1.2	2.7	1.7	2.2	0.99	0.97
	PLACE1002547	2	1.7	1.2	4.1	1.2	2	0.95	1
	PLACE1003573	0	0	0	0.1	0	0	1	0.98
	PLACE1004199	0.1	0.2	0	0	0	0	0.99	0.97
	PLACE1004305	0	0	0	0.3	0	0.2	0.96	0.99
35	PLACE1004450	0.9	0.3	0	0.1	0	0	0.98	0.98
	PLACE1005031	0.9	0	0	0.5	0	0	0.98	0.99
	PLACE1007845	0.8	1	0.4	0.4	0.1	0.1	1	0.98
	PLACE1008984	1.4	1.2	0.4	1.9	0.6	0.5	0.98	0.98
	PLACE1011116	2.6	1.5	1.6	1.6	0.3	0.4	1	1
40	PLACE1000986	0.6	0.2	0.2	0.3	0.1	0.1	1	0.98
	PLACE1004492	1.9	1.9	1.5	3.3	1	1	1	0.97
	PLACE1005569	2.6	0.4	0	1.1	0.3	0.1	0.98	0.99
	PLACE1005601	1.7	1.3	1	2.3	0.6	0.3	0.93	1
	PLACE1006079	0.6	0.3	0	0.1	0.1	0	0.98	0.99
45	PLACE1007077	1.1	0	0	0.3	0.1	0	0.97	0.98
	PLACE1008744	0.4	0.1	0.1	1.1	0.1	0	0.98	1
	PLACE1011181	0.6	0.3	0.5	1.6	0.3	0.5	0.98	0.99
	PLACE1005539	0.4	0	0.2	0.3	0.2	0	1	0.93
	PLACE1008282	1.1	0.7	0.6	1.2	0.4	0.4	0.98	1
50	PLACE1010713	0.6	0.7	0	1.4	0.5	0.4	0.99	0.95
	PLACE1010011	1.2	1.4	0.2	2.7	1.5	1.7	1	0.99
	PLACE3000213	1.9	0.2	0.1	0.8	0.1	0	0.99	1
	PLACE1002080	6.7	3.9	0.3	1.7	0.8	0.5	0.95	0.98
55	SKNMC1000082	1.3	0.1	1.1	0.7	0	0	1	1

	Y79AA1000127	1.8	1.8	1.1	2.1	0.5	0.6	1	1
	Y79AA1000226	1.4	0.8	0.6	0.9	0.3	0.4	0.99	0.99
5	Y79AA1000776	0.3	0.1	0	1.1	0.3	0.5	0.99	0.99
	Y79AA1000876	1.1	1.5	1.2	1.3	0.5	0.8	0.97	1
	Y79AA1001056	1.7	1.7	0.8	1.4	0.9	0.7	1	1
	Y79AA1000777	3.1	3.1	1.2	3.8	0.7	0.5	0.98	0.99
10	Y79AA1000030	1	1.3	0.2	1.3	0	0.6	0.98	0.96
	Y79AA1001212	1.5	1.2	1	2	0.8	0.5	1	0.99
	Y79AA1001427	2.3	3	0.6	2	0.8	0.4	1	1
	Y79AA1001530	0.9	0.9	0.5	1.1	0.4	0.4	1	1
	Y79AA1001592	0.6	0.2	0	0.7	0	0	0.97	1
15	Y79AA1001727	0.8	0.4	0.2	0.9	0.2	0.1	1	1
	Y79AA1001803	0.1	0	0	0.2	0.1	0	0.97	0.99
	Y79AA1002373	0	0	0	0	0	0	0.99	1
	Y79AA1002376	0.9	0.1	0	1.2	0.1	0.4	0.98	1
20	Y79AA1001523	0.5	0.5	0.3	0.6	0.3	0.1	1	0.98
	Y79AA1000888	1.1	1	0.7	1.4	0.7	0.5	1	1
	Y79AA1002129	0.2	0.2	0.1	0.5	0.2	0.2	0.99	1

25 **[0285]** The present invention has provided a total of 830 novel full length cDNA clones. As has not yet proceeded the isolation of full length cDNA within the human, the invention has a large significance. Those proteins such as secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription are known to be associated with many diseases. Those genes and proteins associating with diseases are useful for developing medicines as they can be used as a diagnostic marker, or a target for gene therapy or developing medicines that is capable of regulating their expression and activity. Especially, the cDNA clones encoding a secretion protein are extremely important for medicinal industry since the protein itself is expected to be effective as a medicine, and also the gene may have potential to be associating with many diseases. Moreover, those proteins such as membrane proteins, and proteins associated with signal transduction, glycoprotein, transcription, and diseases, and the genes encoding the proteins may be used as a disease marker. These cDNA clones are also important for medicinal industry as they may be effective for treating diseases through the regulation of the expression and activity of their encoded proteins.

Table 368

40 The names of the representative sequences of the clusters (groups) and the corresponding SEQ IDs.

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45	HRIFA000071a : 1574	HRIFA017921a : 1980
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	HRIFA000432a : 1581	HRIFA018287a : 1987
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	HRIFA000695a : 1587	HRIFA018794a : 1993
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	HRIFA001138a : 1596	HRIFA019175a : 2002
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	HRIFA008989a : 1771	HRIFA026089a : 2177
	HRIFA009071a : 1772	HRIFA026121a : 2178
35	HRIFA009101a : 1773	HRIFA026151a : 2179
	HRIFA009123a : 1774	HRIFA026153a : 2180
	HRIFA009136a : 1775	HRIFA026203a : 2181
	HRIFA009171a : 1776	HRIFA026210a : 2182
	HRIFA009214a : 1777	HRIFA026242a : 2183
40	HRIFA009220a : 1778	HRIFA026265a : 2184
	HRIFA009339a : 1779	HRIFA026303a : 2185
	HRIFA009372a : 1780	HRIFA026316a : 2186
	HRIFA009392a : 1781	HRIFA026346a : 2187
	HRIFA009414a : 1782	HRIFA026351a : 2188
45	HRIFA009451a : 1783	HRIFA026364a : 2189
	HRIFA009482a : 1784	HRIFA026382a : 2190
	HRIFA009578a : 1785	HRIFA026465a : 2191
	HRIFA009762a : 1786	HRIFA026490a : 2192
	HRIFA009764a : 1787	HRIFA026496a : 2193
50	HRIFA009783a : 1788	HRIFA026519a : 2194
	HRIFA009825a : 1789	HRIFA026564a : 2195
	HRIFA009852a : 1790	HRIFA026576a : 2196
	HRIFA009881a : 1791	HRIFA026615a : 2197
	HRIFA009983a : 1792	HRIFA026618a : 2198
55	HRIFA010005a : 1793	HRIFA026659a : 2199

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	HRIFA010070a : 1795	HRIFA026764a : 2201
5	HRIFA010078a : 1796	HRIFA026789a : 2202
	HRIFA010085a : 1797	HRIFA026813a : 2203
	HRIFA010090a : 1798	HRIFA026860a : 2204
	HRIFA010130a : 1799	HRIFA026889a : 2205
	HRIFA010152a : 1800	HRIFA026899a : 2206
10	HRIFA010176a : 1801	HRIFA026918a : 2207
	HRIFA010206a : 1802	HRIFA026923a : 2208
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15	HRIFA010361a : 1806	HRIFA027173a : 2212
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50	HRIFA012151a : 1840	HRIFA028401a : 2246
	HRIFA012167a : 1841	HRIFA028402a : 2247
	HRIFA012278a : 1842	HRIFA028440a : 2248
	HRIFA012282a : 1843	HRIFA028465a : 2249
	HRIFA012283a : 1844	HRIFA028468a : 2250
55	HRIFA012290a : 1845	HRIFA028497a : 2251

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	HRIFA012436a : 1850	HRIFA028592a : 2256
	HRIFA012480a : 1851	HRIFA028614a : 2257
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10	HRIFA012584a : 1854	HRIFA028654a : 2260
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	HRIFA012692a : 1856	HRIFA028790a : 2262
	HRIFA012702a : 1857	HRIFA028804a : 2263
15	HRIFA012737a : 1858	HRIFA028867a : 2264
	HRIFA012761a : 1859	HRIFA028911a : 2265
	HRIFA012795a : 1860	HRIFA028926a : 2266
	HRIFA012881a : 1861	HRIFA028983a : 2267
	HRIFA012885a : 1862	HRIFA029002a : 2268
20	HRIFA012914a : 1863	HRIFA029050a : 2269
	HRIFA012969a : 1864	HRIFA029107a : 2270
	HRIFA012990a : 1865	HRIFA029208a : 2271
	HRIFA012999a : 1866	HRIFA029209a : 2272
	HRIFA013092a : 1867	HRIFA029256a : 2273
25	HRIFA013103a : 1868	HRIFA029263a : 2274
	HRIFA013135a : 1869	HRIFA029274a : 2275
	HRIFA013235a : 1870	HRIFA029278a : 2276
	HRIFA013254a : 1871	HRIFA029285a : 2277
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30	HRIFA013276a : 1873	HRIFA029327a : 2279
	HRIFA013279a : 1874	HRIFA029349a : 2280
	HRIFA013288a : 1875	HRIFA029393a : 2281
	HRIFA013376a : 1876	HRIFA029398a : 2282
	HRIFA013477a : 1877	HRIFA029425a : 2283
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	HRIFA013620a : 1880	HRIFA029460a : 2286
	HRIFA013668a : 1881	HRIFA029467a : 2287
	HRIFA013726a : 1882	HRIFA029508a : 2288
40	HRIFA013744a : 1883	HRIFA029511a : 2289
	HRIFA013899a : 1884	HRIFA029577a : 2290
	HRIFA013911a : 1885	HRIFA029602a : 2291
	HRIFA013919a : 1886	HRIFA029649a : 2292
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	HRIFA013980a : 1888	HRIFA029730a : 2294
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	HRIFA014133a : 1893	HRIFA029932a : 2299
	HRIFA014178a : 1894	HRIFA030025a : 2300
	HRIFA014185a : 1895	HRIFA030045a : 2301
	HRIFA014303a : 1896	HRIFA030097a : 2302
55	HRIFA014336a : 1897	HRIFA030103a : 2303

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	HRIFA014465a : 1901	HRIFA030237a : 2307
	HRIFA014467a : 1902	HRIFA030248a : 2308
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	HRIFA014500a : 1904	HRIFA030264a : 2310
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	HRIFA014568a : 1906	HRIFA030370a : 2312
	HRIFA014590a : 1907	HRIFA030371a : 2313
	HRIFA014598a : 1908	HRIFA030381a : 2314
	HRIFA014620a : 1909	HRIFA030385a : 2315
15	HRIFA014621a : 1910	HRIFA030394a : 2316
	HRIFA014688a : 1911	HRIFA030408a : 2317
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	HRIFA014702a : 1913	HRIFA030448a : 2319
	HRIFA014819a : 1914	HRIFA030456a : 2320
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	HRIFA014953a : 1917	HRIFA030509a : 2323
	HRIFA014967a : 1918	HRIFA030511a : 2324
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	HRIFA015070a : 1920	HRIFA030566a : 2326
	HRIFA015122a : 1921	HRIFA030599a : 2327
	HRIFA015129a : 1922	HRIFA030629a : 2328
	HRIFA015219a : 1923	HRIFA030642a : 2329
30	HRIFA015236a : 1924	HRIFA030662a : 2330
	HRIFA015246a : 1925	HRIFA030839a : 2331
	HRIFA015351a : 1926	HRIFA030981a : 2332
	HRIFA015409a : 1927	HRIFA031062a : 2333
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35	HRIFA015443a : 1929	HRIFA031091a : 2335
	HRIFA015453a : 1930	HRIFA031126a : 2336
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	HRIFA015486a : 1932	HRIFA031336a : 2338
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40	HRIFA015536a : 1934	HRIFA031395a : 2340
	HRIFA015547a : 1935	HRIFA031397a : 2341
	HRIFA015568a : 1936	HRIFA031438a : 2342
	HRIFA015671a : 1937	HRIFA031472a : 2343
	HRIFA015682a : 1938	HRIFA031510a : 2344
45	HRIFA015756a : 1939	HRIFA031672a : 2345
	HRIFA015764a : 1940	HRIFA031869a : 2346
	HRIFA015802a : 1941	HRIFA031871a : 2347
	HRIFA015811a : 1942	HRIFA031895a : 2348
	HRIFA015902a : 1943	HRIFA031935a : 2349
50	HRIFA015947a : 1944	HRIFA031986a : 2350
	HRIFA015995a : 1945	HRIFA032009a : 2351
	HRIFA016070a : 1946	HRIFA032011a : 2352
	HRIFA016129a : 1947	HRIFA032066a : 2353
	HRIFA016214a : 1948	HRIFA032067a : 2354
55	HRIFA016240a : 1949	HRIFA032070a : 2355

HRIFA016255a : 1950	HRIFA032073a : 2356
HRIFA016290a : 1951	HRIFA032079a : 2357
HRIFA016430a : 1952	HRIFA032097a : 2358
HRIFA016599a : 1953	HRIFA032161a : 2359
HRIFA016623a : 1954	HRIFA032186a : 2360
HRIFA016639a : 1955	HRIFA032224a : 2361
HRIFA016654a : 1956	HRIFA032257a : 2362
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HRIFA016758a : 1958	HRIFA032274a : 2364
HRIFA016838a : 1959	HRIFA032275a : 2365
HRIFA016963a : 1960	HRIFA032360a : 2366
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HRIFA017643a : 1971	HRIFA032696a : 2377
HRIFA017670a : 1972	HRIFA032730a : 2378
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HRIFA017729a : 1974	HRIFA032984a : 2380
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HRIFA017801a : 1976	HRIFA033718a : 2382
HRIFA017818a : 1977	HRIFA034010a : 2383
HRIFA017836a : 1978	

Table 369

The names of the internal sequences that are used in the selection of the clones from the representative sequences, and the corresponding SEQ IDs.

AA533598 : 2384	HRIFA036799a : 2463
AI051329 : 2385	HRIFA037138a : 2464
HRIFA000595a : 2386	HRIFA037776a : 2465
HRIFA000667a : 2387	HRIFA037838a : 2466
HRIFA000878a : 2388	HRIRA000001a : 2467
HRIFA001269a : 2389	HRIRA000041a : 2468
HRIFA001283a : 2390	HRIRA000058a : 2469
HRIFA002000a : 2391	HRIRA000260a : 2470
HRIFA002196a : 2392	HRIRA000490a : 2471
HRIFA003583a : 2393	HRIRA000522a : 2472
HRIFA005077a : 2394	HRIRA000553a : 2473
HRIFA005781a : 2395	HRIRA000563a : 2474
HRIFA006216a : 2396	HRIRA000640a : 2475
HRIFA006468a : 2397	HRIRA000725a : 2476
HRIFA006822a : 2398	HRIRA000998a : 2477
HRIFA007048a : 2399	HRIRA001053a : 2478
HRIFA007661a : 2400	HRIRA001314a : 2479

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	HRIFA007777a : 2401	HRIRA001443a : 2480
	HRIFA007997a : 2402	HRIRA001473a : 2481
5	HRIFA008312a : 2403	HRIRA001648a : 2482
	HRIFA009250a : 2404	HRIRA001690a : 2483
	HRIFA009495a : 2405	HRIRA001726a : 2484
	HRIFA009607a : 2406	HRIRA001884a : 2485
	HRIFA009923a : 2407	HRIRA002098a : 2486
10	HRIFA009978a : 2408	HRIRA002100a : 2487
	HRIFA010730a : 2409	HRIRA002155a : 2488
	HRIFA011029a : 2410	HRIRA002307a : 2489
	HRIFA011416a : 2411	HRIRA002442a : 2490
	HRIFA011461a : 2412	HRIRA002446a : 2491
15	HRIFA012670a : 2413	HRIRA002479a : 2492
	HRIFA012717a : 2414	HRIRA002945a : 2493
	HRIFA012802a : 2415	HRIRA003028a : 2494
	HRIFA013357a : 2416	HRIRA003108a : 2495
	HRIFA013484a : 2417	HRIRA003139a : 2496
20	HRIFA015333a : 2418	HRIRA003819a : 2497
	HRIFA015375a : 2419	HRIRA004049a : 2498
	HRIFA015663a : 2420	HRIRA004286a : 2499
	HRIFA016287a : 2421	HRIRA004583a : 2500
25	HRIFA016302a : 2422	HRIRA004691a : 2501
	HRIFA016782a : 2423	HRIRA004783a : 2502
	HRIFA018555a : 2424	HRIRA005152a : 2503
	HRIFA019338a : 2425	HRIRA005221a : 2504
	HRIFA020315a : 2426	HRIRA005227a : 2505
30	HRIFA020806a : 2427	HRIRA005305a : 2506
	HRIFA022264a : 2428	HRIRA005563a : 2507
	HRIFA022923a : 2429	HRIRA006263a : 2508
	HRIFA023027a : 2430	HRIRA006324a : 2509
	HRIFA023218a : 2431	HRIRA006517a : 2510
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	HRIFA023434a : 2433	HRIRA007665a : 2512
	HRIFA023444a : 2434	HRIRA007680a : 2513
	HRIFA023551a : 2435	HRIRA008129a : 2514
	HRIFA023558a : 2436	HRIRA008152a : 2515
40	HRIFA023641a : 2437	HRIRA008276a : 2516
	HRIFA023798a : 2438	HRIRA008329a : 2517
	HRIFA024330a : 2439	HRIRA008854a : 2518
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	HRIFA025565a : 2445	HRIRA012442a : 2524
50	HRIFA025651a : 2446	HRIRA012921a : 2525
	HRIFA026224a : 2447	HRIRA013325a : 2526
	HRIFA026729a : 2448	HRIRA013644a : 2527
	HRIFA026925a : 2449	HRIRA013675a : 2528
	HRIFA028501a : 2450	HRIRA013702a : 2529
55	HRIFA029454a : 2451	HRIRA013757a : 2530
	HRIFA030181a : 2452	HRIRA013951a : 2531

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HRIFA032801a : 2454	HRIRA014380a : 2533
HRIFA033384a : 2455	HRIRA015831a : 2534
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HRIFA033930a : 2457	HRIRA016124a : 2536
HRIFA034817a : 2458	HRIRA017071a : 2537
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HRIFA035542a : 2460	HRIRA020304a : 2539
HRIFA035577a : 2461	HRIRA000579a : 2540
<u>HRIFA036630a : 2462</u>	

[0286] The internal sequences include EST, HRIFA(the representative sequence of the 5'-end), and HRIRA (the representative sequence of the 3'-end).

Table 370

clone	the name of full-length nucleotide sequences	SEQ ID NO of the full-length nucleotide sequences	SEQ ID NO of the deduced amino acid sequences	SEQ ID NO
HEMBA1000006	C-HEMBA1000006	2547	2548	
nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn	
HEMBA1000121	C-HEMBA1000121	2551	2552	
HEMBA1000128	C-HEMBA1000128	2553	2554	
HEMBA1000275	C-HEMBA1000275	2555	2556	
HEMBA1000300	C-HEMBA1000300	2557		
HEMBA1000349	C-HEMBA1000349	2558	2559	
HEMBA1000443	C-HEMBA1000443	2560	2561	
HEMBA1000590	C-HEMBA1000590	2562	2563	
HEMBA1000634	C-HEMBA1000634	2564	2565	
HEMBA1000713	C-HEMBA1000713	2566	2567	
HEMBA1000745	C-HEMBA1000745	2568	2569	
HEMBA1000907	C-HEMBA1000907	2570	2571	
HEMBA1000940	C-HEMBA1000940	2572	2573	
HEMBA1000962	C-HEMBA1000962	2574	2575	
HEMBA1001221	C-HEMBA1001221	2576	2577	
HEMBA1001228	C-HEMBA1001228	2578	2579	
HEMBA1001297	C-HEMBA1001297	2580		
HEMBA1001390	C-HEMBA1001390	2581	2582	
HEMBA1001563	C-HEMBA1001563	2583		
HEMBA1001621	C-HEMBA1001621	2584	2585	
nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn	
HEMBA1001878	C-HEMBA1001878	2588	2589	
HEMBA1002131	C-HEMBA1002131	2590	2591	
HEMBA1002163	C-HEMBA1002163	2592	2593	
HEMBA1002164	C-HEMBA1002164	2594	2595	
HEMBA1002167	C-HEMBA1002167	2596	2597	
HEMBA1002178	C-HEMBA1002178	2598	2599	
nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn	

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	HEMBA1002195	C-HEMBA1002195	2602	2603
	HEMBA1002227	C-HEMBA1002227	2604	2605
	HEMBA1002239	C-HEMBA1002239	2606	
5	HEMBA1002316	C-HEMBA1002316	2607	2608
	HEMBA1002420	C-HEMBA1002420	2609	2610
	HEMBA1002421	C-HEMBA1002421	2611	2612
	HEMBA1002524	C-HEMBA1002524	2613	2614
10	HEMBA1002551	C-HEMBA1002551	2615	2616
	HEMBA1002767	C-HEMBA1002767	2617	2618
	HEMBA1002992	C-HEMBA1002992	2619	2620
	HEMBA1003047	C-HEMBA1003047	2621	2622
	HEMBA1003072	C-HEMBA1003072	2623	2624
15	HEMBA1003101	C-HEMBA1003101	2625	2626
	HEMBA1003230	C-HEMBA1003230	2627	2628
	HEMBA1003294	C-HEMBA1003294	2629	
	HEMBA1003315	C-HEMBA1003315	2630	2631
	HEMBA1003392	C-HEMBA1003392	2632	2633
20	HEMBA1003399	C-HEMBA1003399	2634	2635
	HEMBA1003487	C-HEMBA1003487	2636	2637
	HEMBA1003530	C-HEMBA1003530	2638	2639
	HEMBA1003602	C-HEMBA1003602	2640	2641
	HEMBA1003732	C-HEMBA1003732	2642	2643
25	HEMBA1003945	C-HEMBA1003945	2644	2645
	HEMBA1004110	C-HEMBA1004110	2646	2647
	HEMBA1004250	C-HEMBA1004250	2648	2649
	HEMBA1004391	C-HEMBA1004391	2650	2651
30	HEMBA1004444	C-HEMBA1004444	2652	2653
	HEMBA1004454	C-HEMBA1004454	2654	2655
	HEMBA1004505	C-HEMBA1004505	2656	2657
	HEMBA1004797	C-HEMBA1004797	2658	2659
	HEMBA1004982	C-HEMBA1004982	2660	2661
35	HEMBA1005070	C-HEMBA1005070	2662	2663
	HEMBA1005084	C-HEMBA1005084	2664	2665
	HEMBA1005145	C-HEMBA1005145	2666	2667
	HEMBA1005430	C-HEMBA1005430	2668	2669
	HEMBA1005449	C-HEMBA1005449	2670	2671
40	HEMBA1005489	C-HEMBA1005489	2672	2673
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	HEMBB1001573	C-HEMBB1001573	2739	2740
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55	THYRO1000999	C-THYRO1000999	3508	
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55	NT2RM1000899	C-NT2RM1000899	4109	4110

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	NT2RP3000232	C-NT2RP3000232	4129	4130
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	NT2RP3001650	C-NT2RP3001650	4134	4135
	NT2RP3002409	C-NT2RP3002409	4136	
	NT2RP3002411	C-NT2RP3002411	4137	4138
20	NT2RP3003448	C-NT2RP3003448	4139	
	NT2RP4002715	C-NT2RP4002715	4140	4141
	OVARC1000307	C-OVARC1000307	4142	4143
	PLACE1000907	C-PLACE1000907	4144	4145
25	PLACE1007081	C-PLACE1007081	4146	4147
	PLACE1010011	C-PLACE1010011	4148	4149
	PLACE3000213	C-PLACE3000213	4150	4151
	PLACE4000354	C-PLACE4000354	4152	4153
30	PLACE4000455	C-PLACE4000455	4154	
	THYRO1000776	C-THYRO1000776	4155	4156
	THYRO1001593	C-THYRO1001593	4157	4158
	Y79AA1000750	C-Y79AA1000750	4159	4160
	Y79AA1000888	C-Y79AA1000888	4161	4162
35	Y79AA1002129	C-Y79AA1002129	4163	4164
	Y79AA1002334	C-Y79AA1002334	4165	4166
	MAMMA1002224	C-MAMMA1002224	4167	
40	NT2RP1000271	C-NT2RP1000271	4168	4169
	NT2RP3000481	C-NT2RP3000481	4170	4171
	NT2RP3004481	C-NT2RP3004481	4172	4173
	HEMBA1006658	C-HEMBA1006658	4174	4175
45	NT2RP2006099	C-NT2RP2006099	4176	4177
	NT2RP2006580	C-NT2RP2006580	4178	4179

Homology search result 1

[0287] The result of the homology search in the SwissProt using the representative sequences of the 5'-ends.

Indicated are from the top,
the name of the representative sequence of the cluster,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the organism of which the top hit data is obtained,
the Accession No. of the top hit data.

[0288] Homology search results of the representative sequences of the 5'-end cluster to the data in SwissProt database are shown only for the representative sequences of the cluster from which clones were selected based on the homology search results.

[0289] The P-value is the score which is determined by taking into account the statistic probability of occurrence between the two sequences, and generally low score reflects high similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

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10
HRIFA000016a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
9.2e-05:178:32
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496

15
HRIFA000071a
CIRCUMSPOROZOITE PROTEB PRECURSOR (CS).
5.8e-05:194:29
PLASMODIUM SIMIUM.
Q03110

20
HRIFA000116a
HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.
6.2e-06:83:27
CAENORHABDITIS ELEGANS.
25
P34679

HRIFA000123a
PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).
6.2e-08:89:34
30
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P33154

HRIFA000264a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
35
1.4e-06:231:34
GALLUS GALLUS (CHICKEN).
P02457

40
HRIFA000327a
ATP-BINDING CASSETTE TRANSPORTER 1.
2.0e-16:238:31
MUS MUSCULUS (MOUSE).
P41233

45
HRIFA000415a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-06:120:35
MUS MUSCULUS (MOUSE).
P05142

50
HRIFA000432a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
2.2e-21:86:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
55
Q09818

HRIFA000446a
HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

2.5e-09:138:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40085

5

HRIFA000553a

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

1.7e-27:117:48

GALLUS GALLUS (CHICKEN).

P05099

10

HRIFA000564a

ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).

2.9e-28:163:38

MUS MUSCULUS (MOUSE).

15

P54116

HRIFA000631a

ZINC FINGER PROTEIN 140.

8.2e-45:155:47

20

HOMO SAPIENS (HUMAN).

P52738

HRIFA000683a

FIBRILLIN 1 PRECURSOR.

25

4.8e-18:77:46

HOMO SAPIENS (HUMAN).

P35555

HRIFA000695a

30

"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].

4.0e-06:105:33

HOMO SAPIENS (HUMAN).

P04280

35

HRIFA000776a

FIBRILLIN 2 PRECURSOR.

1.6e-42:214:44

HOMO SAPIENS (HUMAN).

40

P35556

HRIFA000814a

ZINC FINGER PROTEIN 133.

4.4e-16:49:87

45

HOMO SAPIENS (HUMAN).

P52736

HRIFA000845a

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

50

6.0e-06:172:34

MUS MUSCULUS (MOUSE).

P11087

HRIFA001099a

55

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-5 (FRAGMENT).

0.92:38:34

HOMO SAPIENS (HUMAN).

P18849

EP 1 130 094 A2

- 5 HRIFA001132a
AGRN PRECURSOR.
1.3e-26:239:32
GALLUS GALLUS (CHICKEN).
P31696
- 10 HRIFA001138a
CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).
5.9e-114:147:83
HOMO SAPIENS (HUMAN).
P49747
- 15 HRIFA001200a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.035:119:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 20 HRIFA001337a
LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
2.4e-17:98:42
CRICETULUS GRISEUS (CHINESE HAMSTER).
P35950
- 25 HRIFA001341a
NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L)
(NF68).
1.2e-102:248:87
RATTUS NORVEGICUS (RAT).
30 P19527
- 35 HRIFA001413a
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
0.0032:33:63
BOS TAURUS (BOVINE).
P19661
- 40 HRIFA001439a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
0.00031:34:61
HOMO SAPIENS (HUMAN).
P20931
- 45 HRIFA001489a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
8.4e-65:105:72
HOMO SAPIENS (HUMAN).
P35414
- 50 HRIFA001558a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
0.0048:80:31
PLASMODIUM LOPHURAE.
P04929
- 55 HRIFA001712a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.5e-19:169:31

THERMOMONOSPORA CURVATA.
P49695

HRIFA001720a

5 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.4e-94:273:64
HOMO SAPIENS (HUMAN).
Q03923

10 HRIFA001866a

EARLY ANTIGEN PROTEIN D (EA-D).
0.10:93:34
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03191

15 HRIFA001942a

"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1)."
4.7e-12:140:30
20 GALLUS GALLUS (CHICKEN).
P24802

HRIFA001971a

25 HYPOTHETICAL 46.3 KD PROTEIN IN PTA1-CDC24 INTERGENIC REGION.
2.5e-10:86:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39727

HRIFA001972a

30 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.10:100:34
MUS MUSCULUS (MOUSE).
P19137

35 HRIFA001975a

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
6.5e-30:243:33
MUS MUSCULUS (MOUSE).
P21836

40 HRIFA001984a

"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1)."
1.2e-11:140:30
45 GALLUS GALLUS (CHICKEN).
P24802

HRIFA002063a

50 GNS1 PROTEIN.
1.3e-05:127:30
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P25358

HRIFA002102a

55 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
2.9e-07:241:30
HOMO SAPIENS (HUMAN).
Q02817

EP 1 130 094 A2

HRIFA002284a

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

3.8e-05:104:34

RATTUS NORVEGICUS (RAT).

P04474

HRIFA002309a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

1.5e-08:110:37

THERMOMONOSPORA CURVATA.

P49695

HRIFA002384a

GAP JUNCTION ALPHA-6 PROTEIN (CONNEXIN 45) (CX45).

1.8e-31:94:42

HOMO SAPIENS (HUMAN).

P36383

HRIFA002503a

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

6.1e-92:246:67

MUS MUSCULUS (MOUSE).

P15535

HRIFA002689a

TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6) (DNA BINDING PROTEIN GATA-GT2).

0.38:49:34

RATTUS NORVEGICUS (RAT).

P46153

HRIFA002694a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

4.7e-05:93:37

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA002743a

BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).

1.2e-23:216:31

HOMO SAPIENS (HUMAN).

P13497

HRIFA002762a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

5.1e-09:129:41

MUS MUSCULUS (MOUSE).

P05142

HRIFA002766a

FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).

1.8e-12:139:34

HOMO SAPIENS (HUMAN).

Q06828

HRIFA002787a

PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.

1.6e-10:124:37
HOMO SAPIENS (HUMAN).
P08123

5 HRIFA002805a
ZINC FINGER PROTEIN 140.
3.6e-23:43:74
HOMO SAPIENS (HUMAN).
P52738

10 HRIFA002891a
"FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)."
2.0e-41:239:39
MUS MUSCULUS (MOUSE).
15 Q08878

HRIFA002919a
BEM46 PROTEIN (FRAGMENT).
1.0e-12:171:32
20 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069

HRIFA002980a
25 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-
ROGLOBULIN RECEPTOR) (A2MR).
8.7e-32:202:37
GALLUS GALLUS (CHICKEN).
P98157

30 HRIFA003055a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.4e-08:175:29
MUS MUSCULUS (MOUSE).
P05142

35 HRIFA003063a
B-CELL LYMPHOMA 6 PROTEIN HOMOLOG.
2.8e-15:123:34
MUS MUSCULUS (MOUSE).
40 P41183

HRIFA003093a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.3e-11:142:37
45 MUS MUSCULUS (MOUSE).
P05142

HRIFA003340a
50 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
2.3e-05:200:31
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

55 HRIFA003357a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
0.0023:190:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

HRIFA003402a

COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).

3.6e-05:194:27

BOS TAURUS (BOVINE).

P02459

HRIFA003504a

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

1.4e-08:150:33

DROSOPHILA MELANOGASTER (FRUIT FLY).

P33450

HRIFA003592a

CD9 ANTIGEN.

0.0053:24:70

BOS TAURUS (BOVINE).

P30932

HRIFA003635a

"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE)."

5.3e-45:239:43

DROSOPHILA MELANOGASTER (FRUIT FLY).

P53624

HRIFA003640a

PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).

0.00018:28:64

TRYPANOSOMA BRUCEI BRUCEI.

P09791

HRIFA003883a

TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (YIN AND YANG 1) (YY-1) (DELTA TRANSCRIPTION FACTOR) (NF-E1) (UCR-MOTIF DNA-BINDING PROTEIN).

1.0:57:35

MUS MUSCULUS (MOUSE).

Q00899

HRIFA003892a

MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).

6.5e-08:144:25

BACILLUS SUBTILIS.

P39843

HRIFA003946a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

1.4e-06:85:37

MUS MUSCULUS (MOUSE).

P05142

HRIFA004006a

ZINC FINGER PROTEIN 140.

6.2e-20:83:66

HOMO SAPIENS (HUMAN).

P52738

EP 1 130 094 A2

- 1
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45
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55
- HRIFA004034a
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).
1.4e-15:192:32
HOMO SAPIENS (HUMAN).
P20749
 - HRIFA004112a
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
7.2e-26:193:37
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450
 - HRIFA004162a
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
3.6e-10:117:29
MUS MUSCULUS (MOUSE).
P54116
 - HRIFA004401a
LACTOSE OPERON REPRESSOR.
1.1e-07:36:86
ESCHERICHIA COLI.
P03023
 - HRIFA004426a
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
5.1e-11:85:41
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P15287
 - HRIFA004490a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
5.3e-19:101:44
MUS MUSCULUS (MOUSE).
P23780
 - HRIFA004523a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
2.6e-36:180:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
 - HRIFA004663a
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
1.2e-40:112:75
MUS MUSCULUS (MOUSE).
Q00417
 - HRIFA004696a
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
1.1e-62:145:84
CANIS FAMILIARIS (DOG).
P38377
 - HRIFA004714a
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
2.3e-50:127:54
CAENORHABDITIS ELEGANS.

Q09201

HRIFA004745a

MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.

5.0e-17:107:43

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23500

HRIFA004780a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

7.2e-07:142:30

ZEA MAYS (MAIZE).

P14918

HRIFA004919a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).

1.5e-25:156:46

PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).

P10496

HRIFA005072a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).

8.3e-05:24:62

LYCOPERSICON ESCULENTUM (TOMATO).

Q01157

HRIFA005102a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

2.5e-07:188:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA005184a

CYTOCHROME B5.

3.4e-11:117:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40312

HRIFA005214a

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

5.9e-05:141:33

HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

HRIFA005231a

ORM1 PROTEIN.

1.7e-18:137:35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

HRIFA005240a

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

6.3e-81:194:70

HOMO SAPIENS (HUMAN).

Q03923

HRIFA005255a

HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.

1.5e-07:202:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38176

5 HRIFA005271a
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
1.2e-55:86:81
HOMO SAPIENS (HUMAN).
Q00325

10 HRIFA005296a
INSULIN PROMOTER FACTOR 1 (IPF-1) (ISLET/DUODENUM HOMEODOMAIN-1) (IDX-1) (SOMATOSTATIN
TRANSACTIVATING FACTOR-1) (STF-1) (PANCREAS/DUODENUM HOMEODOMAIN-1) (GLUCOSE SENSITIVE
FACTOR) (GSF).
15 0.82:90:34
HOMO SAPIENS (HUMAN).
P52945

20 HRIFA005300a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-07:178:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

25 HRIFA005369a
EBNA-1 NUCLEAR PROTEIN.
2.3e-07:101:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

30 HRIFA005372a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
BOX DNA BINDING PROTEIN SUBUNIT B).
1.1e-14:97:38
35 PETROMYZON MARINUS (SEA LAMPREY).
P25210

40 HRIFA005392a
SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN)
(HSPG) (SYND2).
1.3e-50:126:84
HOMO SAPIENS (HUMAN).
P34741

45 HRIFA005409a
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).
7.1e-66:197:64
50 HOMO SAPIENS (HUMAN).
P30825

55 HRIFA005420a
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
1.5e-33:221:41
MUS MUSCULUS (MOUSE).
P19182

EP 1 130 094 A2

HRIFA005438a

SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP)
(FLAVOPROTEIN SUBUNIT OF COMPLEX II).

6.4e-71:175:68

HOMO SAPIENS (HUMAN).

P31040

HRIFA005462a

CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).

1.4e-19:137:37

OVIS ARIES (SHEEP).

P08060

HRIFA005500a

EBNA-1 NUCLEAR PROTEIN.

0.00042:54:50

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA005540a

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).

0.12:47:29

HOMO SAPIENS (HUMAN).

P18850

HRIFA005644a

VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).

1.2e-102:233:87

BOS TAURUS (BOVINE).

P40682

HRIFA005702a

CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN MUC18)
(MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 AN-
TIGEN) (MELANOMA ADHESION MOLECULE).

8.7e-05:174:28

HOMO SAPIENS (HUMAN).

P43121

HRIFA005720a

F-SPONDIN PRECURSOR.

8.9e-12:155:31

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P35447

HRIFA005728a

SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).

1.7e-05:126:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08458

HRIFA005732a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

4.4e-26:159:38

THERMOMONOSPORA CURVATA.

P49695

HRIFA005760a

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FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOS-
YLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).
3.8e-15:53:54

HOMO SAPIENS (HUMAN).
P16442

HRIFA005781a

ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
DROXYSTEROID DEHYDROGENASE).

5.2e-47:228:47

HOMO SAPIENS (HUMAN).
P37058

HRIFA005944a

PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].

2.5e-06:142:35

MUS MUSCULUS (MOUSE).
P28481

HRIFA006183a

ZINC FINGER PROTEIN 136.

1.3e-42:129:62

HOMO SAPIENS (HUMAN).
P52737

HRIFA006250a

HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).

0.0038:75:37

DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

HRIFA006298a

EBNA-1 NUCLEAR PROTEIN.

1.4e-05:80:42

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA006448a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

8.5e-05:183:28

XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA006494a

AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).

1.2e-18:201:33

HOMO SAPIENS (HUMAN).
Q02246

HRIFA006510a

CORNICHON PROTEIN.

6.0e-53:144:66

DROSOPHILA MELANOGASTER (FRUIT FLY).
P49858

HRIFA006566a

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-

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BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).
P25210

HRIFA006572a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
7.2e-05:158:29
MUS MUSCULUS (MOUSE).
P11087

HRIFA006586a
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.3e-13:219:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

HRIFA006596a
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
7.2e-22:241:32
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071

HRIFA006609a
PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
0.61:28:46
"GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY)."
P01306

HRIFA006633a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
7.8e-07:170:34
HOMO SAPIENS (HUMAN).
Q07092

HRIFA006642a
AMALGAM PROTEIN PRECURSOR.
1.5e-09:185:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P15364

HRIFA006649a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.7e-50:166:50
HOMO SAPIENS (HUMAN).
Q03923

HRIFA006667a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
6.8e-45:180:43
HOMO SAPIENS (HUMAN).
Q03923

HRIFA006730a
SYG1 PROTEIN.
1.8e-14:164:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

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P40528

HRIFA006798a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

5 0.22:149:34

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

HRIFA006926a

10 SYNAPTOTAGMIN IV.

3.6e-19:168:38

RATTUS NORVEGICUS (RAT).

P50232

HRIFA007013a

15 MIC1 PROTEIN.

1.4e-13:115:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53258

20

HRIFA007032a

CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).

0.00013:92:35

CANIS FAMILIARIS (DOG).

25

P39881

HRIFA007068a

EBNA-1 NUCLEAR PROTEIN.

7.0e-10:145:33

30 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA007152a

TRANSCRIPTION FACTOR SOX-4.

35

0.90:47:44

HOMO SAPIENS (HUMAN).

Q06945

HRIFA007219a

40 THROMBOSPONDIN 3 PRECURSOR.

1.3e-105:209:88

HOMO SAPIENS (HUMAN).

P49746

HRIFA007228a

45 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.

2.3e-11:174:24

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39981

50

HRIFA007243a

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

3.0e-18:163:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

55

P39986

HRIFA007244a

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

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4.2e-05:81:33
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

5 HRIFA007256a
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
2.3e-77:186:75
HOMO SAPIENS (HUMAN).
P53355

10 HRIFA007262a
PAIRED AMPHIPATHIC HELIX PROTEIN.
1.3e-06:152:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
15 P22579

HRIFA007352a
5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).
4.2e-36:146:57
20 HOMO SAPIENS (HUMAN).
Q15583

HRIFA007424a
F-SPONDIN PRECURSOR.
25 8.9e-34:84:89
RATTUS NORVEGICUS (RAT).
P35446

HRIFA007435a
30 PROTEIN KINASE CEK1 (EC 2.7.1.-).
1.0e-37:159:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P38938

35 HRIFA007463a
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).
4.8e-32:85:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53685

40 HRIFA007493a
UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN
CARRIER PROTEIN).
1.2e-47:171:56
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33296

HRIFA007512a
50 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
8.0e-07:173:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

HRIFA007532a
55 "CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEIN-
ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE
SUBUNIT)."
1.8e-10:110:37

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HOMO SAPIENS (HUMAN).
P20807

HRIFA007547a

5 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.068:51:45
BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).
P29836

10 HRIFA007565a

COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.1e-08:121:37
HOMO SAPIENS (HUMAN).
Q03692

15 HRIFA007571a

ORM1 PROTEIN.
5.8e-17:106:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
20 P53224

HRIFA007659a

HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
2.5e-47:213:41
25 CAENORHABDITIS ELEGANS.
P49191

HRIFA007722a

30 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
7.7e-13:146:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

HRIFA007728a

35 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
9.1e-05:124:31
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

40 HRIFA007745a

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).
7.0e-15:109:36
TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
P04058

45 HRIFA007829a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00045:16:68
LYCOPERSICON ESCULENTUM (TOMATO).
50 Q01157

HRIFA007909a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
6.1e-06:173:34
55 BOS TAURUS (BOVINE).
P02453

HRIFA007985a

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T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).

0.00079:97:37

ORYCTOLAGUS CUNICULUS (RABBIT).

P06333

5

HRIFA008000a

"DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR."

1.6e-37:165:42

ORYCTOLAGUS CUNICULUS (RABBIT).

10

P13806

HRIFA008174a

COLLAGEN 1(X) CHAIN PRECURSOR.

4.5e-05:215:28

15

BOS TAURUS (BOVINE).

P23206

HRIFA008186a

ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).

20

2.1e-25:118:46

HOMO SAPIENS (HUMAN).

P37058

25

HRIFA008200a

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

7.9e-17:139:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

30

P32802

HRIFA008212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.035:135:28

35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA008252a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

40

0.00015:128:32

MUS MUSCULUS (MOUSE).

P05142

HRIFA008284a

NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).

45

3.9e-18:153:30

HOMO SAPIENS (HUMAN).

P32004

50

HRIFA008314a

HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.

2.1e-18:99:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38800

55

HRIFA008362a

PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).

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9.1e-42:135:57
GALLUS GALLUS (CHICKEN).
P53760

5 HRIFA008426a
HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).
1.3e-08:104:45
GALLUS GALLUS (CHICKEN).
Q90655

10 HRIFA008459a
CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).
5.5e-15:96:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
15 P06782

HRIFA008483a
PROBABLE LONG-CHAIN FATTY ACID TRANSPORT PROTEIN.
7.4e-26:154:41
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38225

HRIFA008547a
ZINC FINGER PROTEIN 136.
25 7.2e-57:228:50
HOMO SAPIENS (HUMAN).
P52737

HRIFA008596a
30 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-05:97:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

35 HRIFA008611a
NPL1 PROTEIN (SEC63 PROTEIN).
8.1e-15:113:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14906

40 HRIFA008661a
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
2.7e-16:184:29
ESCHERICHIA COLI.
45 P37021

HRIFA008717a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
6.9e-32:198:41
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

HRIFA008784a
55 HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.
2.2e-16:93:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38869

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HRIFA008790a
HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.
4.2e-08:121:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47111

HRIFA008976a
ACROSIN PRECURSOR (EC 3.4.21.10).
0.31:20:70
HOMO SAPIENS (HUMAN).
P10323

HRIFA008981a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.0e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923

HRIFA008989a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
1.2e-05:134:33
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA009071 a
CELLULAR TUMOR ANTIGEN P53 (PHOSPHOPROTEIN P53).
0.14:104:31
HOMO SAPIENS (HUMAN).
P04637

HRIFA009101a
ZINC FINGER PROTEIN 136.
6.5e-47:126:67
HOMO SAPIENS (HUMAN).
P52737

HRIFA009123a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.010:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA009136a
REGULATORY PROTEIN E2.
0.032:100:37
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787

HRIFA009171a
BUTYROPHILIN PRECURSOR (BT).
1.6e-15:168:31
BOS TAURUS (BOVINE).
P18892

HRIFA009220a
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.
2.2e-48:268:41

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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09895

HRIFA009339a
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
0.63:57:35
MUS MUSCULUS (MOUSE).
Q01149

HRIFA009451a
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA)
(TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLA-
GENASE INHIBITOR).
1.7e-57:163:73
HOMO SAPIENS (HUMAN).
P01033

HRIFA009482a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
7.7e-25:86:59
MUS MUSCULUS (MOUSE).
P23780

HRIFA009578a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
8.8e-10:199:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

HRIFA009762a
CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).
0.17:116:32
RATTUS NORVEGICUS (RAT).
P53565

HRIFA009783a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
6.2e-48:231:48
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782

HRIFA009825a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
4.0e-06:70:38
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

HRIFA009852a
"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM
140]."
4.0e-07:198:27
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P16170

HRIFA009881a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.5e-11:106:35
SORGHUM VULGARE (SORGHUM).

P24152

HRIFA009983a

G-BOX BINDING FACTOR (GBF).

3.8e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

HRIFA010005a

"M PROTEIN, SEROTYPE 49 PRECURSOR."

1.6e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

HRIFA010078a

HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.

4.7e-05:194:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53214

HRIFA010085a

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

2.9e-92:243:69

HOMO SAPIENS (HUMAN).

Q03923

HRIFA010090a

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

6.7e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

HRIFA010130a

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

5.6e-13:99:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

HRIFA010152a

"ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)."

2.3e-05:73:43

CANIS FAMILIARIS (DOG).

P30803

HRIFA010176a

HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).

0.066:105:31

MUS MUSCULUS (MOUSE).

P35583

HRIFA010301a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

1.1e-09:120:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

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- HRIFA010319a
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
(DBH).
4.8e-23:185:32
5 RATTUS NORVEGICUS (RAT).
Q05754
- HRIFA010361a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
10 2.6e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA010394a
15 HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
3.3e-36:144:47
CAENORHABDITIS ELEGANS.
P49191
- HRIFA010425a
20 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-09:199:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- HRIFA010460a
25 TRANSCRIPTIONAL ACTIVATOR FE65.
2.3e-27:101:54
RATTUS NORVEGICUS (RAT).
30 P46933
- HRIFA010466a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
5.3e-07:123:34
35 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA010490a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
40 0.0031:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129
- HRIFA010736a
45 PROTEIN Q300.
0.018:14:85
MUS MUSCULUS (MOUSE).
Q02722
- HRIFA010790a
50 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-
PORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-
NAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
1.6e-82:197:72
55 HOMO SAPIENS (HUMAN).
Q06495
- HRIFA010799a

EP 1 130 094 A2

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.7e-05:220:30

GALLUS GALLUS (CHICKEN).

P02457

HRIFA010859a

ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4).

0.063:134:33

HOMO SAPIENS (HUMAN).

P18825

HRIFA010891a

HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.

0.044:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P36015

HRIFA010975a

TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).

8.5e-113:144:86

HOMO SAPIENS (HUMAN).

P43405

HRIFA010988a

GASTRIN PRECURSOR.

0.084:59:37

HOMO SAPIENS (HUMAN).

P01350

HRIFA011016a

PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).

3.1e-15:127:37

RATTUS NORVEGICUS (RAT).

P38659

HRIFA011105a

SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.

0.97:41:43

DROSOPHILA MELANOGASTER (FRUIT FLY).

P02841

HRIFA011128a

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).

0.0046:30:63

LYCOPERSICON ESCULENTUM (TOMATO).

Q01157

HRIFA011179a

PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).

1.1e-20:127:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34244

HRIFA011197a

DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).

5.8e-26:169:40

MUS MUSCULUS (MOUSE).

P28843

HRIFA011449a

GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).

1.9e-26:109:53

MUS MUSCULUS (MOUSE).

P24788

HRIFA011484a

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.00055:115:33

HOMO SAPIENS (HUMAN).

P21917

HRIFA011512a

POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).

0.00024:139:25

HOMO SAPIENS (HUMAN).

P51531

HRIFA011580a

VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI) PHOSVITIN (PV) LIPOVITELLIN II (LVII) YGP40].

4.0e-08:182:32

GALLUS GALLUS (CHICKEN).

P02845

HRIFA011659a

VON WILLEBRAND FACTOR PRECURSOR.

9.8e-17:210:25

HOMO SAPIENS (HUMAN).

P04275

HRIFA011820a

ZINC FINGER PROTEIN 136.

1.9e-10:42:73

HOMO SAPIENS (HUMAN).

P52737

HRIFA011926a

TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).

1.0:149:22

PSEUDOMONAS AERUGINOSA.

P15276

HRIFA011947a

ZINC FINGER PROTEIN 136.

1.3e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

HRIFA012069a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.0027:205:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA012151a

EP 1 130 094 A2

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.
0.00028:72:37
RATTUS NORVEGICUS (RAT).
Q07008

5

HRIFA012167a
HYPOTHETICAL SYMPORTER IN GLTS-SELC INTERGENIC REGION.
6.4e-09:145:28
ESCHERICHIA COLI.
P31435

10

HRIFA012278a
ZINC FINGER PROTEIN 140.
3.1e-14:88:52
HOMO SAPIENS (HUMAN).
P52738

15

HRIFA012354a
"SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT."
2.1e-05:120:32
RATTUS NORVEGICUS (RAT).
P04775

20

HRIFA012427a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.3e-08:250:28
MUS MUSCULUS (MOUSE).
P11087

25

HRIFA012436a
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
4.7e-09:95:31
HOMO SAPIENS (HUMAN).
Q04941

30

HRIFA012515a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
3.5e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170

35

HRIFA012584a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
4.9e-14:136:29
NEUROSPORA CRASSA.
P23231

45

HRIFA012625a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."
9.6e-12:103:40
RATTUS NORVEGICUS (RAT).
P13386

55

HRIFA012692a

BLOOM'S SYNDROME PROTEIN.

6.3e-26:203:34

HOMO SAPIENS (HUMAN).

P54132

5

HRIFA012702a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

1.9e-07:153:30

ZEA MAYS (MAIZE).

10

P14918

HRIFA012737a

LEUCOCYTE ANTIGEN CD97 PRECURSOR.

1.6e-09:170:24

15

HOMO SAPIENS (HUMAN).

P48960

HRIFA012795a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).

20

3.0e-34:189:39

RATTUS NORVEGICUS (RAT).

P15387

HRIFA012885a

25

HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.

2.9e-21:159:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47032

30

HRIFA012914a

ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70 TRANSMEMBRANE PROTEIN P20E].

3.4e-29:134:47

BABOON ENDOGENOUS VIRUS (STRAIN M7).

35

P10269

HRIFA012969a

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

40

1.2e-30:228:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

HRIFA012990a

45

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

7.4e-20:181:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39986

50

HRIFA013092a

OUTER MEMBRANE PROTEIN H.8 PRECURSOR.

0.0039:51:39

NEISSERIA GONORRHOEAE.

P11910

55

HRIFA013103a

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-

FERASE) (GT).

0.25:50:34

MUS MUSCULUS (MOUSE).

P15535

5

HRIFA013135a

CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).

1.6e-05:214:28

CLOSTRIDIUM THERMOCELLUM.

10

Q06852

HRIFA013235a

PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.

1.9e-05:113:40

15

HOMO SAPIENS (HUMAN).

P02461

HRIFA013254a

COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].

20

3.8e-13:123:41

MUS MUSCULUS (MOUSE).

P01029

HRIFA013265a

25

CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).

7.0e-107:225:86

HOMO SAPIENS (HUMAN).

P07711

30

HRIFA013276a

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

2.2e-117:270:85

HOMO SAPIENS (HUMAN).

P21589

35

HRIFA013279a

CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).

4.9e-05:127:37

PLASMODIUM VIVAX.

40

P08677

HRIFA013376a

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

45

8.0e-23:230:31

NEUROSPORA CRASSA.

P23231

50

HRIFA013477a

OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).

5.8e-87:197:87

HOMO SAPIENS (HUMAN).

P41217

55

HRIFA013586a

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

3.8e-31:93:64
BOS TAURUS (BOVINE).
P07106

5 HRIFA013589a
T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).
5.0e-06:95:35
HOMO SAPIENS (HUMAN).
P40200

10 HRIFA013620a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."
7.1e-08:95:37
15 MUS MUSCULUS (MOUSE).
P20490

HRIFA013726a
SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).
20 1.5e-33:99:50
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03497

HRIFA013744a
25 ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).
7.5e-15:105:38
BOS TAURUS (BOVINE).
P07106

30 HRIFA013911a
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
7.8e-37:104:46
HOMO SAPIENS (HUMAN).
35 P43251

HRIFA013919a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
1.2e-10:170:32
40 HOMO SAPIENS (HUMAN).
Q02817

HRIFA013932a
45 "SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].
2.6e-05:168:34
HOMO SAPIENS (HUMAN).
P04280

50 HRIFA013980a
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
0.00036:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
55 P18480

HRIFA014006a
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).

EP 1 130 094 A2

9.4e-16:185:28
MUS MUSCULUS (MOUSE).
P20937

5 HRIFA014024a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.0013:102:44
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

10 HRIFA014056a
PROTEIN Q300.
5.1e-05:24:70
MUS MUSCULUS (MOUSE).
15 Q02722

HRIFA014111a
TOLL PROTEIN PRECURSOR.
5.5e-08:203:27
20 DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953

HRIFA014133a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
25 1.6e-06:143:33
MUS MUSCULUS (MOUSE).
P05142

HRIFA014185a
30 LEUCOCYTE ANTIGEN CD97 PRECURSOR.
6.0e-14:192:30
HOMO SAPIENS (HUMAN).
P48960

35 HRIFA014336a
"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT)."
2.8e-70:198:58
SUS SCROFA (PIG).
P20305

40 HRIFA014396a
CREB-BINDING PROTEIN.
2.6e-07:101:34
MUS MUSCULUS (MOUSE).
45 P45481

HRIFA014397a
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.
5.2e-05:147:30
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25655

HRIFA014465a
55 HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
2.8e-11:166:30
CAENORHABDITIS ELEGANS.
P30638

EP 1 130 094 A2

- 5 HRIFA014500a
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
1.0e-14:149:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862
- 10 HRIFA014561a
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
4.1e-70:156:89
HOMO SAPIENS (HUMAN).
P46091
- 15 HRIFA014568a
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
2.4e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684
- 20 HRIFA014590a
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.18:26:30
GALLUS GALLUS (CHICKEN).
P14093
- 25 HRIFA014598a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
4.9e-05:124:29
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 30 HRIFA014620a
ENL PROTEIN.
0.58:170:30
HOMO SAPIENS (HUMAN).
35 Q03111
- 40 HRIFA014621a
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
2.7e-50:150:74
HOMO SAPIENS (HUMAN).
P11462
- 45 HRIFA014688a
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
6.9e-31:189:39
HOMO SAPIENS (HUMAN).
P18564
- 50 HRIFA014702a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
6.4e-05:89:40
MUS MUSCULUS (MOUSE).
P05142
- 55 HRIFA014819a
MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.
7.8e-26:117:46
HOMO SAPIENS (HUMAN).

P55083

HRIFA014868a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
8.9e-08:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

HRIFA014951a
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
4.1e-23:132:39
EQUUS CABALLUS (HORSE).
P80010

HRIFA014967a
CHLORINE CHANNEL PROTEIN P64.
2.0e-52:142:76
BOS TAURUS (BOVINE).
P35526

HRIFA015063a
ZINC FINGER PROTEIN 136.
6.6e-53:229:48
HOMO SAPIENS (HUMAN).
P52737

HRIFA015070a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
9.3e-24:143:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

HRIFA015122a
REGULATORY PROTEIN E2.
0.45:129:30
HUMAN PAPILLOMAVIRUS TYPE 5.
P06921

HRIFA015219a
FIBRILLIN 1 PRECURSOR (MP340).
9.9e-09:132:32
BOS TAURUS (BOVINE).
P98133

HRIFA015246a
PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
2.4e-33:184:46
HOMO SAPIENS (HUMAN).
Q00888

HRIFA015351a
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.0021:122:30
RATTUS NORVEGICUS (RAT).
P03994

HRIFA015423a
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).

1.2e-11:148:35

HOMO SAPIENS (HUMAN).

P20749

5

HRIFA015453a

RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).

6.8e-11:91:37

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P54644

10

HRIFA015486a

BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR).

2.0e-22:208:27

15

MUS MUSCULUS (MOUSE).

Q01339

HRIFA015506a

COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).

20

1.3e-12:73:50

HOMO SAPIENS (HUMAN).

P23508

HRIFA015536a

25

CHLORINE CHANNEL PROTEIN P64.

1.2e-49:115:79

BOS TAURUS (BOVINE).

P35526

30

HRIFA015547a

BEM46 PROTEIN (FRAGMENT).

1.4e-33:137:49

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P54069

35

HRIFA015568a

HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.

2.4e-16:152:34

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

40

Q09875

HRIFA015756a

EBNA-2 NUCLEAR PROTEIN.

2.9e-15:28:75

45

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P12978

HRIFA015802a

PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).

50

0.0035:122:30

RATTUS NORVEGICUS (RAT).

P03994

HRIFA015811a

55

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

6.2e-39:171:43

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

EP 1 130 094 A2

- 5 HRIFA015902a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.0075:161:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 10 HRIFA015947a
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.035:98:28
MUS MUSCULUS (MOUSE).
P10925
- 15 HRIFA015995a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
6.2e-08:221:37
HOMO SAPIENS (HUMAN).
P02461
- 20 HRIFA016070a
"COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR."
1.0e-18:179:35
HOMO SAPIENS (HUMAN).
P02745
- 25 HRIFA016214a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.0e-05:96:42
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA016240a
HYPOTHETICAL 65.3 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION.
8.5e-05:103:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
35 P47082
- 40 HRIFA016255a
EBNA-1 NUCLEAR PROTEIN.
4.5e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 45 HRIFA016290a
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
6.7e-21:182:41
HOMO SAPIENS (HUMAN).
P12259
- 50 HRIFA016430a
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
7.1e-50:120:86
HOMO SAPIENS (HUMAN).
P24390
- 55 HRIFA016599a
MEIOTIC RECOMBINATION PROTEIN REC104.
0.57:73:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33323

HRIFA016639a

"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."

8.0e-06:206:23

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08640

HRIFA016654a

HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).

1.1e-78:181:86

ORYCTOLAGUS CUNICULUS (RABBIT).

P33279

HRIFA016669a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

1.4e-08:87:36

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA016758a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

9.5e-17:158:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

HRIFA016963a

FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.

6.2e-08:131:32

LYMNAEA STAGNALIS (GREAT POND SNAIL).

P42565

HRIFA017031a

MYOSIN HEAVY CHAIN KINASE A (EC 2.7.1.129) (MHCK A).

2.6e-11:152:34

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P42527

HRIFA017146a

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.0014:78:37

HOMO SAPIENS (HUMAN).

P21917

HRIFA017190a

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0026:89:30

HOMO SAPIENS (HUMAN).

Q01543

HRIFA017257a

"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)."

2.5e-79:261:57

HOMO SAPIENS (HUMAN).

P06396

HRIFA017295a

EP 1 130 094 A2

"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."

3.4e-20:66:78

HOMO SAPIENS (HUMAN).

Q10469

HRIFA017312a

C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).

2.7e-19:221:33

HOMO SAPIENS (HUMAN).

P04003

HRIFA017456a

LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).

0.11:94:35

MUS MUSCULUS (MOUSE).

P19137

HRIFA017457a

SYNAPTOTAGMIN II.

7.2e-07:98:35

MUS MUSCULUS (MOUSE).

P46097

HRIFA017643a

NOV PROTEIN HOMOLOG PRECURSOR (NOVH).

2.2e-07:81:41

HOMO SAPIENS (HUMAN).

P48745

HRIFA017670a

TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.

4.9e-06:172:27

RATTUS NORVEGICUS (RAT).

P19814

HRIFA017703a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

1.9e-16:129:34

THERMOMONOSPORA CURVATA.

P49695

HRIFA017791a

MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).

0.012:71:38

HOMO SAPIENS (HUMAN).

Q02817

HRIFA017801a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

4.5e-07:86:39

MUS MUSCULUS (MOUSE).

P05142

HRIFA017818a

ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN).

1.0:32:40

STREPTOMYCES LIVIDANS.
P50014

HRIFA017836a
"TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H))."
1.3e-08:113:31
PASTEURELLA MULTOCIDA.
P51564

HRIFA017855a
ORM1 PROTEIN.
1.7e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

HRIFA017921a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
2.0e-09:182:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA018092a
"DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)."
2.1e-20:119:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P17898

HRIFA018131a
ORM1 PROTEIN.
2.6e-20:137:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

HRIFA018134a
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
1.1e-11:147:32
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Q05609

HRIFA018238a
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).
8.6e-06:74:44
MUS MUSCULUS (MOUSE).
Q01705

HRIFA018262a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
6.4e-10:71:38
THERMOMONOSPORA CURVATA.
P49695

HRIFA018287a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
1.5e-06:214:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214

EP 1 130 094 A2

HRIFA018447a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00065:133:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA018580a
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

HRIFA018666a
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).
1.7e-06:191:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P16621

HRIFA018688a
PHLB PROTEIN PRECURSOR.
1.9e-06:110:35
SERRATIA LIQUEFACIENS.
P18954

HRIFA018754a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."
1.8e-06:195:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

HRIFA018794a
MSP1 PROTEIN HOMOLOG.
3.2e-06:93:25
CAENORHABDITIS ELEGANS.
P54815

HRIFA018827a
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.1e-17:180:28
CAENORHABDITIS ELEGANS.
P30638

HRIFA018870a
HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.
4.7e-09:70:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47088

HRIFA018904a
MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).
5.5e-12:142:32
HOMO SAPIENS (HUMAN).
Q09013

HRIFA018931a

ZINC FINGER PROTEIN 140.

2.9e-10:47:74

HOMO SAPIENS (HUMAN).

P52738

5

HRIFA018993a

HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.

1.2e-13:117:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

10

P53073

HRIFA019105a

DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).

7.5e-22:203:32

15

DROSOPHILA MELANOGASTER (FRUIT FLY).

P25723

HRIFA019136a

"MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)."

20

1.0e-25:74:81

HOMO SAPIENS (HUMAN).

P29966

25

HRIFA019175a

PROTEIN KINASE WIS1 (EC 2.7.1.-).

1.3e-14:84:39

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

30

P33886

HRIFA019262a

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

2.5e-55:188:50

35

HOMO SAPIENS (HUMAN).

Q03923

HRIFA019412a

CATHEPSIN E PRECURSOR (EC 3.4.23.34).

1.4e-09:121:33

40

CAVIA PORCELLUS (GUINEA PIG).

P25796

HRIFA019437a

REGULATORY PROTEIN E2.

45

0.26:77:37

HUMAN PAPILLOMAVIRUS TYPE 14.

P36783

HRIFA019466a

EBNA-1 NUCLEAR PROTEIN.

50

2.7e-19:130:43

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

55

HRIFA019490a

TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).

1.1e-09:132:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

HRIFA019498a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAL (SHAL2).

5.6e-05:87:36

DROSOPHILA MELANOGASTER (FRUIT FLY).

P17971

HRIFA019532a

EBNA-1 NUCLEAR PROTEIN.

1.8e-05:67:49

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA019651a

ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).

6.1e-05:31:64

PLASMODIUM CHABAUDI.

Q02752

HRIFA019867a

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

8.2e-34:103:71

RATTUS NORVEGICUS (RAT).

Q06496

HRIFA019869a

SERINE/THREONINE-PROTEIN KINASE FUSED (EC 2.7.1.-).

7.2e-29:83:49

DROSOPHILA MELANOGASTER (FRUIT FLY).

P23647

HRIFA019958a

REPRESSOR PROTEIN CI (FRAGMENT).

0.99:45:37

BACTERIOPHAGE 434.

P16117

HRIFA020144a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

2.8e-06:176:30

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

HRIFA020184a

NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).

1.9e-10:102:37

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P18160

HRIFA020272a

MUSCARINIC ACETYLCHOLINE RECEPTOR M3.

5.5e-91:211:85

HOMO SAPIENS (HUMAN).

P20309

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- 5
HRIFA020335a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
5.0e-104:275:72
HOMO SAPIENS (HUMAN).
P27448
- 10
HRIFA020349a
BRITTLE-1 PROTEIN PRECURSOR.
6.0e-30:214:35
ZEA MAYS (MAIZE).
P29518
- 15
HRIFA020453a
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
2.5e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214
- 20
HRIFA020693a
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).
3.9e-09:96:35
HOMO SAPIENS (HUMAN).
P43146
- 25
HRIFA020707a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).
3.4e-09:95:33
TRYPANOSOMA BRUCEI BRUCEI.
30
Q06084
- 35
HRIFA020748a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
3.2e-09:210:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 40
HRIFA020862a
MODIFIER 3 PROTEIN (M33).
5.6e-26:76:61
MUS MUSCULUS (MOUSE).
P30658
- 45
HRIFA020883a
PROTEIN Q300.
0.00054:21:66
MUS MUSCULUS (MOUSE).
Q02722
- 50
HRIFA021007a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.092:73:36
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
55
P08393
- HRIFA021040a
TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).

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0.98:63:39
HOMO SAPIENS (HUMAN).
P43694

5 HRIFA021061a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-09:162:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

10 HRIFA021213a
OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.
2.0e-38:96:72
CAENORHABDITIS ELEGANS.
P46975

15 HRIFA021224a
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
2.8e-06:55:52
20 RATTUS NORVEGICUS (RAT).
Q02975

HRIFA021398a
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
25 2.5e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139

HRIFA021445a
30 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEBOX PROTEIN PBX1) (HOMEBOX PROTEIN PRL).
0.38:146:31
HOMO SAPIENS (HUMAN).
P40424

35 HRIFA021494a
EBNA-1 NUCLEAR PROTEIN.
6.8e-07:116:41
40 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA021499a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.1e-34:159:50
45 GALLUS GALLUS (CHICKEN).
P05099

HRIFA021543a
50 ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).
0.0087:50:40
GALLUS GALLUS (CHICKEN).
Q03352

55 HRIFA021620a
PLATELET FACTOR 4 (PF-4).
0.019:65:27
SUS SCROFA (PIG).
P30034

- 5 HRIFA021637a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
6.0e-37:147:53
GALLUS GALLUS (CHICKEN).
P05099
- 10 HRIFA021651a
CARG-BINDING FACTOR-A (CBF-A).
2.6e-11:170:30
MUS MUSCULUS (MOUSE).
Q99020
- 15 HRIFA021754a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.2e-37:137:51
GALLUS GALLUS (CHICKEN).
P05099
- 20 HRIFA021781a
DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COM-
PLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).
7.1e-19:199:31
HOMO SAPIENS (HUMAN).
P18074
- 25 HRIFA021787a
PROTEIN Q300.
0.051:13:84
MUS MUSCULUS (MOUSE).
30 Q02722
- 35 HRIFA021794a
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
1.6e-07:90:32
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 40 HRIFA021855a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.6e-06:163:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 45 HRIFA021906a
S-ANTIGEN PROTEIN PRECURSOR.
2.1e-09:226:28
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593
- 50 HRIFA022055a
BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).
0.63:118:31
ACHROMOBACTER LYTICUS.
P27458
- 55 HRIFA022065a
BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.
9.7e-24:235:34

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HOMO SAPIENS (HUMAN).
P16279

5 HRIFA022139a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.1e-57:232:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782

10 HRIFA022156a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR."
1.4e-07:133:35
TRITICUM AESTIVUM (WHEAT).
P08489

15 HRIFA022166a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.5e-28:194:35
HOMO SAPIENS (HUMAN).
20 Q03468

HRIFA022177a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.2e-12:137:32
25 THERMOMONOSPORA CURVATA.
P49695

HRIFA022182a
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).
30 1.2e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793

HRIFA022203a
35 COLLAGEN ALPHA 1 (III) CHAIN.
1.1e-05:211:33
BOS TAURUS (BOVINE).
P04258

40 HRIFA022227a
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
3.2e-31:229:36
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
45 Q10071

HRIFA022234a
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
1.8e-08:110:30
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P09620

HRIFA022249a
55 ZINC FINGER PROTEIN 133.
1.1e-34:84:48
HOMO SAPIENS (HUMAN).
P52736

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- HRIFA022265a
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
5.1e-26:188:40
5 RATTUS NORVEGICUS (RAT).
P13234
- HRIFA022328a
SCO1 PROTEIN PRECURSOR.
10 5.4e-25:84:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23833
- HRIFA022335a
15 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.21:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 20 HRIFA022348a
AGAMOUS PROTEIN.
1.0:40:42
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
25 P17839
- HRIFA022411a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
30 0.00059:111:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- HRIFA022423a
35 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
2.5e-15:106:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857
- HRIFA022462a
40 RETINOIC ACID RECEPTOR RXR-BETA.
0.0010:124:33
HOMO SAPIENS (HUMAN).
P28702
- 45 HRIFA022493a
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
0.0018:130:34
MUS MUSCULUS (MOUSE).
50 Q01338
- HRIFA022528a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
3.2e-23:230:28
55 ZEA MAYS (MAIZE).
P14918
- HRIFA022546a

NINAC SHORT PROTEIN (EC 2.7.1.-).
8.5e-42:209:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P10677

5

HRIFA022564a
ZINC FINGER PROTEIN 140.
7.9e-23:116:51
HOMO SAPIENS (HUMAN).
P52738

10

HRIFA022616a
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
7.4e-36:172:43
HOMO SAPIENS (HUMAN).
Q07954

15

HRIFA022671a
PAIRED AMPHIPATHIC HELIX PROTEIN.
2.0e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

20

HRIFA022691a
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
1.4e-44:229:41
PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).
P19477

25

30

HRIFA022702a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.1e-08:146:38
GALLUS GALLUS (CHICKEN).
P02457

35

HRIFA022707a
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).
7.0e-40:229:37
HOMO SAPIENS (HUMAN).
P16383

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HRIFA022714a
"AMELOGENIN, CLASS I PRECURSOR."
0.62:96:31
BOS TAURUS (BOVINE).
P02817

45

HRIFA022728a
ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).
1.7e-06:28:64
SUS SCROFA (PIG).
P08001

50

HRIFA022729a
"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."

55

7.7e-29:69:84

HOMO SAPIENS (HUMAN).

Q10469

- 5 HRIFA022737a
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).
6.7e-19:170:37
GALLUS GALLUS (CHICKEN).
10 P10039
- HRIFA022776a
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
4.0e-20:199:31
15 MEDICAGO SATIVA (ALFALFA).
P38661
- HRIFA022782a
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
20 3.7e-09:184:36
PLASMODIUM CYNOMOLGI (STRAIN BEROK).
P08672
- HRIFA022865a
25 COLLAGEN ALPHA 1(III) CHAIN.
2.5e-09:169:33
BOS TAURUS (BOVINE).
P04258
- HRIFA022875a
30 BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
9.1e-14:115:33
BOS TAURUS (BOVINE).
P21793
- HRIFA022890a
35 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.8e-10:237:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
40 P17437
- HRIFA022895a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.4e-106:283:67
45 HOMO SAPIENS (HUMAN).
Q03923
- HRIFA022985a
50 PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).
3.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.
Q06084
- HRIFA023007a
55 MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).
1.1e-27:66:54
HOMO SAPIENS (HUMAN).

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P22670

HRIFA023048a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

2.2e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

HRIFA023069a

BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).

3.4e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

HRIFA023129a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

4.2e-06:37:51

PLASMODIUM LOPHURAE.

P04929

HRIFA023154a

GLYCOPROTEIN X PRECURSOR.

8.2e-05:140:27

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

HRIFA023212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

8.3e-10:249:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA023227a

GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).

9.2e-15:180:30

ESCHERICHIA COLI.

P37021

HRIFA023257a

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

2.4e-118:229:88

RATTUS NORVEGICUS (RAT).

P38378

HRIFA023304a

PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-ATPASE).

1.3e-23:222:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39524

HRIFA023434a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

0.00018:157:30

RATTUS NORVEGICUS (RAT).

P17659

- 5 HRIFA023464a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 10 HRIFA023489a
HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.
4.4e-09:230:23
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10297
- 15 HRIFA023634a
EBNA-1 NUCLEAR PROTEIN.
1.8e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 20 HRIFA023767a
CYTOCHROME B5.
1.1e-12:92:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312
- 25 HRIFA023894a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-05:80:40
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA023923a
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
4.2e-76:128:85
HOMO SAPIENS (HUMAN).
35 P00395
- 40 HRIFA024088a
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).
1.1e-05:118:32
MUS MUSCULUS (MOUSE).
P98084
- 45 HRIFA024132a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
6.5e-40:136:61
HOMO SAPIENS (HUMAN).
P51787
- 50 HRIFA024185a
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.55:128:29
HOMO SAPIENS (HUMAN).
P50548
- 55 HRIFA024197a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP (CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).

7.5e-09:93:34
NEUROSPORA CRASSA.
P23231

5 HRIFA024218a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.7e-06:180:36
HOMO SAPIENS (HUMAN).
P02452

10 HRIFA024255a
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
4.8e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
15 Q10496

HRIFA024305a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.047:47:29
20 HOMO SAPIENS (HUMAN).
P18850

HRIFA024392a
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
25 6.7e-24:119:43
HOMO SAPIENS (HUMAN).
P51805

HRIFA024423a
30 COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

35 HRIFA024473a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
3.3e-05:106:41
BOS TAURUS (BOVINE).
P02453

40 HRIFA024482a
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
1.2e-07:99:31
NICOTIANA TABACUM (COMMON TOBACCO).
45 Q03211

HRIFA024504a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
50 DROXYSTEROID DEHYDROGENASE).
2.6e-43:205:49
HOMO SAPIENS (HUMAN).
P37058

55 HRIFA024543a
GLYCOPROTEIN X PRECURSOR.
1.5e-06:257:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

- 5 HRIFA024718a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
5.3e-45:168:52
MUS MUSCULUS (MOUSE).
P23780
- 10 HRIFA024767a
SODIUM CHANNEL PROTEIN (NA⁺ CHANNEL).
7.4e-30:221:31
ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
P02719
- 15 HRIFA024884a
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.0089:23:65
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245
- 20 HRIFA024893a
REGULATORY PROTEIN E2.
0.0021:167:31
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422
- 25 HRIFA024937a
GNS1 PROTEIN.
1.0e-15:173:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358
- 30 HRIFA024978a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.00019:150:32
HOMO SAPIENS (HUMAN).
35 Q02817
- 40 HRIFA024994a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
5.3e-22:145:46
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 45 HRIFA025033a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.50:215:29
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- 50 HRIFA025046a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
1.7e-41:104:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 55 HRIFA025250a
"PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR))."
7.4e-17:126:34
DROSOPHILA MELANOGASTER (FRUIT FLY).

P05130

HRIFA025261a
MYOSIN I ALPHA (MMI-ALPHA).
2.3e-64:141:84
MUS MUSCULUS (MOUSE).
P46735

HRIFA025290a
EBNA-1 NUCLEAR PROTEIN.
0.016:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA025327a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
2.3e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

HRIFA025353a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834

HRIFA025479a
PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
3.0e-05:112:33
ESCHERICHIA COLI.
P31137

HRIFA025488a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR (FRAGMENTS).
9.5e-05:104:40
MUS MUSCULUS (MOUSE).
P08121

HRIFA025492a
SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
1.8e-53:159:69
HOMO SAPIENS (HUMAN).
Q13627

HRIFA025636a
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (EC 3.4.24.-) (TAT-BIND-
ING HOMOLOG 12).
4.7e-32:81:66
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40341

HRIFA025695a
PEREGRIN (BR140 PROTEIN).
3.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

HRIFA025703a

EP 1 130 094 A2

CELL SURFACE ANTIGEN 114/A10 PRECURSOR.

1.8e-08:71:42

MUS MUSCULUS (MOUSE).

P19467

5

HRIFA025706a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

1.2e-28:111:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

10

P43636

HRIFA025766a

CYTOCHROME B5.

4.2e-13:133:33

ORYCTOLAGUS CUNICULUS (RABBIT).

15

P00169

HRIFA025771a

HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.

20

6.7e-10:129:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53288

HRIFA025778a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

25

1.5e-05:212:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA025800a

HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.

30

3.7e-18:165:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40544

35

HRIFA025904a

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

2.6e-05:211:28

HOMO SAPIENS (HUMAN).

40

P17927

HRIFA025907a

INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUPI-5111).

2.1e-38:176:38

HOMO SAPIENS (HUMAN).

45

Q06323

HRIFA025913a

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

50

2.5e-32:185:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

HRIFA025936a

TRANSCRIPTIONAL ACTIVATOR FE65.

55

3.4e-09:43:46

RATTUS NORVEGICUS (RAT).

P46933

5 HRIFA025966a
SYNAPTOTAGMIN III.
4.5e-05:93:33
RATTUS NORVEGICUS (RAT).
P40748

10 HRIFA025978a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR."
3.5e-06:224:28
TRITICUM AESTIVUM (WHEAT).
P10388

15 HRIFA026089a
BUTYROPHILIN PRECURSOR (BT).
1.1e-12:146:29
BOS TAURUS (BOVINE).
P18892

20 HRIFA026121a
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
9.7e-06:72:43
HOMO SAPIENS (HUMAN).
P48023

25 HRIFA026242a
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
7.4e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566

30 HRIFA026265a
DNA BINDING PROTEIN S1FA.
0.67:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551

35 HRIFA026303a
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.014:88:32
HOMO SAPIENS (HUMAN).
P10163

45 HRIFA026316a
EBNA-2 NUCLEAR PROTEIN.
1.5e-07:82:35
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978

50 HRIFA026351a
FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
0.019:89:31
HOMO SAPIENS (HUMAN).
Q01543

55 HRIFA026364a
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.
8.3e-40:167:49
RATTUS NORVEGICUS (RAT).

P48303

HRIFA026382a

T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).

5 6.2e-10:135:38

ORYCTOLAGUS CUNICULUS (RABBIT).

P06333

HRIFA026465a

10 COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).

8.6e-07:158:35

GALLUS GALLUS (CHICKEN).

P12106

HRIFA026496a

15 ZINC FINGER PROTEIN 140.

5.9e-24:122:52

HOMO SAPIENS (HUMAN).

P52738

20

HRIFA026519a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

1.3e-08:130:36

MUS MUSCULUS (MOUSE).

25

P05142

HRIFA026564a

GLYCOPROTEIN X PRECURSOR

1.8e-10:225:25

30

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

HRIFA026576a

35 "ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)."

1.7e-09:116:34

HOMO SAPIENS (HUMAN).

P12235

HRIFA026615a

40 REGULATORY PROTEIN E2.

0.0024:132:31

HUMAN PAPILLOMAVIRUS TYPE 9.

P36780

45

HRIFA026618a

PROTEIN Q300.

1.2e-05:27:66

MUS MUSCULUS (MOUSE).

50

Q02722

HRIFA026659a

SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KINASE).

55

2.0e-10:81:45

RATTUS NORVEGICUS (RAT).

Q06226

EP 1 130 094 A2

- HRIFA026764a
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
3.4e-05:162:25
RATTUS NORVEGICUS (RAT).
5 P10252
- HRIFA026789a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
8.1e-22:175:38
10 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818
- HRIFA026813a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."
15 7.1e-89:256:67
HOMO SAPIENS (HUMAN).
Q15139
- HRIFA026860a
20 MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).
2.6e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988
- HRIFA026923a
25 CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.18:119:36
CANIS FAMILIARIS (DOG).
P39881
30
- HRIFA027012a
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSI-
DASE) (ALPHA-MANNOSIDASE 1A)."
1.8e-44:234:41
35 MUS MUSCULUS (MOUSE).
P45700
- HRIFA027045a
40 HYPOTHETICAL PROTEIN HI0519.
2.7e-27:181:38
HAEMOPHILUS INFLUENZAE.
P44742
- HRIFA027125a
45 ZINC FINGER PROTEIN 133.
3.9e-33:70:61
HOMO SAPIENS (HUMAN).
P52736
- HRIFA027173a
50 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.15:137:27
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
55
- HRIFA027179a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.6e-30:90:77

HOMO SAPIENS (HUMAN).
Q03468

5 HRIFA027187a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
4.7e-11:44:61
HOMO SAPIENS (HUMAN).
P20931

10 HRIFA027327a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
3.8e-07:184:35
HOMO SAPIENS (HUMAN).
Q03692

15 HRIFA027329a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
9.1e-08:195:29
20 DROSOPHILA ERECTA (FRUIT FLY).
P13730

HRIFA027355a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
1.9e-06:33:72
25 HOMO SAPIENS (HUMAN).
P20931

HRIFA027485a
COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
30 0.00099:174:36
HOMO SAPIENS (HUMAN).
P12107

HRIFA027536a
35 VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
0.0042:104:35
DROSOPHILA MELANOGASTER (FRUIT FLY).
P13238

40 HRIFA027549a
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00023:101:44
HOMO SAPIENS (HUMAN).
P21917

45 HRIFA027622a
GUANOSINE-DIPHOSPHATASE (EC 3.6.1.42) (GDPASE).
2.2e-23:146:45
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32621

HRIFA027625a
CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).
1.1e-57:220:54
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P13586

HRIFA027644a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
7.5e-05:72:40
RATTUS NORVEGICUS (RAT).
P02454

5

HRIFA027656a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
1.6e-13:149:34
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

10

HRIFA027673a
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
6.4e-06:47:57
HOMO SAPIENS (HUMAN).
P29279

15

HRIFA027681a
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.1e-13:158:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458

20

HRIFA027714a
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
7.2e-06:146:30
CAENORHABDITIS ELEGANS.
P46580

25

HRIFA027722a
SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
2.7e-105:242:85
CANIS FAMILIARIS (DOG).
Q00004

30

HRIFA027860a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.3e-08:168:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

35

HRIFA027867a
STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-
EOCALCIN).
1.0:100:27
ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
P18301

45

HRIFA027940a
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
8.7e-15:149:38
HOMO SAPIENS (HUMAN).
P55103

50

HRIFA028061a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
9.7e-07:157:26
THERMOMONOSPORA CURVATA.

55

P49695

HRIFA028157a

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

2.8e-71:201:68

HOMO SAPIENS (HUMAN).

P30825

HRIFA028187a

EBNA-1 NUCLEAR PROTEIN.

1.5e-09:131:38

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA028262a

CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).

7.2e-09:99:33

MUS MUSCULUS (MOUSE).

P53996

HRIFA028371a

PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).

1.0e-08:103:33

RATTUS NORVEGICUS (RAT).

Q01177

HRIFA028402a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

3.2e-33:204:39

THERMOMONOSPORA CURVATA.

P49695

HRIFA028440a

COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.

1.9e-07:192:36

HOMO SAPIENS (HUMAN).

P53420

HRIFA028468a

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].

5.8e-32:178:44

RATTUS NORVEGICUS (RAT).

P13234

HRIFA028501a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

6.3e-05:161:31

RATTUS NORVEGICUS (RAT).

P17659

HRIFA028511a

ANKYRIN HOMOLOG PRECURSOR.

3.0e-19:176:34

CHROMATIUM VINOSUM.

Q06527

- 5
HRIFA028576a
ACROSIN PRECURSOR (EC 3.4.21.10).
4.8e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038
- 10
HRIFA028614a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
1.0e-08:82:39
PLASMODIUM LOPHURAE.
P04929
- 15
HRIFA028651a
BAND 3 ANION TRANSPORT PROTEIN.
1.3e-18:156:32
GALLUS GALLUS (CHICKEN).
P15575
- 20
HRIFA028790a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
5.0e-18:212:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 25
HRIFA028804a
CCAAT-BINDING FACTOR (CBF).
0.98:232:23
MUS MUSCULUS (MOUSE).
P53569
- 30
HRIFA028867a
REGULATORY PROTEIN E2.
0.0057:124:31
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787
- 35
HRIFA028911a
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.
1.2e-09:206:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47179
- 45
HRIFA028983a
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0051:115:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439
- 50
HRIFA029002a
FIBRINOGEN BETA CHAIN.
3.2e-25:121:45
BOS TAURUS (BOVINE).
P02676
- 55
HRIFA029050a
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
1.2e-10:134:32
GALLUS GALLUS (CHICKEN).

P24503

HRIFA029208a

RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).

1.4e-14:64:59

RATTUS NORVEGICUS (RAT).

Q02975

HRIFA029209a

"ALPHA-MANNOSIDASE II (EC 3.2.1.114) (MANNOsyl-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II)."

2.3e-12:114:37

MUS MUSCULUS (MOUSE).

P27046

HRIFA029256a

GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26).

1.8e-35:89:75

HOMO SAPIENS (HUMAN).

P29033

HRIFA029263a

SARCALUMENIN PRECURSOR.

2.1e-16:161:31

ORYCTOLAGUS CUNICULUS (RABBIT).

P13666

HRIFA029278a

"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].

3.5e-10:204:32

HOMO SAPIENS (HUMAN).

P04280

HRIFA029285a

GLYCOPROTEIN 25L PRECURSOR (GP25L).

4.9e-58:197:55

CANIS FAMILIARIS (DOG).

P27869

HRIFA029317a

HIGH AFFINITY SULPHATE TRANSPORTER 2.

2.3e-25:83:50

STYLOSANTHES HAMATA.

P53392

HRIFA029327a

MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).

9.1e-34:227:37

BOS TAURUS (BOVINE).

P22292

HRIFA029349a

CUTICLE COLLAGEN 12 PRECURSOR.

5.1e-09:190:33

CAENORHABDITIS ELEGANS.

P20630

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- 5 HRIFA029393a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
9.7e-69:165:84
HOMO SAPIENS (HUMAN).
P35414
- 10 HRIFA029398a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.011:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 15 HRIFA029425a
ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN).
2.0e-08:99:32
BOS TAURUS (BOVINE).
P02510
- 20 HRIFA029434a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CPS) [CONTAINS: BASIC PEP-
TIDE IB-6" PEPTIDE P-H].
2.6e-05:232:32
HOMO SAPIENS (HUMAN).
P04280
- 25 HRIFA029440a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00046:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 30 HRIFA029460a
SYNAPTOTAGMIN III.
1.5e-08:102:35
RATTUS NORVEGICUS (RAT).
P40748
- 40 HRIFA029467a
GLYCOPROTEIN X PRECURSOR.
5.2e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 45 HRIFA029508a
PROPERDIN PRECURSOR.
1.9e-06:218:32
HOMO SAPIENS (HUMAN).
P27918
- 50 HRIFA029511a
POTASSIUM CHANNEL PROTEIN EAG.
2.3e-66:139:61
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q02280
- 55 HRIFA029602a
SEX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR).
1.0:37:37

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SUS SCROFA (PIG).
P36393

HRIFA029649a

5 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.30:99:34

HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

10 HRIFA029715a

GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP).
0.54:95:30

HOMO SAPIENS (HUMAN).

15 P35638

HRIFA029730a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
3.8e-05:131:29

20 PLASMODIUM LOPHURAE.
P04929

HRIFA029792a

25 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
9.0e-09:178:30

THERMOMONOSPORA CURVATA.
P49695

HRIFA029802a

30 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).
7.2e-73:204:69
CANIS FAMILIARIS (DOG).
Q01685

35 HRIFA029866a

PROTEIN KINASE BYR2 (EC 2.7.1.-) (PROTEIN KINASE STE8) (MAPK KINASE KINASE) (MAPKKK).
1.2e-27:144:45
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P28829

40 HRIFA029932a

F-SPONDIN PRECURSOR.
9.1e-24:191:37

45 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447

HRIFA030025a

50 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
1.0e-11:138:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802

55 HRIFA030045a

SARCALUMENIN PRECURSOR.
2.4e-20:151:32

ORYCTOLAGUS CUNICULUS (RABBIT).
P13666

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- HRIFA030103a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.1e-05:215:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214
- HRIFA030106a
SCO-SPONDIN (FRAGMENT).
0.53:60:36
BOS TAURUS (BOVINE).
P98167
- HRIFA030147a
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
1.8e-10:93:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53257
- HRIFA030250a
ENAMELIN (TUFTELIN).
3.7e-108:250:86
BOS TAURUS (BOVINE).
P27628
- HRIFA030264a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
3.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170
- HRIFA030342a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
1.5e-42:203:49
HOMO SAPIENS (HUMAN).
P37058
- HRIFA030370a
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
8.0e-12:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555
- HRIFA030371a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."
1.6e-68:228:59
HOMO SAPIENS (HUMAN).
Q15139
- HRIFA030381a
COLLAGEN 1(X) CHAIN PRECURSOR.
3.0e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125
- HRIFA030385a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

0.029:162:31

HOMO SAPIENS (HUMAN).

Q03692

5 HRIFA030411a
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).

1.2e-27:115:53

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

10 Q09925

HRIFA030448a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).

2.5e-92:225:77

15 HOMO SAPIENS (HUMAN).

P27448

HRIFA030456a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

20 9.3e-08:127:35

MUS MUSCULUS (MOUSE).

P05142

HRIFA030461a

25 CUTICLE COLLAGEN 12 PRECURSOR.

0.046:140:31

CAENORHABDITIS ELEGANS.

P20630

30 HRIFA030472a

NUC-1 NEGATIVE REGULATORY PROTEIN PREG.

0.0030:98:31

NEUROSPORA CRASSA.

35 Q06712

HRIFA030509a

"INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE)."

2.5e-09:65:43

40 HOMO SAPIENS (HUMAN).

P19525

HRIFA030511a

T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN.

45 0.00010:99:33

HOMO SAPIENS (HUMAN).

P21145

HRIFA030545a

50 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).

7.6e-21:165:35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53974

55 HRIFA030566a

"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."

2.7e-07:221:30

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

HRIFA030599a
GLYCOPROTEIN X PRECURSOR.
2.8e-05:236:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA030629a
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).
3.5e-16:115:38
BOS TAURUS (BOVINE).
P05307

HRIFA030642a
SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).
2.5e-12:93:47
VOLVOX CARTERI.
P21997

HRIFA030662a
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
9.1e-120:279:83
HOMO SAPIENS (HUMAN).
P03886

HRIFA030839a
HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.
1.0:66:27
ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).
Q00135

HRIFA031091a
PROTEIN Q300.
0.0042:27:62
MUS MUSCULUS (MOUSE).
Q02722

HRIFA031126a
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (RB INTRON ENCODED G-PROTEIN COUPLED RECEPTOR).
1.3e-06:70:34
HOMO SAPIENS (HUMAN).
P43657

HRIFA031249a
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
5.9e-05:166:31
RATTUS NORVEGICUS (RAT).
P04474

HRIFA031336a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).

P25210

HRIFA031395a

COLD SHOCK PROTEIN CSPB (FRAGMENT).

5 0.95:32:40

BACILLUS GLOBISPORUS.

P41018

HRIFA031397a

10 REGULATORY PROTEIN E2.

0.0077:145:35

HUMAN PAPILLOMAVIRUS TYPE 47.

P22420

HRIFA031438a

15 GLUCOSE REPRESSION MEDIATOR PROTEIN.

1.3e-06:176:26

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

20

HRIFA031869a

TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (RHL).

1.7e-18:163:41

RATTUS NORVEGICUS (RAT).

25 Q04666

HRIFA031935a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

1.8e-06:192:32

30 ZEA MAYS (MAIZE).

P14918

HRIFA031986a

35 SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).

2.4e-49:222:47

RATTUS NORVEGICUS (RAT).

P35465

HRIFA032009a

40 PROBABLE G PROTEIN-COUPLED RECEPTOR FROM T-CELLS PRECURSOR (GLUCOCORTICOID-INDUCED RECEPTOR).

1.0e-17:118:36

MUS MUSCULUS (MOUSE).

45 P30731

HRIFA032011a

MUSCARINIC ACETYLCHOLINE RECEPTOR M4.

7.8e-35:184:32

50 HOMO SAPIENS (HUMAN).

P08173

HRIFA032070a

MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.

55 2.1e-18:107:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23500

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HRIFA032073a
SECRETOTRANIN III PRECURSOR (SGIII).
9.7e-69:182:76
MUS MUSCULUS (MOUSE).
P47867

5

HRIFA032079a
HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.
3.5e-12:96:39
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09906

10

HRIFA032097a
GLYCOPROTEIN J.
0.023:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480

15

HRIFA032161a
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.22:56:42
HOMO SAPIENS (HUMAN).
P49716

20

25

HRIFA032186a
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN) (TAXREB302).
0.86:50:38
HOMO SAPIENS (HUMAN).
Q10586

30

HRIFA032224a
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
2.6e-43:196:45
CAENORHABDITIS ELEGANS.
Q03567

35

HRIFA032257a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
4.7e-07:204:25
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922

40

HRIFA032274a
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
7.8e-60:163:74
MUS MUSCULUS (MOUSE).
Q07231

45

HRIFA032275a
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
7.2e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546

50

55

HRIFA032360a
HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.
3.0e-05:198:28

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CAENORHABDITIS ELEGANS.
Q09625

5 HRIFA032389a
EBNA-1 NUCLEAR PROTEIN.
1.3e-05:86:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P03211

10 HRIFA032433a
GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).
3.1e-14:54:53
RATTUS NORVEGICUS (RAT).
P30969

15 HRIFA032453a
BUTYROPHILIN PRECURSOR (BT).
5.9e-13:162:32
BOS TAURUS (BOVINE).
P18892

20 HRIFA032478a
GLYCOPROTEIN X PRECURSOR.
3.8e-06:253:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
25 P28968

HRIFA032506a
COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR.
1.2e-06:226:34
30 HOMO SAPIENS (HUMAN).
P12111

HRIFA032511a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
35 8.7e-09:229:34
HOMO SAPIENS (HUMAN).
Q07092

HRIFA032530a
40 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
9.0e-05:159:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

45 HRIFA032587a
SYNAPTOTAGMIN (P65).
3.2e-08:72:52
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P41823

50 HRIFA032605a
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER
PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESS-
ING 1).
55 8.4e-37:192:41
HOMO SAPIENS (HUMAN).
Q03518

HRIFA032642a
 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
 5.0e-05:127:33
 MUS MUSCULUS (MOUSE).
 P05142

HRIFA032696a
 COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
 1.4e-13:200:38
 BOS TAURUS (BOVINE).
 P02459

HRIFA032730a
 K-GLYPICAN PRECURSOR.
 4.8e-67:180:68
 MUS MUSCULUS (MOUSE).
 P51655

HRIFA032820a
 GLUTAMIC ACID-RICH PROTEIN PRECURSOR.
 7.5e-05:192:23
 PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).
 P13816

Homology search result 2

[0290] Homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database

[0291] Representative sequence of the 5'-end cluster exhibiting relatively high homology (304 cluster: "exhibiting relatively high homology" means that the P value is 10^{-10} or less)

HRIFA000327a, HRIFA000432a, HRIFA000553a, HRIFA000564a, HRIFA000631a, HRIFA000683a, HRIFA000776a,
 HRIFA000814a, HRIFA001132a, HRIFA001138a, HRIFA001337a, HRIFA001341a, HRIFA001489a, HRIFA001712a,
 HRIFA001720a, HRIFA001942a, HRIFA001975a, HRIFA001984a, HRIFA002384a, HRIFA002503a, HRIFA002743a,
 HRIFA002766a, HRIFA002805a, HRIFA002891a, HRIFA002919a, HRIFA002980a, HRIFA003063a, HRIFA003093a,
 HRIFA003635a, HRIFA004006a, HRIFA004034a, HRIFA004112a, HRIFA004426a, HRIFA004490a, HRIFA004523a,
 HRIFA004663a, HRIFA004696a, HRIFA004714a, HRIFA004745a, HRIFA004919a, HRIFA005184a, HRIFA005231a,
 HRIFA005240a, HRIFA005271a, HRIFA005372a, HRIFA005392a, HRIFA005409a, HRIFA005420a, HRIFA005438a,
 HRIFA005462a, HRIFA005644a, HRIFA005720a, HRIFA005732a, HRIFA005760a, HRIFA005781a, HRIFA006183a,
 HRIFA006494a, HRIFA006510a, HRIFA006566a, HRIFA006586a, HRIFA006596a, HRIFA006649a, HRIFA006667a,
 HRIFA006730a, HRIFA006926a, HRIFA007013a, HRIFA007219a, HRIFA007228a, HRIFA007243a, HRIFA007352a,
 HRIFA007424a, HRIFA007435a, HRIFA007463a, HRIFA007493a, HRIFA007571a, HRIFA007659a, HRIFA007722a,
 HRIFA007745a, HRIFA008000a, HRIFA008200a, HRIFA008284a, HRIFA008314a, HRIFA008362a, HRIFA008459a,
 HRIFA008483a, HRIFA008547a, HRIFA008611a, HRIFA008661a, HRIFA008717a, HRIFA008784a, HRIFA008981a,
 HRIFA009101a, HRIFA009171a, HRIFA009220a, HRIFA009451a, HRIFA009482a, HRIFA009783a, HRIFA009881a,
 HRIFA010085a, HRIFA010090a,
 HRIFA010130a, HRIFA010319a, HRIFA010394a, HRIFA010460a, HRIFA010790a, HRIFA010975a, HRIFA011016a,
 HRIFA011179a, HRIFA011197a, HRIFA011449a, HRIFA011659a, HRIFA011947a, HRIFA012278a, HRIFA012584a,
 HRIFA012625a, HRIFA012692a, HRIFA012795a, HRIFA012885a, HRIFA012914a, HRIFA012969a, HRIFA012990a,
 HRIFA013254a, HRIFA013265a, HRIFA013276a, HRIFA013376a, HRIFA013477a, HRIFA013586a, HRIFA013726a,
 HRIFA013744a, HRIFA013911a, HRIFA014006a, HRIFA014185a, HRIFA014336a, HRIFA014465a, HRIFA014500a,
 HRIFA014561a, HRIFA014568a, HRIFA014621a, HRIFA014688a, HRIFA014819a, HRIFA014951a, HRIFA014967a,
 HRIFA015063a, HRIFA015070a, HRIFA015246a, HRIFA015423a, HRIFA015453a, HRIFA015486a, HRIFA015506a,
 HRIFA015536a, HRIFA015547a, HRIFA015568a, HRIFA015756a, HRIFA015811a, HRIFA016070a, HRIFA016290a,
 HRIFA016430a, HRIFA016654a, HRIFA016758a, HRIFA017031a, HRIFA017257a, HRIFA017295a, HRIFA017312a,
 HRIFA017703a, HRIFA017855a, HRIFA018092a, HRIFA018131a, HRIFA018134a, HRIFA018580a, HRIFA018827a,
 HRIFA018904a, HRIFA018993a, HRIFA019105a, HRIFA019136a, HRIFA019175a, HRIFA019262a, HRIFA019466a,
 HRIFA019867a, HRIFA019869a, HRIFA020272a, HRIFA020335a, HRIFA020349a, HRIFA020862a, HRIFA021213a,
 HRIFA021398a, HRIFA021499a, HRIFA021637a, HRIFA021651a, HRIFA021754a, HRIFA021781a, HRIFA022065a,
 HRIFA022139a, HRIFA022166a, HRIFA022177a, HRIFA022182a, HRIFA022227a, HRIFA022249a, HRIFA022265a,

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HRIFA022328a, HRIFA022423a, HRIFA022528a, HRIFA022546a, HRIFA022564a, HRIFA022616a, HRIFA022671a, HRIFA022691a, HRIFA022707a, HRIFA022729a, HRIFA022737a, HRIFA022776a, HRIFA022875a, HRIFA022895a, HRIFA023007a, HRIFA023227a, HRIFA023257a, HRIFA023304a, HRIFA023464a, HRIFA023767a, HRIFA023923a, HRIFA024132a, HRIFA024255a, HRIFA024392a, HRIFA024423a, HRIFA024504a, HRIFA024718a, HRIFA024767a, 5 HRIFA024937a, HRIFA024994a, HRIFA025046a, HRIFA025250a, HRIFA025261a, HRIFA025353a, HRIFA025492a, HRIFA025636a, HRIFA025695a, HRIFA025706a, HRIFA025766a, HRIFA025800a, HRIFA025907a, HRIFA025913a, HRIFA026089a, HRIFA026364a, HRIFA026496a, HRIFA026789a, HRIFA026813a, HRIFA026860a, HRIFA027012a, HRIFA027045a, HRIFA027125a, HRIFA027179a, HRIFA027187a, HRIFA027622a, HRIFA027625a, HRIFA027656a, HRIFA027681a, HRIFA027722a, HRIFA027940a, HRIFA028157a, HRIFA028402a, HRIFA028468a, HRIFA028511a, 10 HRIFA028651a, HRIFA028790a, HRIFA029002a, HRIFA029208a, HRIFA029209a, HRIFA029256a, HRIFA029263a, HRIFA029285a, HRIFA029317a, HRIFA029327a, HRIFA029393a, HRIFA029511a, HRIFA029802a, HRIFA029866a, HRIFA029932a, HRIFA030025a, HRIFA030045a, HRIFA030250a, HRIFA030342a, HRIFA030370a, HRIFA030371a, HRIFA030411a, HRIFA030448a, HRIFA030545a, HRIFA030629a, HRIFA030642a, HRIFA030662a, HRIFA031336a, HRIFA031869a, HRIFA031986a, HRIFA032009a, HRIFA032011a, HRIFA032070a, HRIFA032073a, HRIFA032079a, 15 HRIFA032224a, HRIFA032274a, HRIFA032275a, HRIFA032433a, HRIFA032453a, HRIFA032605a, HRIFA032696a, HRIFA032730a,

Homology search result 3

20 **[0292]** Representative sequence of the 5'-end cluster exhibiting relatively low homology (221 cluster: "exhibiting relatively low homology" means that the P value is higher than 10^{-10} and 10^{-4} or less)
HRIFA000016a, HRIFA000071a, HRIFA000116a, HRIFA000123a, HRIFA000264a, HRIFA000415a, HRIFA000446a, HRIFA000695a, HRIFA000845a, HRIFA001971a, HRIFA002063a, HRIFA002102a, HRIFA002284a, HRIFA002309a, HRIFA002694a, HRIFA002762a, HRIFA002787a, HRIFA003055a, HRIFA003340a, HRIFA003402a, HRIFA003504a, 25 HRIFA003892a, HRIFA003946a, HRIFA004162a, HRIFA004401a, HRIFA004780a, HRIFA005072a, HRIFA005102a, HRIFA005214a, HRIFA005255a, HRIFA005300a, HRIFA005369a, HRIFA005702a, HRIFA005728a, HRIFA005944a, HRIFA006298a, HRIFA006448a, HRIFA006572a, HRIFA006633a, HRIFA006642a, HRIFA007068a, HRIFA007244a, HRIFA007262a, HRIFA007512a, HRIFA007532a, HRIFA007565a, HRIFA007728a, HRIFA007909a, HRIFA008174a, HRIFA008426a, HRIFA008596a, HRIFA008790a, HRIFA008989a, HRIFA009578a, HRIFA009825a, HRIFA009852a, 30 HRIFA009983a, HRIFA010005a, HRIFA010078a, HRIFA010152a, HRIFA010301a, HRIFA010361a, HRIFA010425a, HRIFA010466a, HRIFA010799a, HRIFA011580a, HRIFA011820a, HRIFA012167a, HRIFA012354a, HRIFA012427a, HRIFA012436a, HRIFA012515a, HRIFA012702a, HRIFA012737a, HRIFA013135a, HRIFA013235a, HRIFA013279a, HRIFA013589a, HRIFA013620a, HRIFA013919a, HRIFA013932a, HRIFA014056a, HRIFA014111a, HRIFA014133a, HRIFA014396a, HRIFA014397a, HRIFA014598a, HRIFA014702a, HRIFA014868a, HRIFA015219a, HRIFA015995a, 35 HRIFA016214a, HRIFA016240a, HRIFA016255a, HRIFA016639a, HRIFA016669a, HRIFA016963a, HRIFA017457a, HRIFA017643a, HRIFA017670a, HRIFA017801a, HRIFA017836a, HRIFA017921a, HRIFA018238a, HRIFA018262a, HRIFA018287a, HRIFA018666a, HRIFA018688a, HRIFA018754a, HRIFA018794a, HRIFA018870a, HRIFA018931a, HRIFA019412a, HRIFA019490a, HRIFA019498a, HRIFA019532a, HRIFA019651a, HRIFA0201440, HRIFA020184a, HRIFA020453a, HRIFA020693a, 40 HRIFA020707a, HRIFA020748a, HRIFA021061a, HRIFA021224a, HRIFA021494a, HRIFA021794a, HRIFA021855a, HRIFA021906a, HRIFA022156a, HRIFA022203a, HRIFA022234a, HRIFA022702a, HRIFA022728a, HRIFA022782a, HRIFA022865a, HRIFA022890a, HRIFA022985a, HRIFA023048a, HRIFA023069a, HRIFA023129a, HRIFA023154a, HRIFA023212a, HRIFA023489a, HRIFA023634a, HRIFA023894a, HRIFA024088a, HRIFA024197a, HRIFA024218a, HRIFA024473a, HRIFA024482a, HRIFA024543a, HRIFA025327a, HRIFA025479a, HRIFA025488a, HRIFA025703a, 45 HRIFA025771a, HRIFA025778a, HRIFA025904a, HRIFA025966a, HRIFA025978a, HRIFA026121a, HRIFA026242a, HRIFA026316a, HRIFA026382a, HRIFA026465a, HRIFA026519a, HRIFA026564a, HRIFA026576a, HRIFA026618a, HRIFA026659a, HRIFA026764a, HRIFA027327a, HRIFA027329a, HRIFA027355a, HRIFA027644a, HRIFA027673a, HRIFA027714a, HRIFA027860a, HRIFA028061a, HRIFA028187a, HRIFA028262a, HRIFA028371a, HRIFA028440a, HRIFA028501a, HRIFA028576a, HRIFA028614a, HRIFA028911a, HRIFA029050a, HRIFA029278a, HRIFA029349a, 50 HRIFA029425a, HRIFA029434a, HRIFA029460a, HRIFA029467a, HRIFA029508a, HRIFA029730a, HRIFA029792a, HRIFA030103a, HRIFA030147a, HRIFA030264a, HRIFA030381a, HRIFA030456a, HRIFA030509a, HRIFA030511a, HRIFA030566a, HRIFA030599a, HRIFA031126a, HRIFA031249a, HRIFA031438a, HRIFA031935a, HRIFA032257a, HRIFA032360a, HRIFA032389a, HRIFA032478a, HRIFA032506a, HRIFA032511a, HRIFA032530a, HRIFA032587a, HRIFA032642a, HRIFA032820a, 55

Homology search result 4

[0293] Representative sequence of the 5'-end cluster exhibiting low homology (115 cluster: "exhibiting low homology"

means that the P value is higher than 10^{-4} and 1 or less)

HRIFA001099a, HRIFA001200a, HRIFA001413a, HRIFA001439a, HRIFA001558a, HRIFA001866a, HRIFA001972a,
 HRIFA002689a, HRIFA003357a, HRIFA003592a, HRIFA003640a, HRIFA003883a, HRIFA005296a, HRIFA005500a,
 HRIFA005540a, HRIFA006250a, HRIFA006609a, HRIFA006798a, HRIFA007032a, HRIFA007152a, HRIFA007547a,
 5 HRIFA007829a, HRIFA007985a, HRIFA008212a, HRIFA008252a, HRIFA008976a, HRIFA009071a, HRIFA009123a,
 HRIFA009136a, HRIFA009339a, HRIFA009762a, HRIFA010176a, HRIFA010490a, HRIFA010736a, HRIFA010859a,
 HRIFA010891a, HRIFA010988a, HRIFA011105a, HRIFA011128a, HRIFA011484a, HRIFA011512a, HRIFA011926a,
 HRIFA012069a, HRIFA012151a, HRIFA013092a, HRIFA013103a, HRIFA013980a, HRIFA014024a, HRIFA014590a,
 HRIFA014620a, HRIFA015122a, HRIFA015351a, HRIFA015802a, HRIFA015902a, HRIFA015947a, HRIFA016599a,
 10 HRIFA017146a, HRIFA017190a, HRIFA017456a, HRIFA017791a, HRIFA017818a, HRIFA018447a, HRIFA019437a,
 HRIFA019958a, HRIFA020883a, HRIFA021007a, HRIFA021040a, HRIFA021445a, HRIFA021543a, HRIFA021620a,
 HRIFA021787a, HRIFA022055a, HRIFA022335a, HRIFA022348a, HRIFA022411a, HRIFA022462a, HRIFA022493a,
 HRIFA022714a, HRIFA023434a, HRIFA024185a, HRIFA024305a, HRIFA024884a, HRIFA024893a, HRIFA024978a,
 HRIFA025033a, HRIFA025290a, HRIFA026265a, HRIFA026303a, HRIFA026351a, HRIFA026615a, HRIFA026923a,
 15 HRIFA027173a, HRIFA027485a, HRIFA027536a, HRIFA027549a, HRIFA027867a, HRIFA028804a, HRIFA028867a,
 HRIFA028983a, HRIFA029398a,
 HRIFA029440a, HRIFA029602a, HRIFA029649a, HRIFA029715a, HRIFA030106a, HRIFA030385a, HRIFA030461a,
 HRIFA030472a, HRIFA030839a, HRIFA031091a, HRIFA031395a, HRIFA031397a, HRIFA032097a, HRIFA032161a,
 HRIFA032186a,

Homology search result 5

[0294] The result of the homology search in the SwissProt using the clone sequences of the 5'-ends.

Indicated are from the top,
 the name of the clone sequence,
 definition of the top hit data,
 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
 the organism of which the top hit data is obtained,
 30 the Accession No. of the top hit data.

[0295] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020
 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
 1.2e-119:279:83
 HOMO SAPIENS (HUMAN).
 P03886

F-BNGH41000087
 PROPERDIN PRECURSOR.
 2.5e-06:218:32
 HOMO SAPIENS (HUMAN).
 P27918

F-BNGH41000091
 POTASSIUM CHANNEL PROTEIN EAG.
 3.1e-66:139:61
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q02280

F-HEMBA1000006
 S-ANTIGEN PROTEIN PRECURSOR.
 3.0e-05:164:31
 55 PLASMODIUM FALCIPARUM (ISOLATE V1).
 P09593

F-HEMBA1000121

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HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.

8.2e-06:83:27

CAENORHABDITIS ELEGANS.

P34679

5

F-HEMBA1000128

PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).

8.2e-08:89:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

10

P33154

F-HEMBA1000275

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.9e-06:231:34

15

GALLUS GALLUS (CHICKEN).

P02457

F-HEMBA1000300

!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!

20

1.4e-13:73:56

HOMO SAPIENS (HUMAN).

P39195

F-HEMBA1000349

25

ATP-BINDING CASSETTE TRANSPORTER 1.

2.6e-16:238:31

MUS MUSCULUS (MOUSE).

P41233

30

F-HEMBA1000443

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

4.8e-06:120:35

MUS MUSCULUS (MOUSE).

P05142

35

F-HEMBA1000462

PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.

2.9e-21:86:52

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

40

Q09818

F-HEMBA1000477

HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

3.3e-09:138:34

45

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40085

F-HEMBA1000590

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

2.2e-27:117:48

50

GALLUS GALLUS (CHICKEN).

P05099

F-HEMBA1000634

55

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.00027:85:43

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-HEMBA1000671
ZINC FINGER PROTEIN 140.
1.1e-44:155:47
HOMO SAPIENS (HUMAN).
P52738

F-HEMBA1000713
BLADDER CANCER 10 KD PROTEIN.
1.5e-42:81:97
HOMO SAPIENS (HUMAN).
060629

F-HEMBA1000732
FIBRILLIN 1 PRECURSOR.
6.3e-18:77:46
HOMO SAPIENS (HUMAN).
P35555

F-HEMBA1000745
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6; PEPTIDE P-H].
5.2e-06:105:33
HOMO SAPIENS (HUMAN).
P04280

F-HEMBA1000835
FIBRILLIN 2 PRECURSOR.
2.1e-42:214:44
HOMO SAPIENS (HUMAN).
P35556

F-HEMBA1000875
ZINC FINGER PROTEIN 133.
5.8e-16:49:87
HOMO SAPIENS (HUMAN).
P52736

F-HEMBA1000907
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
2.2e-05:172:34
MUS MUSCULUS (MOUSE).
P11087

F-HEMBA1000940
GAP JUNCTION CX43.4 PROTEIN (CONNEXIN 43.4) (CX43.4).
1.4e-20:90:42
BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
Q92052

F-HEMBA1000962
WATER-STRESS INDUCIBLE PROTEIN RAB21.
0.089:122:25
ORYZA SATIVA (RICE).
P12253

F-HEMBA1001184

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SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).

4.9e-33:100:60

HOMO SAPIENS (HUMAN).

P55822

5

F-HEMBA1001221

AGRIN PRECURSOR.

1.7e-26:239:32

GALLUS GALLUS (CHICKEN).

10

P31696

F-HEMBA1001228

CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).

7.7e-114:147:83

15

HOMO SAPIENS (HUMAN).

P49747

F-HEMBA1001272

SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).

5.8e-06:129:33

20

HOMO SAPIENS (HUMAN).

Q15427

F-HEMBA1001296

TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).

0.0019:115:36

25

GALLUS GALLUS (CHICKEN).

Q98937

F-HEMBA1001297

50S RIBOSOMAL PROTEIN L37E (L35E).

0.65:40:40

30

HALOARCUA MARISMORTUI (HALOBACTERIUM MARISMORTUI).

P32410

35

F-HEMBA1001390

SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).

0.00050:89:33

NEPHILA CLAVIPES (ORB SPIDER).

40

P46804

F-HEMBA1001563

B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).

0.00041:34:61

45

HOMO SAPIENS (HUMAN).

P20931

F-HEMBA1001621

PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.

1.1e-64:105:72

50

HOMO SAPIENS (HUMAN).

P35414

F-HEMBA1001878

VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.

1.3e-24:170:35

55

PODOSPORA ANSERINA.

Q00808

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- 5 F-HEMBA1001886
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.8e-94:273:64
HOMO SAPIENS (HUMAN).
Q03923
- 10 F-HEMBA1002048
EARLY ANTIGEN PROTEIN D (EA-D).
0.13:93:34
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03191
- 15 F-HEMBA1002131
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1).
6.3e-12:140:30
GALLUS GALLUS (CHICKEN).
P24802
- 20 F-HEMBA1002163
HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.
2.1e-10:204:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q04651
- 25 F-HEMBA1002164
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-
CP).
0.022:62:32
30 GLYCINE MAX (SOYBEAN).
Q42783
- 35 F-HEMBA1002167
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
5.2e-31:247:31
BUNGARUS FASCIATUS (BANDED KRAIT).
Q92035
- 40 F-HEMBA1002178
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1).
1.5e-11:140:30
GALLUS GALLUS (CHICKEN).
P24802
- 45 F-HEMBA1002195
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
5.0e-07:52:36
50 PODOSPORA ANSERINA.
Q00808
- 55 F-HEMBA1002227
MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (ACAMP-81).
0.00063:21:100
BOS TAURUS (BOVINE).
P12624
- F-HEMBA1002239

!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!

1.5e-33:101:70

HOMO SAPIENS (HUMAN).

P39192

F-HEMBA1002316

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

4.6e-08:186:32

SORGHUM VULGARE (SORGHUM).

P24152

F-HEMBA1002420

WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

0.0078:19:68

MUS MUSCULUS (MOUSE).

P70315

F-HEMBA1002421

SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2).

1.1e-52:107:97

HOMO SAPIENS (HUMAN).

P34741

F-HEMBA1002524

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

5.0e-05:104:34

RATTUS NORVEGICUS (RAT).

P04474

F-HEMBA1002551

HYPOTHETICAL WD-REPEAT PROTEIN SLR0143.

9.9e-09:128:29

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

P74442

F-HEMBA1002767

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

8.0e-92:246:67

MUS MUSCULUS (MOUSE).

P15535

F-HEMBA1002985

TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6).

0.060:49:34

MUS MUSCULUS (MOUSE).

Q61169

F-HEMBA1002992

HOLOTRICIN 3 PRECURSOR.

0.0035:64:37

HOLOTRICHIA DIOMPHALIA.

Q25055

F-HEMBA1003047

BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).

1.5e-23:216:31
HOMO SAPIENS (HUMAN).
P13497

5 F-HEMBA1003072
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
6.8e-09:129:41
MUS MUSCULUS (MOUSE).
P05142

10 F-HEMBA1003101
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
2.2e-10:124:37
HOMO SAPIENS (HUMAN).
15 P08123

F-HEMBA1003120
ZINC FINGER PROTEIN 140.
4.8e-23:43:74
20 HOMO SAPIENS (HUMAN).
P52738

F-HEMBA1003230
FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90).
25 2.7e-41:239:39
MUS MUSCULUS (MOUSE).
Q08878

F-HEMBA1003294
30 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
7.0e-34:84:69
HOMO SAPIENS (HUMAN).
P39194

35 F-HEMBA1003315
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
0.00012:178:32
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496

40 F-HEMBA1003392
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-
ROGLOBULIN RECEPTOR) (A2MR).
1.1e-31:202:37
45 GALLUS GALLUS (CHICKEN).
P98157

F-HEMBA1003399
MVP1 PROTEIN.
50 5.6e-12:67:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40959

F-HEMBA1003487
55 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.5e-08:175:29
MUS MUSCULUS (MOUSE).
P05142

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F-HEMBA1003497

ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1)
(ZINC FINGER PROTEIN Z13).

9.3e-18:171:33

MUS MUSCULUS (MOUSE).

Q60821

F-HEMBA1003530

SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).

9.9e-12:122:35

HOMO SAPIENS (HUMAN).

P81489

F-HEMBA1003602

PROLINE-RICH PROTEIN MP-3 (FRAGMENT).

0.98:114:33

MUS MUSCULUS (MOUSE).

P05143

F-HEMBA1003732

TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).

0.35:225:28

PSEUDOMONAS AERUGINOSA.

P15276

F-HEMBA1003945

HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.

2.9e-48:268:41

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09895

F-HEMBA1004007

THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1) (FRAGMENT).

0.90:60:30

CAVIA PORCELLUS (GUINEA PIG).

P97273

F-HEMBA1004067

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

3.0e-05:200:31

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-HEMBA1004085

GLUCOSE REPRESSION MEDIATOR PROTEIN.

0.0030:190:26

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

F-HEMBA1004110

EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).

1.2e-14:102:36

MUS MUSCULUS (MOUSE).

P42567

F-HEMBA1004250

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

1.8e-08:150:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450

5 F-HEMBA1004391
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
4.5e-09:96:35
MUS MUSCULUS (MOUSE).
P70211

10 F-HEMBA1004444
GLYCOPROTEIN 25L PRECURSOR (GP25L).
4.6e-41:148:52
CANIS FAMILIARIS (DOG).
15 P27869

F-HEMBA1004454
CD9 ANTIGEN.
0.0070:24:70
20 BOS TAURUS (BOVINE).
P30932

F-HEMBA1004505
25 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).
7.0e-45:239:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P53624

30 F-HEMBA1004785
MODIFIER 3 PROTEIN (M33).
7.4e-26:76:61
MUS MUSCULUS (MOUSE).
P30658

35 F-HEMBA1004797
PROTEIN Q300.
0.00071:21:66
MUS MUSCULUS (MOUSE).
40 Q02722

F-HEMBA1004952
EBNA-1 NUCLEAR PROTEIN.
2.4e-05:67:49
45 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

F-HEMBA1004971

50 F-HEMBA1004982
MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).
8.6e-08:144:25
BACILLUS SUBTILIS.
P39843

55 F-HEMBA1005070
HYPOTHETICAL PROTEIN KIAA0310.
1.0e-38:140:68

HOMO SAPIENS (HUMAN).
O15027

F-HEMBA1005084

NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
2.5e-10:102:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

F-HEMBA1005145

PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.8e-06:85:37
MUS MUSCULUS (MOUSE).
P05142

F-HEMBA1005230

ZINC FINGER PROTEIN 140.
8.2e-20:83:66
HOMO SAPIENS (HUMAN).
P52738

F-HEMBA1005246

TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).
1.5e-09:132:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

F-HEMBA1005267

B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).
1.9e-15:192:32
HOMO SAPIENS (HUMAN).
P20749

F-HEMBA1005337

ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).
8.0e-05:31:64
PLASMODIUM CHABAUDI.
Q02752

F-HEMBA1005430

MALE SPECIFIC SPERM PROTEIN MST84DB.
0.34:42:42
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643

F-HEMBA1005449

PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).
4.5e-09:95:33
TRYPANOSOMA BRUCEI BRUCEI.
Q06084

F-HEMBA1005489

CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110).
7.2e-05:90:36
HOMO SAPIENS (HUMAN).
Q15700

- 5 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
3.3e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139
- 10 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3.
7.2e-91:211:85
HOMO SAPIENS (HUMAN).
P20309
- 15 F-HEMBA1005698
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
3.3e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214
- 20 F-HEMBA1005913
HYPOTHETICAL 5.8 KD PROTEIN.
0.97:43:30
CLOVER YELLOW MOSAIC VIRUS (CYMV).
P16485
- 25 F-HEMBA1005929
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
6.6e-104:275:72
HOMO SAPIENS (HUMAN).
P27448
- 30 F-HEMBA1005945
BRITTLE-1 PROTEIN PRECURSOR.
7.8e-30:214:35
ZEA MAYS (MAIZE).
P29518
- 35 F-HEMBA1006016
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
1.9e-07:34:76
HOMO SAPIENS (HUMAN).
P39188
- 40 F-HEMBA1006171
PROBABLE E5 PROTEIN.
0.98:66:31
HUMAN PAPILLOMAVIRUS TYPE 33.
P06426
- 45 F-HEMBA1006276
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
4.1e-07:56:57
MUS MUSCULUS (MOUSE).
Q61967
- 50 F-HEMBA1006299
BASIC PROLINE-RICH PEPTIDE P-E (IB-9).
0.11:38:28
HOMO SAPIENS (HUMAN).

P02811

F-HEMBA1006311

ZINC FINGER PROTEIN 23 (ZINC FINGER PROTEIN KOX16) (FRAGMENT).

0.91:22:45

HOMO SAPIENS (HUMAN).

P17027

F-HEMBA1006335

PERIPHERAL MYELIN PROTEIN 22 (PMP-22) (GROWTH-ARREST-SPECIFIC PROTEIN 3) (GAS3).

0.017:125:27

MUS MUSCULUS (MOUSE).

P16646

F-HEMBA1006357

SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.

5.2e-40:136:52

HOMO SAPIENS (HUMAN).

O15127

F-HEMBA1006430

OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.

2.7e-38:96:72

CAENORHABDITIS ELEGANS.

P46975

F-HEMBA1006482

SCO1 PROTEIN PRECURSOR.

7.1e-25:84:45

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23833

F-HEMBA1006517

HYPOTHETICAL 93.4 KD PROTEIN IN STE3-GIN10 INTERGENIC REGION.

0.48:145:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34239

F-HEMBA1006544

TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

7.0e-11:210:37

HOMO SAPIENS (HUMAN).

000268

F-HEMBA1006572

ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).

0.011:50:40

GALLUS GALLUS (CHICKEN).

Q03352

F-HEMBA1006658

SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).

4.6e-44:234:45

CAENORHABDITIS ELEGANS.

Q23356

F-HEMBA1006707

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

9.3e-34:159:50
GALLUS GALLUS (CHICKEN).
P05099

5 F-HEMBA1006724
PLATELET FACTOR 4 (PF-4).
0.025:65:27
SUS SCROFA (PIG).
P30034

10 F-HEMBA1006749
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.9e-37:147:53
GALLUS GALLUS (CHICKEN).
15 P05099

F-HEMBA1006770
FLOWERING TIME CONTROL PROTEIN FCA.
3.4e-27:139:39
20 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
004425

F-HEMBA1006902
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
25 1.5e-37:137:51
GALLUS GALLUS (CHICKEN).
P05099

F-HEMBA1006912
30 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.27:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

35 F-HEMBA1006916
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.1e-05:163:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
40 P17437

F-HEMBA1006960
SMALL PROLINE-RICH PROTEIN 2-1.
1.0:34:35
45 HOMO SAPIENS (HUMAN).
P35326

F-HEMBA1007013
S-ANTIGEN PROTEIN PRECURSOR.
50 2.8e-09:226:28
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593

F-HEMBA1007057
55 PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).
4.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.

Q06084

F-HEMBA1007063

AGAMOUS PROTEIN.

1.0:40:42

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P17839

F-HEMBA1007226

PUTATIVE CUTICLE COLLAGEN C09G5.5.

0.10:105:38

CAENORHABDITIS ELEGANS.

Q09456

F-HEMBA1007241

HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

3.3e-15:106:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

F-HEMBA1007291

RETINOIC ACID RECEPTOR RXR-BETA.

0.0013:124:33

HOMO SAPIENS (HUMAN).

P28702

F-HEMBA1007332

ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).

0.0024:130:34

MUS MUSCULUS (MOUSE).

Q01338

F-HEMBB1000106

CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).

9.5e-09:99:33

MUS MUSCULUS (MOUSE).

P53996

F-HEMBB1000276

F-HEMBB1000309

F-HEMBB1000407

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

0.38:99:34

HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

F-HEMBB1000447

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

0.0076:80:31

PLASMODIUM LOPHURAE.

P04929

F-HEMBB1000542

BETA-2 BUNGAROTOXIN B CHAIN PRECURSOR (BUNGAROTOXIN, B2 CHAIN).

0.017:53:33

BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).

P00989

F-HEMBB1000567

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

5.0e-05:131:29

PLASMODIUM LOPHURAE.

P04929

F-HEMBB1000642

BASIC PROLINE-RICH PEPTIDE IB-1.

0.0074:66:31

HOMO SAPIENS (HUMAN).

P04281

F-HEMBB1000668

VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.

7.3e-10:184:32

PODOSPORA ANSERINA.

Q00808

F-HEMBB1000679

TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).

9.5e-73:204:69

CANIS FAMILIARIS (DOG).

Q01685

F-HEMBB1000881

F-SPONDIN PRECURSOR.

1.2e-23:191:37

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P35447

F-HEMBB1000905

TRANSCRIPTIONAL REPRESSOR RCO-1.

0.068:105:34

NEUROSPORA CRASSA.

P78706

F-HEMBB1001026

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.3e-11:138:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

F-HEMBB1001048

SARCALUMENIN PRECURSOR.

3.1e-20:151:32

ORYCTOLAGUS CUNICULUS (RABBIT).

P13666

F-HEMBB1001200

HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.

1.0:66:27

ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).

Q00135

F-HEMBB1001407

!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!

2.0e-24:58:60

HOMO SAPIENS (HUMAN).

P39194

5

F-HEMBB1001530

SLS1 PROTEIN PRECURSOR.

0.0012:37:51

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).

10

Q99158

F-HEMBB1001547

HYPOTHETICAL 71.7 KD PROTEIN F52H3.2 IN CHROMOSOME II.

4.1e-49:200:55

15

CAENORHABDITIS ELEGANS.

Q20680

F-HEMBB1001573

PROTEIN Q300.

20

0.0055:27:62

MUS MUSCULUS (MOUSE).

Q02722

F-HEMBB1001847

25

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

7.8e-05:166:31

RATTUS NORVEGICUS (RAT).

P04474

30

F-HEMBB1001959

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).

8.8e-15:97:38

PETROMYZON MARINUS (SEA LAMPREY).

35

P25210

F-HEMBB1001978

MICROCIN B17 PROCESSING PROTEIN MCBC.

0.049:100:31

40

ESCHERICHIA COLI.

P23185

F-HEMBB1002039

COLD SHOCK PROTEIN CSPB (FRAGMENT).

45

0.98:32:40

BACILLUS GLOBISPORUS.

P41018

F-HEMBB1002041

50

REGULATORY PROTEIN E2.

0.010:145:35

HUMAN PAPILLOMAVIRUS TYPE 47.

P22420

55

F-HEMBB1002051

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0056:89:31

HOMO SAPIENS (HUMAN).

Q01543

F-HEMBB1002120

UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).

1.4e-08:154:30

RATTUS NORVEGICUS (RAT).

P56558

F-HEMBB1002162

IMMEDIATE-EARLY PROTEIN IE180.

0.86:130:31

PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).

P11675

F-HEMBB1002228

PTB-ASSOCIATED SPLICING FACTOR (PSF).

0.00092:97:34

HOMO SAPIENS (HUMAN).

P23246

F-HEMBB1002245

PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).

2.5e-55:128:88

RATTUS NORVEGICUS (RAT).

Q62786

F-HEMBB1002302

REGULATORY PROTEIN E2.

0.042:100:37

HUMAN PAPILLOMAVIRUS TYPE 25.

P36787

F-HEMBB1002427

FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).

5.0e-15:53:54

HOMO SAPIENS (HUMAN).

P16442

F-HEMBB1002465

ACYL-COA DEHYDROGENASE (EC 1.3.99.-).

8.2e-35:162:50

BACILLUS SUBTILIS.

P45857

F-HEMBB1002661

TRANSCRIPTION FACTOR HES-1 (C-HAIRY1).

2.2e-18:159:40

GALLUS GALLUS (CHICKEN).

057337

F-HEMBB1002663

F-HEMBB1002693

GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN

EP 1 130 094 A2

P30; NUCLEOPROTEIN P10].
0.83:74:28
DUPLAN MURINE LEUKEMIA VIRUS.
P23090

5

F-MAMMA1000046
!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!
2.3e-24:98:67
HOMO SAPIENS (HUMAN).
P39191

10

F-MAMMA1000102
APOLIPOPROTEIN L PRECURSOR (APO-L).
4.3e-22:213:34
HOMO SAPIENS (HUMAN).
O14791

15

F-MAMMA1000106
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
1.6e-07:99:31
NICOTIANA TABACUM (COMMON TOBACCO).
Q03211

20

F-MAMMA1000118
HYPOTHETICAL 29.3 KD PROTEIN (ORF92).
0.00059:155:30
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341

25

F-MAMMA1000141
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
0.00011:39:66
HOMO SAPIENS (HUMAN).
P39195

30

F-MAMMA1000204
SYNAPTOTAGMIN III (SYTIII).
5.9e-05:93:33
MUS MUSCULUS (MOUSE).
035681

35

F-MAMMA1000226
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR.
4.6e-06:224:28
TRITICUM AESTIVUM (WHEAT).
P10388

40

F-MAMMA1000403
COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).
1.1e-06:158:35
GALLUS GALLUS (CHICKEN).
P12106

50

F-MAMMA1000449
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
6.3e-05:137:32
HOMO SAPIENS (HUMAN).
P17600

55

- 5 F-MAMMA1000457
NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2).
7.6e-48:151:62
BOS TAURUS (BOVINE).
P07514
- 10 F-MAMMA1000473
SPERM PROTAMINE P1.
0.024:29:44
DROMICIOPS AUSTRALIS (MONITO DEL MONTE) (DROMICIOPS GLIROIDES). P42132
- 15 F-MAMMA1000496
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
9.8e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566
- 20 F-MAMMA1000528
DNA BINDING PROTEIN S1FA.
0.77:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551
- 25 F-MAMMA1000591
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.018:88:32
HOMO SAPIENS (HUMAN).
P10163
- 30 F-MAMMA1000614
HYPOTHETICAL 29.3 KD PROTEIN (ORF92).
7.5e-08:148:36
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341
- 35 F-MAMMA1000652
!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!
5.3e-36:56:85
HOMO SAPIENS (HUMAN).
P39189
- 40 F-MAMMA1000681
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.
7.5e-41:167:51
MUS MUSCULUS (MOUSE).
45 008530
- 50 F-MAMMA1000706
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
8.1e-10:135:38
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- 55 F-MAMMA1000788
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.0e-06:214:32
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P53214

5 F-MAMMA1000810
 REGULATORY PROTEIN E2.
 0.0031:132:31
 HUMAN PAPILLOMAVIRUS TYPE 9.
 P36780

10 F-MAMMA1000814
 PROTEIN Q300.
 1.6e-05:27:66
 MUS MUSCULUS (MOUSE).
 Q02722

15 F-MAMMA1000881
 SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KI-
 NASE).
 2.7e-10:81:45
 RATTUS NORVEGICUS (RAT).
 Q06226

20 F-MAMMA1000986
 INVOLUCRIN.
 0.95:125:24
 SUS SCROFA (PIG).
 P18175

25 F-MAMMA1000994
 CUTICLE COLLAGEN 2C (FRAGMENT).
 0.00062:97:34
 HAEMONCHUS CONTORTUS.
 30 P16252

35 F-MAMMA1001043
 MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
 4.5e-05:162:25
 RATTUS NORVEGICUS (RAT).
 P10252

40 F-MAMMA1001066
 B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
 2.6e-06:33:72
 HOMO SAPIENS (HUMAN).
 P20931

45 F-MAMMA1001094
 PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
 1.1e-21:175:38
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 Q09818

50 F-MAMMA1001141
 PTB-ASSOCIATED SPLICING FACTOR (PSF).
 0.13:196:27
 HOMO SAPIENS (HUMAN).
 P23246

55 F-MAMMA1001150
 PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
 9.4e-89:256:67

HOMO SAPIENS (HUMAN).
Q15139

5 F-MAMMA1001237
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).
3.5e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988

10 F-MAMMA1001284
AUTOIMMUNE REGULATOR (APECED PROTEIN).
0.027:178:30
HOMO SAPIENS (HUMAN).
043918

15 F-MAMMA1001310
HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC RE-
GION.
1.9e-14:151:31
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q04225

F-MAMMA1001344
25 MALE SPECIFIC SPERM PROTEIN MST84DC.
0.16:35:42
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01644

30 F-MAMMA1001418
HYPOTHETICAL PROTEIN HI0519.
3.5e-27:181:38
HAEMOPHILUS INFLUENZAE.
P44742

35 F-MAMMA1001532
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
1.1e-34:78:58
MUS MUSCULUS (MOUSE).
Q61967

40 F-MAMMA1001609
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.20:137:27
45 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

F-MAMMA1001615
5E5 ANTIGEN.
2.3e-07:205:34
50 RATTUS NORVEGICUS (RAT).
Q63003

F-MAMMA1001623
55 EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
4.8e-30:90:77
HOMO SAPIENS (HUMAN).
Q03468

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F-MAMMA1001634
 B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
 6.1e-11:44:61
 HOMO SAPIENS (HUMAN).
 5 P20931

F-MAMMA1001893
 COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
 0.0013:174:36
 10 HOMO SAPIENS (HUMAN).
 P12107

F-MAMMA1001901
 !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
 15 1.3e-21:65:66
 HOMO SAPIENS (HUMAN).
 P39195

F-MAMMA1001957
 20 VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
 0.0055:104:35
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P13238

F-MAMMA1001978
 25 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
 0.00030:101:44
 HOMO SAPIENS (HUMAN).
 30 P21917

F-MAMMA1002070
 PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
 1.4e-08:103:33
 RATTUS NORVEGICUS (RAT).
 35 Q01177

F-MAMMA1002080
 FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.
 8.2e-08:131:32
 40 LYMNAEA STAGNALIS (GREAT POND SNAIL).
 P42565

F-MAMMA1002087
 45 MALE SPECIFIC SPERM PROTEIN MST84DD.
 0.65:24:45
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q01645

F-MAMMA1002091
 50 APYRASE PRECURSOR (EC 3.6.1.5) (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE)
 (ATP-DIPHOSPHOHYDROLASE).
 2.6e-24:155:43
 SOLANUM TUBEROSUM (POTATO).
 P80595
 55

F-MAMMA1002095
 CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).
 2.3e-58:213:56

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
043108

5 F-MAMMA1002128
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
9.9e-05:72:40
RATTUS NORVEGICUS (RAT).
P02454

10 F-MAMMA1002142
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
2.1e-13:149:34
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

15 F-MAMMA1002165
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
8.4e-06:47:57
HOMO SAPIENS (HUMAN).
20 P29279

F-MAMMA1002205
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
5.9e-26:56:78
25 HOMO SAPIENS (HUMAN).
P39188

F-MAMMA1002224
!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
30 3.7e-16:62:67
HOMO SAPIENS (HUMAN).
P39194

F-MAMMA1002234
35 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
3.5e-105:242:85
CANIS FAMILIARIS (DOG).
Q00004

40 F-MAMMA1002586
MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSI-
DASE) (ALPHA-MANNOSIDASE 1A).
4.7e-24:203:35
MUS MUSCULUS (MOUSE).
45 P45700

F-MAMMA1002633
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
7.3e-27:49:73
50 HOMO SAPIENS (HUMAN).
P39188

F-MAMMA1003126
55 SARCALUMENIN PRECURSOR.
7.9e-30:156:35
ORYCTOLAGUS CUNICULUS (RABBIT).
P13666

- 5 F-NT2RM1000407
LACTOSE OPERON REPRESSOR.
1.4e-07:36:86
ESCHERICHIA COLI.
P03023
- 10 F-NT2RM1000462
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
6.7e-11:85:41
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P15287
- 15 F-NT2RM1000542
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
3.5e-19:104:48
FELIS SILVESTRIUS CATUS (CAT).
O19015
- 20 F-NT2RM1000580
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
3.4e-36:180:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
- 25 F-NT2RM1000789
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
1.5e-40:112:75
MUS MUSCULUS (MOUSE).
Q00417
- 30 F-NT2RM1000855
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
2.5e-81:152:94
CANIS FAMILIARIS (DOG).
P38377
- 35 F-NT2RM1000858
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
3.1e-50:127:54
CAENORHABDITIS ELEGANS.
Q09201
- 40 F-NT2RM1000899
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
6.6e-17:107:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500
- 50 F-NT2RM2000241
DOUBLESEX PROTEIN, MALE-SPECIFIC.
0.0021:64:32
DROSOPHILA MELANOGASTER (FRUIT FLY).
P23023
- 55 F-NT2RM2000306
PUTATIVE GTP-BINDING PROTEIN W08E3.3.
1.1e-69:198:69
CAENORHABDITIS ELEGANS.

P91917

F-NT2RM2000410

BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).

0.73:118:31

ACHROMOBACTER LYTICUS.

P27458

F-NT2RM2000423

BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.

1.3e-23:235:34

HOMO SAPIENS (HUMAN).

P16279

F-NT2RM2000497

DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).

9.4e-19:199:31

CRICETULUS GRISEUS (CHINESE HAMSTER).

Q60452

F-NT2RM2000514

HYPOTHETICAL PROTEIN HI1558.

7.7e-06:82:34

HAEMOPHILUS INFLUENZAE.

P45252

F-NT2RM2000565

HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.

2.8e-57:232:52

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09782

F-NT2RM2000582

PROTEIN Q300.

0.066:13:84

MUS MUSCULUS (MOUSE).

Q02722

F-NT2RM2000589

RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).

2.1e-07:90:32

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P54644

F-NT2RM2000622

GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.

1.9e-07:133:35

TRITICUM AESTIVUM (WHEAT).

P08489

F-NT2RM2000632

EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).

4.6e-28:194:35

HOMO SAPIENS (HUMAN).

Q03468

F-NT2RM2000773

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MYC-ASSOCIATED ZINC FINGER PROTEIN (MAZI) (PUR-1) (ZF87).

3.4e-24:156:47

HOMO SAPIENS (HUMAN).

P56270

F-NT2RM2001126

NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).

1.5e-05:118:32

MUS MUSCULUS (MOUSE).

P98084

F-NT2RM2001558

MAJOR FIBROUS SHEATH PROTEIN PRECURSOR (FSC1) (P82).

1.9e-24:164:40

MUS MUSCULUS (MOUSE).

Q60662

F-NT2RM2001626

HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.

1.6e-09:206:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47179

F-NT2RM2001643

HYPOTHETICAL PROTEIN MJ1025.

0.21:203:22

METHANOCOCCUS JANNASCHII.

Q58431

F-NT2RM2001738

REGULATORY PROTEIN E2.

0.0076:124:31

HUMAN PAPILLOMAVIRUS TYPE 25.

P36787

F-NT2RM2001767

HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).

0.0068:115:33

DROSOPHILA MELANOGASTER (FRUIT FLY).

P25439

F-NT2RM2001792

FIBRINOGEN BETA CHAIN.

4.3e-25:121:45

BOS TAURUS (BOVINE).

P02676

F-NT2RM2001818

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.4e-06:192:32

ZEA MAYS (MAIZE).

P14918

F-NT2RM2001902

SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (P65-PAK).

2.3e-52:250:45

RATTUS NORVEGICUS (RAT).

Q62829

F-NT2RM2001939

PROBABLE G PROTEIN-COUPLEID RECEPTOR GPR19 (GPR-NGA).

4.0e-97:204:92

HOMO SAPIENS (HUMAN).

Q15760

F-NT2RM2001941

MUSCARINIC ACETYLCHOLINE RECEPTOR M4.

1.0e-34:184:32

HOMO SAPIENS (HUMAN).

P08173

F-NT2RM4000100

EBNA-1 NUCLEAR PROTEIN.

1.7e-05:86:39

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

F-NT2RM4000115

DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1).

9.5e-05:116:35

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P36594

F-NT2RM4000198

BUTYROPHILIN PRECURSOR (BT).

8.6e-14:162:33

MUS MUSCULUS (MOUSE).

Q62556

F-NT2RM4000284

COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).

0.86:95:37

HOMO SAPIENS (HUMAN).

P12110

F-NT2RM4000295

COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.

1.1e-08:229:34

HOMO SAPIENS (HUMAN).

Q07092

F-NT2RM4000326

SH3 DOMAIN-BINDING PROTEIN 3BP-2.

6.1e-05:187:31

HOMO SAPIENS (HUMAN).

P78314

F-NT2RM4000417

SYNAPTOTAGMIN (P65).

4.2e-08:72:52

APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).

P41823

F-NT2RM4000444

ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER

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PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESS-
ING 1).

1.1e-36:192:41

HOMO SAPIENS (HUMAN).

Q03518

F-NT2RM4000587

COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).

1.8e-13:200:38

BOS TAURUS (BOVINE).

P02459

F-NT2RM4000593

F-NT2RM4000648

K-GLYPICAN PRECURSOR.

6.4e-67:180:68

MUS MUSCULUS (MOUSE).

P51655

F-NT2RM4000761

CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).

2.3e-53:107:81

RATTUS NORVEGICUS (RAT).

P05503

F-NT2RM4000965

PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).

4.9e-14:188:34

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

060100

F-NT2RM4000997

HISTONE H1C (CLONE XLHW2).

0.88:73:26

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P15866

F-NT2RM4001321

HOMEBOX PROTEIN HOX-A2.

0.27:77:37

GALLUS GALLUS (CHICKEN).

Q08727

F-NT2RM4001325

CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).

3.8e-30:184:39

GALLUS GALLUS (CHICKEN).

Q92179

F-NT2RM4001377

HYPOTHETICAL BHLF1 PROTEIN.

5.9e-06:216:33

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03181

F-NT2RM4001735

GNS 1 PROTEIN.

0.0028:114:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358

5 F-NT2RM4001768
PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).
8.6e-24:205:36
STREPTOMYCES ANTIBIOTICUS.
Q03326

10 F-NT2RM4001843
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).
4.6e-33:258:37
XANTHOMONAS MANIHOTIS.
15 P48982

F-NT2RM4002352
BASEMENT MEMBRANE PROTEOGLYCAN PRECURSOR (PERLECAN HOMOLOG).
1.0e-15:85:45
20 CAENORHABDITIS ELEGANS.
Q06561

F-NT2RP1000002
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
25 0.00011:24:62
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

F-NT2RP1000050
30 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
2.5e-07:198:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

35 F-NT2RP1000181
CYTOCHROME B5.
4.4e-11:117:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
40 P40312

F-NT2RP1000239
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
7.8e-05:141:33
45 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

F-NT2RP1000261
ORM1 PROTEIN.
2.2e-18:137:35
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

F-NT2RP1000271
55 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
8.3e-81:194:70
HOMO SAPIENS (HUMAN).
Q03923

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F-NT2RP1000300
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.
2.0e-07:202:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38176

F-NT2RP1000325
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
1.6e-55:86:81
HOMO SAPIENS (HUMAN).
Q00325

F-NT2RP1000448
PROLINE-RICH PEPTIDE P-B.
0.094:32:43
HOMO SAPIENS (HUMAN).
P02814

F-NT2RP1000465
EBNA-1 NUCLEAR PROTEIN.
3.1e-07:101:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

F-NT2RP1000468
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DIVA BINDING PROTEIN SUBUNIT B).
1.4e-14:97:38
PETROMYZON MARINUS (SEA LAMPREY).
P25210

F-NT2RP1000551
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
1.9e-33:221:41
MUS MUSCULUS (MOUSE).
P19182

F-NT2RP1000579
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX II).
3.4e-68:247:62
HOMO SAPIENS (HUMAN).
P31040

F-NT2RP1000613
CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).
1.9e-19:137:37
OVIS ARIES (SHEEP).
P08060

F-NT2RP1000679
EBNA-1 NUCLEAR PROTEIN.
0.00055:54:50
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

F-NT2RP1000740
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

0.071:71:45
HOMO SAPIENS (HUMAN).
000268

5 F-NT2RP1000903
SPORE COAT PROTEIN SP96.
0.016:124:26
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P14328

10 F-NT2RP1000981
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.1e-08:196:28
HOMO SAPIENS (HUMAN).
15 Q99795

F-NT2RP1001004
F-SPONDIN PRECURSOR.
1.2e-11:155:31
20 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447

F-NT2RP1001020
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
25 2.2e-05:126:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458

F-NT2RP1001031
30 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
5.8e-26:159:38
THERMOMONOSPORA CURVATA.
P49695

35 F-NT2RP1001563
METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
0.00036:42:40
BOS TAURUS (BOVINE).
P37359

40 F-NT2RP2000092
ZINC FINGER PROTEIN 136.
2.9e-44:129:62
HOMO SAPIENS (HUMAN).
45 P52737

F-NT2RP2000178
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0050:75:37
50 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

F-NT2RP2000240
PUTATIVE CUTICLE COLLAGEN C09G5.5.
55 9.2e-08:137:34
CAENORHABDITIS ELEGANS.
Q09456

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F-NT2RP2000394
 PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).
 0.00019:28:64
 TRYPANOSOMA BRUCEI BRUCEI.
 P09791

F-NT2RP2000447
 GOLGIN-95.
 6.4e-25:55:67
 HOMO SAPIENS (HUMAN).
 Q08379

F-NT2RP2000479
 PROBABLE E5B PROTEIN.
 1.0:32:37
 HUMAN PAPILLOMAVIRUS TYPE 6B.
 P06461

F-NT2RP2000514
 AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).
 1.5e-18:201:33
 HOMO SAPIENS (HUMAN).
 Q02246

F-NT2RP2000533
 CORNICHON PROTEIN.
 5.6e-52:144:65
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P49858

F-NT2RP2000610
 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
 BOX DNA BINDING PROTEIN SUBUNIT B).
 8.7e-15:97:38
 PETROMYZON MARINUS (SEA LAMPREY).
 P25210

F-NT2RP2000616
 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 0.028:163:30
 MUS MUSCULUS (MOUSE).
 P11087

F-NT2RP2000649
 POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
 (PPSEP 1).
 9.5e-22:241:32
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 Q10071

F-NT2RP2000663
 PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
 0.71:28:46
 GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY).
 P01306

F-NT2RP2000694
 WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

8.8e-10:90:42
MUS MUSCULUS (MOUSE).
P70315

5 F-NT2RP2000712
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.3e-50:166:50
HOMO SAPIENS (HUMAN).
Q03923

10 F-NT2RP2000739
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
8.9e-45:180:43
HOMO SAPIENS (HUMAN).
15 Q03923

F-NT2RP2000818
SYG1 PROTEIN.
2.4e-14:164:35
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40528

F-NT2RP2000903
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
25 0.28:149:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

F-NT2RP2001200
30 MIC1 PROTEIN.
1.8e-13:115:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53258

35 F-NT2RP2001223
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.00017:92:35
CANIS FAMILIARIS (DOG).
P39881

40 F-NT2RP2001276
NPDC-1 PROTEIN PRECURSOR.
4.9e-35:96:71
MUS MUSCULUS (MOUSE).
45 Q64322

F-NT2RP2001388
CECROPIN B PRECURSOR.
0.98:31:51
50 DROSOPHILA MELANOGASTER (FRUIT FLY).
P14956

F-NT2RP2001469
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
55 6.0e-07:146:22
PODOSPORA ANSERINA.
Q00808

F-NT2RP2001480
THROMBOSPONDIN 3 PRECURSOR.
2.1e-100:209:88
HOMO SAPIENS (HUMAN).
P49746

F-NT2RP2001495
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
3.1e-11:174:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

F-NT2RP2001514
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
4.0e-18:163:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

F-NT2RP2001529
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
4.4e-83:186:78
HOMO SAPIENS (HUMAN).
P53355

F-NT2RP2001538
PAIRED AMPHIPATHIC HELIX PROTEIN.
1.7e-06:152:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

F-NT2RP2001562
CLATHRIN LIGHT CHAIN B (BRAIN AND LYMPHOCYTE LCB).
0.0093:124:27
HOMO SAPIENS (HUMAN).
P09497

F-NT2RP2001662
5'-TG-3'INTERACTING FACTOR (HOMEBOX PROTEIN TGIF).
5.6e-36:146:57
HOMO SAPIENS (HUMAN).
Q15583

F-NT2RP2001755
F-SPONDIN PRECURSOR.
1.2e-33:84:89
RATTUS NORVEGICUS (RAT).
P35446

F-NT2RP2001769
PROTEIN KINASE CEK1 (EC 2.7.1.-).
1.3e-37:159:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P38938

F-NT2RP2001817
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).
6.4e-32:85:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53685

F-NT2RP2001878

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

5 1.1e-06:173:28

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-NT2RP2001903

10 CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEIN-ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT).

2.4e-10:110:37

HOMO SAPIENS (HUMAN).

15 P20807

F-NT2RP2001915

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

0.0069:74:39

20 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

F-NT2RP2001921

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).

25 0.016:51:45

BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).

P29836

F-NT2RP2001948

30 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

6.7e-08:121:37

HOMO SAPIENS (HUMAN).

Q03692

F-NT2RP2001956

ORM1 PROTEIN.

7.6e-17:106:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

F-NT2RP2002015

HOMEBOX PROTEIN HOX-A2.

0.12:77:37

GALLUS GALLUS (CHICKEN).

45 Q08727

F-NT2RP2002063

HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.

3.2e-47:213:41

50 CAENORHABDITIS ELEGANS.

P49191

F-NT2RP2002188

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).

55 9.2e-15:109:36

TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).

P04058

EP 1 130 094 A2

F-NT2RP2002232
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.0e-12:92:50
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782

F-NT2RP2002304
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00059:16:68
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

F-NT2RP2002409
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
0.00039:184:33
BOS TAURUS (BOVINE).
P02453

F-NT2RP2002510
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
0.0010:97:37
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333

F-NT2RP2002527
CYTOCHROME B5.
1.3e-11:77:38
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P40312

F-NT2RP2002533
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR.
2.0e-37:165:42
ORYCTOLAGUS CUNICULUS (RABBIT).
P13806

F-NT2RP2002564
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
4.7e-06:81:35
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

F-NT2RP2002674
SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HY-
DROLASE) (CEH).
2.4e-25:147:41
HOMO SAPIENS (HUMAN).
P34913

F-NT2RP2002721
GLUCOSE 6-PHOSPHATE TRANSLOCASE.
0.0073:88:26
HOMO SAPIENS (HUMAN).
043826

F-NT2RP2002824
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

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1.0e-16:139:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802

5 F-NT2RP2002942
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
5.1e-18:153:30
HOMO SAPIENS (HUMAN).
P32004

10 F-NT2RP2002974
HOMEODOMAIN PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT).
3.6e-80:187:84
15 MUS MUSCULUS (MOUSE).
P70178

F-NT2RP2002976
20 HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.
2.8e-18:99:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38800

25 F-NT2RP2003042
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).
1.2e-41:135:57
GALLUS GALLUS (CHICKEN).
P53760

30 F-NT2RP2003138
5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).
3.3e-09:104:45
MUS MUSCULUS (MOUSE).
35 P70284

F-NT2RP2003179
40 CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).
7.2e-15:96:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P06782

F-NT2RP2003210
45 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).
6.2e-69:235:57
MUS MUSCULUS (MOUSE).
Q60714

50 F-NT2RP2003302
ZINC FINGER PROTEIN 136.
9.7e-52:140:52
HOMO SAPIENS (HUMAN).
P52737

55 F-NT2RP2003369
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).
0.00020:87:32
HOMO SAPIENS (HUMAN).

P10161

F-NT2RP2003383

LONG NEUROTOXIN 2 (TOXINS I AND V).

0.86:38:39

DENDROASPIS VIRIDIS (WESTERN GREEN MAMBA).

P01395

F-NT2RP2003390

NPL1 PROTEIN (SEC63 PROTEIN).

1.1e-14:113:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14906

F-NT2RP2003469

MYO-INOSITOL TRANSPORTER 2.

1.7e-09:148:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P30606

F-NT2RP2003545

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

9.2e-32:198:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38692

F-NT2RP2003593

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

0.00019:128:32

MUS MUSCULUS (MOUSE).

P05142

F-NT2RP2003599

ATP-DEPENDENT BILE ACID PERMEASE.

0.88:69:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32386

F-NT2RP2003655

HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.

2.9e-16:93:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38869

F-NT2RP2003664

HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.

5.6e-08:121:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47111

F-NT2RP2003931

ACROSIN PRECURSOR (EC 3.4.21.10).

0.38:20:70

HOMO SAPIENS (HUMAN).

P10323

F-NT2RP2003940

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

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1.3e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923

5 F-NT2RP2003950
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
1.5e-05:134:33
10 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

F-NT2RP2004069
HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.
4.3e-13:68:54
15 CAENORHABDITIS ELEGANS.
Q09297

F-NT2RP2004108
ZINC FINGER PROTEIN 136.
20 8.6e-47:126:67
HOMO SAPIENS (HUMAN).
P52737

F-NT2RP2004141
25 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.013:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

30 F-NT2RP2004179
GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (GLYCEROPHOSPHODIESTER
PHOSPHODIESTERASE).
5.9e-10:110:36
35 ESCHERICHIA COLI.
P10908

F-NT2RP2004205
MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
4.6e-10:99:34
40 HOMO SAPIENS (HUMAN).
Q16653

F-NT2RP2004447
45 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
0.86:48:37
MUS MUSCULUS (MOUSE).
Q01149

F-NT2RP2004495
50 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
0.031:135:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

55 F-NT2RP2004524
HYPOTHETICAL 18.7 KD PROTEIN IN HMS1-ABF2 INTERGENIC REGION.
0.042:96:23
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q04767

F-NT2RP2004556

SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).

0.0082:87:35

HOMO SAPIENS (HUMAN).

P81489

F-NT2RP2004606

METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).

2.2e-57:163:73

HOMO SAPIENS (HUMAN).

P01033

F-NT2RP2004648

BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).

3.2e-25:90:62

FELIS SILVESTRIIS CATUS (CAT).

O19015

F-NT2RP2004670

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

6.6e-14:108:34

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP2004794

HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

5.7e-11:140:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

F-NT2RP2004837

F-NT2RP2004847

ADULT ENHANCER FACTOR 1 (AEF-1).

7.9e-09:81:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P39413

F-NT2RP2005027

GLUCOSE TRANSPORTER TYPE 3, BRAIN.

3.6e-64:130:96

HOMO SAPIENS (HUMAN).

P11169

F-NT2RP2005069

CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).

0.22:116:32

RATTUS NORVEGICUS (RAT).

P53565

F-NT2RP2005163

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

5.3e-06:70:38

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

F-NT2RP2005181

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

4.2e-54:153:69

HOMO SAPIENS (HUMAN).

P30825

F-NT2RP2005247

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.0e-11:106:35

SORGHUM VULGARE (SORGHUM).

P24152

F-NT2RP2005378

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.11:97:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

F-NT2RP2005391

G-BOX BINDING FACTOR (GBF).

5.1e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

F-NT2RP2005425

M PROTEIN, SEROTYPE 49 PRECURSOR.

2.1e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

F-NT2RP2005463

OVOMUCOID (FRAGMENT).

1.0:21:52

BAMBUSICOLA THORACICA (CHINESE BAMBOO-PARTRIDGE).

P52259

F-NT2RP2005514

MOBC PROTEIN.

1.0:26:53

THIOBACILLUS FERROOXIDANS.

P22899

F-NT2RP2005535

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.8e-92:243:69

HOMO SAPIENS (HUMAN).

Q03923

F-NT2RP2005541

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

8.8e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

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- 5 F-NT2RP2005597
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC
2.4.1.109).
7.4e-13:99:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- 10 F-NT2RP2005632
ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENY-
LYL CYCLASE).
3.0e-05:73:43
CANIS FAMILIARIS (DOG).
P30803
- 15 F-NT2RP2005666
HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).
0.086:105:31
MUS MUSCULUS (MOUSE).
P35583
- 20 F-NT2RP2005774
ZINC FINGER PROTEIN 136.
7.8e-33:128:57
HOMO SAPIENS (HUMAN).
P52737
- 25 F-NT2RP2005878
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
6.8e-23:96:48
MUS MUSCULUS (MOUSE).
070503
- 30 F-NT2RP2005883
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
(DBH).
6.4e-23:185:32
RATTUS NORVEGICUS (RAT).
Q05754
- 35 F-NT2RP2005887
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
1.0:40:30
METHANOCOCCUS JANNASCHII.
Q57650
- 40 F-NT2RP2005941
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
3.5e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 45 F-NT2RP2005994
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
4.4e-36:144:47
CAENORHABDITIS ELEGANS.
P49191
- 50 F-NT2RP2006004

EP 1 130 094 A2

BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG).

0.030:28:50

RATTUS NORVEGICUS (RAT).

Q01129

F-NT2RP2006042

HYPOTHETICAL PROTEIN KIAA0144.

1.2e-22:228:39

HOMO SAPIENS (HUMAN).

Q14157

F-NT2RP2006092

TRANSCRIPTIONAL ACTIVATOR FE65.

3.1e-27:101:54

RATTUS NORVEGICUS (RAT).

P46933

F-NT2RP2006099

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

7.0e-07:123:34

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

F-NT2RP2006134

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).

0.0041:118:30

PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).

P29129

F-NT2RP2006269

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

6.3e-17:119:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

F-NT2RP2006512

GNS1 PROTEIN.

8.6e-14:186:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P25358

F-NT2RP3000011

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

2.9e-12:137:32

THERMOMONOSPORA CURVATA.

P49695

F-NT2RP3000022

SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).

1.6e-47:121:79

RATTUS NORVEGICUS (RAT).

P20793

F-NT2RP3000059

COLLAGEN ALPHA 1(III) CHAIN.

1.5e-05:211:33

BOS TAURUS (BOVINE).

P04258

F-NT2RP3000063

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

4.2e-23:230:28

ZEA MAYS (MAIZE).

P14918

F-NT2RP3000125

CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).

2.3e-08:110:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P09620

F-NT2RP3000148

ZINC FINGER PROTEIN 133.

1.4e-34:84:48

HOMO SAPIENS (HUMAN).

P52736

F-NT2RP3000169

SMALL PROLINE-RICH PROTEIN 2-1.

0.00092:14:57

HOMO SAPIENS (HUMAN).

P35326

F-NT2RP3000171

24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.

4.6e-10:134:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P28707

F-NT2RP3000172

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

1.8e-33:161:42

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP3000201

SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).

4.1e-79:254:64

CAENORHABDITIS ELEGANS.

Q23356

F-NT2RP3000232

ZINC FINGER PROTEIN 184 (FRAGMENT).

8.5e-23:119:45

HOMO SAPIENS (HUMAN).

Q99676

F-NT2RP3000304

LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).

9.8e-36:172:43

HOMO SAPIENS (HUMAN).

Q07954

F-NT2RP3000378

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PAIRED AMPHIPATHIC HELIX PROTEIN.
2.7e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

5

F-NT2RP3000427
5E5 ANTIGEN.
0.086:204:31
RATTUS NORVEGICUS (RAT).
Q63003

10

F-NT2RP3000436
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
1.3e-23:106:33
CAENORHABDITIS ELEGANS.
Q11067

15

F-NT2RP3000444
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
0.00052:166:36
HOMO SAPIENS (HUMAN).
000268

20

F-NT2RP3000460
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
1.0e-98:194:100
RATTUS NORVEGICUS (RAT).
P38378

25

F-NT2RP3000481
NONSENSE-MEDIATED MRNA DECAY PROTEIN 5.
7.4e-19:217:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46970

30

F-NT2RP3000616
BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
1.2e-13:115:33
BOS TAURUS (BOVINE).
P21793

35

F-NT2RP3000645
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.3e-10:237:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

45

F-NT2RP3000652
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
3.1e-106:283:67
HOMO SAPIENS (HUMAN).
Q03923

50

F-NT2RP3000676
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
7.4e-07:102:32
HOMO SAPIENS (HUMAN).

55

P12235

F-NT2RP3000677

MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).

1.5e-27:66:54

HOMO SAPIENS (HUMAN).

P22670

F-NT2RP3000721

HYPOTHETICAL 62.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION.

1.6e-22:208:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43560

F-NT2RP3000789

ONCONEURAL VENTRAL ANTIGEN-1 (NOVA-1) (PARANEOPLASTIC RI ANTIGEN) (VENTRAL NEURON-SPECIFIC PROTEIN 1).

1.0e-07:190:26

HOMO SAPIENS (HUMAN).

P51513

F-NT2RP3000818

HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION.

5.9e-05:100:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34248

F-NT2RP3000820

BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).

0.92:97:26

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

P73538

F-NT2RP3000838

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

6.4e-07:231:31

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

F-NT2RP3000871

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

2.8e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

F-NT2RP3000907

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

2.2e-41:104:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39986

F-NT2RP3000921

BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).

4.5e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

EP 1 130 094 A2

F-NT2RP3001012
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
5.5e-06:37:51
PLASMODIUM LOPHURAE.
P04929

F-NT2RP3001044
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDA.
0.10:61:31
STREPTOMYCES COELICOLOR.
P18182

F-NT2RP3001061
GLYCOPROTEIN X PRECURSOR.
0.00011:140:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

F-NT2RP3001159
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.1e-09:249:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

F-NT2RP3001170
POU DOMAIN PROTEIN 1 (DJPOU1).
0.020:173:29
DUGESIA JAPONICA (PLANARIAN).
P31370

F-NT2RP3001195
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
1.2e-14:180:30
ESCHERICHIA COLI.
P37021

F-NT2RP3001240
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
3.1e-118:229:88
RATTUS NORVEGICUS (RAT).
P38378

F-NT2RP3001271
EBNA-1 NUCLEAR PROTEIN.
2.3e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

F-NT2RP3001322
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-AT-
PASE).
1.7e-23:222:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39524

F-NT2RP3001388
SYNAPTOTAGMIN IV.
4.8e-19:168:38

RATTUS NORVEGICUS (RAT).
P50232

F-NT2RP3001542

5 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).
2.7e-12:132:37
HOMO SAPIENS (HUMAN).
Q13829

10 F-NT2RP3001560

SYNAPSINS IA AND IB.
0.59:104:35
BOS TAURUS (BOVINE).
P17599

15 F-NT2RP3001592

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
20 P29834

F-NT2RP3001650

CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.23:119:36
25 CANIS FAMILIARIS (DOG).
P39881

F-NT2RP3001685

HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).
30 2.2e-48:207:48
PSEUDOMONAS AERUGINOSA.
P28812

F-NT2RP3001738

35 CYTOCHROME B5.
9.5e-13:133:33
ORYCTOLAGUS CUNICULUS (RABBIT).
P00169

40 F-NT2RP3001754

SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
7.9e-05:117:29
HOMO SAPIENS (HUMAN).
P17600

45 F-NT2RP3001858

CUTICLE COLLAGEN 2.
0.030:118:35
CAENORHABDITIS ELEGANS.
50 P17656

F-NT2RP3001976

ZINC FINGER PROTEIN 140.
7.8e-24:122:52
55 HOMO SAPIENS (HUMAN).
P52738

F-NT2RP3002015

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
0.018:224:30
GALLUS GALLUS (CHICKEN).
P02457

5

F-NT2RP3002160
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.0058:206:29
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

10

F-NT2RP3002281
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).
1.3e-14:86:40
HOMO SAPIENS (HUMAN).
P52597

15

F-NT2RP3002286
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.65:128:29
HOMO SAPIENS (HUMAN).
P50548

20

F-NT2RP3002311
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
6.1e-46:172:54
FELIS SILVESTRIS CATUS (CAT).
O19015

25

F-NT2RP3002324
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.012:23:65
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245

30

F-NT2RP3002342
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.8e-13:219:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

35

F-NT2RP3002353
REGULATORY PROTEIN E2.
0.0027:167:31
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422

45

F-NT2RP3002409
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).
9.9e-09:93:34
NEUROSPORA CRASSA.
P23231

50

F-NT2RP3002411
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
5.6e-107:254:80

55

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MUS MUSCULUS (MOUSE).
070503

F-NT2RP3002448

5 TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
1.5e-05:163:33
HOMO SAPIENS (HUMAN).
000268

10 F-NT2RP3002571

HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
6.4e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10496

15 F-NT2RP3002664

CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.062:47:29
HOMO SAPIENS (HUMAN).
20 P18850

F-NT2RP3002721

25 CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
6.2e-140:283:92
SUS SCROFA (PIG).
P00889

F-NT2RP3002737

30 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
4.1e-40:136:61
MUS MUSCULUS (MOUSE).
P97414

F-NT2RP3002738

35 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.029:195:28
HOMO SAPIENS (HUMAN).
P10163

40 F-NT2RP3002790

PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.7e-08:130:36
MUS MUSCULUS (MOUSE).
P05142

45 F-NT2RP3002836

TRANSMEMBRANE PROTEIN SEX PRECURSOR.
8.9e-24:119:43
HOMO SAPIENS (HUMAN).
50 P51805

F-NT2RP3002887

55 SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).
2.9e-11:198:34
HOMO SAPIENS (HUMAN).
P02812

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F-NT2RP3002900
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.8e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

F-NT2RP3002958
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
6.4e-06:172:27
RATTUS NORVEGICUS (RAT).
P19814

F-NT2RP3002983
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
4.4e-05:106:41
BOS TAURUS (BOVINE).
P02453

F-NT2RP3003000
SODIUM CHANNEL PROTEIN (NA⁺ CHANNEL).
9.7e-30:221:31
ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
P02719

F-NT2RP3003076
ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220].
0.00033:173:30
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03200

F-NT2RP3003354
SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
2.0e-54:204:51
MUS MUSCULUS (MOUSE).
035609

F-NT2RP3003448
PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
4.0e-05:112:33
ESCHERICHIA COLI.
P31137

F-NT2RP3003469
!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
1.2e-17:70:64
HOMO SAPIENS (HUMAN).
P39194

F-NT2RP3003473
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
0.0037:33:63
BOS TAURUS (BOVINE).
P19661

F-NT2RP3003527
SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
1.8e-53:159:69
HOMO SAPIENS (HUMAN).

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Q13627

F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
2.3e-114:219:97
HOMO SAPIENS (HUMAN).
P41217

F-NT2RP3003535
HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3 REGION (ORF57).
0.98:36:30
ASTASIA LONGA (EUGLENOPHYCEAN ALGA).
P34774

F-NT2RP3003559
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.047:29:48
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643

F-NT2RP3003614
TRYPSIN INHIBITOR II (BDTI-II).
0.98:23:39
BRYONIA DIOICA (RED BRYONY).
P11968

F-NT2RP3003729
HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.
4.1e-11:204:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03151

F-NT2RP3003849
PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)).
9.7e-17:126:34
DROSOPHILA MELANOGASTER (FRUIT FLY).
P05130

F-NT2RP3003874
MYOSIN I ALPHA (MMI-ALPHA).
3.1e-64:141:84
MUS MUSCULUS (MOUSE).
P46735

F-NT2RP3003939
CELL DIVISION PROTEIN FTSH HOMOLOG 4 (EC 3.4.24.-).
7.1e-34:76:61
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P72991

F-NT2RP3003963
HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.
0.95:31:38
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
Q48251

F-NT2RP3004000
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).

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7.1e-07:187:29
CRICETULUS GRISEUS (CHINESE HAMSTER).
P11414

5 F-NT2RP3004025
EBNA-1 NUCLEAR PROTEIN.
0.022:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-NT2RP3004067
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.0e-07:184:35
HOMO SAPIENS (HUMAN).
15 Q03692

F-NT2RP3004075
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.
2.9e-07:92:40
20 HORDEUM VULGARE (BARLEY).
P17816

F-NT2RP3004083
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
25 0.013:24:45
COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
P50682

F-NT2RP3004090
30 SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
1.2e-07:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

35 F-NT2RP3004119
PEREGRIN (BR140 PROTEIN).
4.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

40 F-NT2RP3004130
CELL SURFACE ANTIGEN 114/A10 PRECURSOR.
2.4e-08:71:42
MUS MUSCULUS (MOUSE).
45 P19467

F-NT2RP3004133
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.5e-28:111:44
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

F-NT2RP3004202
55 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.0e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

- 5 F-NT2RP3004294
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.
8.8e-10:129:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53288
- 10 F-NT2RP3004309
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-05:212:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 15 F-NT2RP3004321
REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP).
2.8e-09:81:40
LEISHMANIA MAJOR.
Q25337
- 20 F-NT2RP3004345
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 25 F-NT2RP3004355
HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPV.
0.81:154:26
AZOTOBACTER CHROOCOCCUM MCD 1.
Q43959
- 30 F-NT2RP3004374
HOMEODOMAIN PROTEIN HOX-A2.
0.28:77:37
GALLUS GALLUS (CHICKEN).
Q08727
- 35 F-NT2RP3004406
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.
4.9e-18:165:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40544
- 40 F-NT2RP3004481
BUTYROPHILIN PRECURSOR (BT).
4.0e-13:152:31
HOMO SAPIENS (HUMAN).
Q13410
- 50 F-NT2RP3004552
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
3.4e-05:211:28
HOMO SAPIENS (HUMAN).
P17927
- 55 F-NT2RP3004557
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUP I-5111).
1.6e-23:129:35
HOMO SAPIENS (HUMAN).

Q06323

F-NT2RP3004625

GLYCOPROTEIN X PRECURSOR.

2.4e-10:225:25

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

F-NT2RP3004640

ENAMELIN (TUFTELIN).

2.6e-70:167:85

BOS TAURUS (BOVINE).

P27628

F-NT2RP3004647

ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).

4.6e-10:116:34

HOMO SAPIENS (HUMAN).

P12235

F-NT2RP4000108

NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L) (NF68).

3.4e-107:255:87

RATTUS NORVEGICUS (RAT).

P19527

F-NT2RP4000634

MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).

7.9e-142:267:88

MUS MUSCULUS (MOUSE).

Q61083

F-NT2RP4000962

SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).

1.5e-13:158:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08458

F-NT2RP4001001

F-NT2RP4001009

POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).

7.7e-24:235:31

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q10071

F-NT2RP4001467

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

1.2e-120:237:97

HOMO SAPIENS (HUMAN).

P21589

F-NT2RP4001877

GLYCINE-RICH RNA-BINDING PROTEIN.

1.4e-08:89:34

DAUCUS CAROTA (CARROT).

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Q03878

F-NT2RP4001879

VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.

5 0.98:49:34

MYCOBACTERIUM TUBERCULOSIS.

P71934

F-NT2RP4002187

10 PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).

4.5e-98:246:78

MUS MUSCULUS (MOUSE).

070503

F-NT2RP4002451

CUTICLE COLLAGEN 2.

0.85:92:35

CAENORHABDITIS ELEGANS.

P17656

20

F-NT2RP4002715

HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.

0.47:31:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

25 P53245

F-NT2RP4002750

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

30

3.3e-63:185:67

HOMO SAPIENS (HUMAN).

P30825

35

F-OVARC1000003

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

2.2e-82:197:72

40

HOMO SAPIENS (HUMAN).

Q06495

F-OVARC1000090

HOMEBOX PROTEIN HOX-B1 (GHOX-LAB).

45

0.049:120:32

GALLUS GALLUS (CHICKEN).

P31259

F-OVARC1000105

UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

50

8.6e-47:159:58

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33296

55

F-OVARC1000137

HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.

0.058:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015

F-OVARC1000208

!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!

2.2e-12:51:74

HOMO SAPIENS (HUMAN).

P39195

F-OVARC1000255

TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).

1.1e-112:144:86

HOMO SAPIENS (HUMAN).

P43405

F-OVARC1000275

GASTRIN PRECURSOR.

0.11:59:37

HOMO SAPIENS (HUMAN).

P01350

F-OVARC1000298

PROLINE-RICH PROTEIN MP-3 (FRAGMENT).

0.014:74:39

MUS MUSCULUS (MOUSE).

P05143

F-OVARC1000307

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

1.0:33:54

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-OVARC1000313

PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).

4.0e-15:127:37

RATTUS NORVEGICUS (RAT).

P38659

F-OVARC1000331

GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).

2.0e-24:64:84

HOMO SAPIENS (HUMAN).

P36959

F-OVARC1000410

FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).

1.9e-44:229:41

PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).

P19477

F-OVARC1000439

SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.

0.99:41:43

DROSOPHILA MELANOGASTER (FRUIT FLY).

P02841

EP 1 130 094 A2

F-OVARC1000467
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0061:30:63
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

5

F-OVARC1000529
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL 101 W (EC 2.7.1.-).
1.5e-20:127:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244

10

F-OVARC1000553
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
7.6e-26:169:40
MUS MUSCULUS (MOUSE).
P28843

15

F-OVARC1000775
METALLOTHIONEIN (MT).
0.91:31:38
CARASSIUS AURATUS (GOLDFISH).
P52723

20

F-OVARC1000811
COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).
2.8e-11:69:43
HOMO SAPIENS (HUMAN).
P00748

25

F-OVARC1000853
CUTICLE COLLAGEN 40.
0.00013:130:33
CAENORHABDITIS ELEGANS.
P34804

30

F-OVARC1000873
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.00015:53:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643

40

F-OVARC1000916
GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).
2.5e-26:109:53
MUS MUSCULUS (MOUSE).
P24788

45

F-OVARC1000956
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00073:115:33
HOMO SAPIENS (HUMAN).
P21917

50

F-OVARC1000995
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).
0.00031:139:25
HOMO SAPIENS (HUMAN).

55

P51531

F-OVARC1001030

5E5 ANTIGEN.

1.9e-09:89:41

RATTUS NORVEGICUS (RAT).

Q63003

F-OVARC1001049

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.5e-08:146:38

GALLUS GALLUS (CHICKEN).

P02457

F-OVARC1001086

VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40].

5.3e-08:182:32

GALLUS GALLUS (CHICKEN).

P02845

F-OVARC1001132

GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).

9.2e-40:229:37

HOMO SAPIENS (HUMAN).

P16383

F-OVARC1001163

HYPOTHETICAL 49.3 KD PROTEIN C30D 11.06C IN CHROMOSOME I.

8.8e-05:38:44

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09906

F-OVARC1001222

AMELOGENIN, CLASS I PRECURSOR.

0.72:96:31

BOS TAURUS (BOVINE).

P02817

F-OVARC1001260

F-OVARC1001336

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-PORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-NAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

1.1e-33:103:71

RATTUS NORVEGICUS (RAT).

Q06496

F-OVARC1001338

SERINE/THREONINE-PROTEIN KINASE UNC-51 (EC 2.7.1.-).

3.8e-30:89:46

CAENORHABDITIS ELEGANS.

Q23023

F-OVARC1001569

ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).

2.2e-06:28:64

SUS SCROFA (PIG).
P08001

F-OVARC1001570
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.8e-09:121:33
CAVIA PORCELLUS (GUINEA PIG).
P25796

F-OVARC1001596
REGULATORY PROTEIN E2.
0.33:77:37
HUMAN PAPILLOMAVIRUS TYPE 14.
P36783

F-OVARC1001607
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).
1.0e-28:69:84
HOMO SAPIENS (HUMAN).
Q10469

F-OVARC1001725

F-OVARC1001727

F-OVARC1001807
EARLY RESPONSE PROTEIN NAK1 (TR3 ORPHAN RECEPTOR).
2.4e-51:153:75
HOMO SAPIENS (HUMAN).
P22736

F-OVARC1001833
CIS-GOLGI MATRIX PROTEIN GM130.
1.2e-55:169:75
RATTUS NORVEGICUS (RAT).
Q62839

F-OVARC1001952
EBNA-1 NUCLEAR PROTEIN.
3.5e-19:130:43
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

F-OVARC1001991
HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).
3.7e-16:141:43
HOMO SAPIENS (HUMAN).
Q14681

F-OVARC1002058
LAMININ ALPHA-5 CHAIN (FRAGMENT).
2.8e-22:163:33
MUS MUSCULUS (MOUSE).
Q61001

F-OVARC1002178

EP 1 130 094 A2

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.12:73:36

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-PLACE1000033

VON WILLEBRAND FACTOR PRECURSOR.

1.7e-19:190:28

CANIS FAMILIARIS (DOG).

Q28295

F-PLACE1000231

DNA-BINDING PROTEIN MNB1A.

0.24:60:33

ZEA MAYS (MAIZE).

P38564

F-PLACE1000258

ZINC FINGER PROTEIN 177.

3.6e-19:55:61

HOMO SAPIENS (HUMAN).

Q13360

F-PLACE1000442

ZINC FINGER PROTEIN 136.

1.7e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

F-PLACE1000560

COLICIN E9 (EC 3.1.21.1).

0.015:47:44

ESCHERICHIA COLI.

P09883

F-PLACE1000740

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3).

1.6e-05:75:36

MUS MUSCULUS (MOUSE).

P31695

F-PLACE1000907

ZINC FINGER PROTEIN 141.

2.8e-15:43:88

HOMO SAPIENS (HUMAN).

Q15928

F-PLACE1000912

PROBABLE E4 PROTEIN (E1^E4).

0.19:46:36

HUMAN PAPILLOMAVIRUS TYPE 6B.

P06459

F-PLACE1000914

MALE SPECIFIC SPERM PROTEIN MST87F.

0.054:27:44

DROSOPHILA MELANOGASTER (FRUIT FLY).

P08175

F-PLACE1000927
HYPOTHETICAL PROTEIN HI0044.
3.9e-07:139:30
HAEMOPHILUS INFLUENZAE.
P44477

F-PLACE1000986

F-PLACE1001016
SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT.
2.7e-05:120:32
RATTUS NORVEGICUS (RAT).
P04775

F-PLACE1001100

F-PLACE1001114
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
2.5e-07:250:28
MUS MUSCULUS (MOUSE).
P11087

F-PLACE1001123
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
6.2e-09:95:31
HOMO SAPIENS (HUMAN).
Q04941

F-PLACE1001183
NONHISTONE CHROMOSOMAL PROTEIN HMG-17.
0.31:52:34
GALLUS GALLUS (CHICKEN).
P02314

F-PLACE1001229
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).
1.0:38:47
ARTEMIA SAUNA (BRINE SHRIMP).
P19047

F-PLACE1001231
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
4.7e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170

F-PLACE1001340
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
6.5e-14:136:29
NEUROSPORA CRASSA.
P23231

F-PLACE1001401

EP 1 130 094 A2

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).

1.3e-11:103:40

RATTUS NORVEGICUS (RAT).

P13386

F-PLACE1001407

INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).

0.013:121:32

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

Q05049

F-PLACE1001464

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

1.4e-119:246:89

HOMO SAPIENS (HUMAN).

P21589

F-PLACE1001500

BLOOM'S SYNDROME PROTEIN.

8.3e-26:203:34

HOMO SAPIENS (HUMAN).

P54132

F-PLACE1001516

GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).

7.4e-07:204:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08640

F-PLACE1001536

F-PLACE1001564

LEUCOCYTE ANTIGEN CD97 PRECURSOR.

2.1e-09:170:24

HOMO SAPIENS (HUMAN).

P48960

F-PLACE1001655

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).

4.0e-34:189:39

RATTUS NORVEGICUS (RAT).

P15387

F-PLACE1001788

HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I.

6.2e-21:75:58

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09695

F-PLACE1001795

HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.

3.8e-21:159:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47032

F-PLACE1001836

EP 1 130 094 A2

ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN)[CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].

4.5e-29:134:47

BABOON ENDOGENOUS VIRUS (STRAIN M7).

P10269

F-PLACE1001918

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.5e-30:228:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

F-PLACE1001949

PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).

5.1e-36:210:46

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q12697

F-PLACE1002080

HYPOTHETICAL PROTEIN KIAA0288 (HA6116).

3.5e-26:207:45

HOMO SAPIENS (HUMAN).

P56524

F-PLACE1002095

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

0.32:50:34

MUS MUSCULUS (MOUSE).

P15535

F-PLACE1002153

CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).

0.00021:214:26

CLOSTRIDIUM THERMOCELLUM.

Q06852

F-PLACE1002329

EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.

1.1e-35:179:44

MUS MUSCULUS (MOUSE).

Q08509

F-PLACE1002355

COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] (FRAGMENTS).

1.0e-14:183:32

BOS TAURUS (BOVINE).

P01030

F-PLACE1002374

CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).

9.2e-107:225:86

HOMO SAPIENS (HUMAN).

P07711

F-PLACE1002518

EP 1 130 094 A2

HYPOTHETICAL 13.2 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.

6.1e-05:59:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38239

5

F-PLACE1002547

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

10

1.0e-22:230:31

NEUROSPORA CRASSA.

P23231

F-PLACE1002726

15

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).

0.61:25:48

ORYCTOLAGUS CUNICULUS (RABBIT).

P02456

F-PLACE1002905

20

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

5.0e-31:93:64

BOS TAURUS (BOVINE).

25

P07106

F-PLACE1002911

T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

6.6e-06:95:35

30

HOMO SAPIENS (HUMAN).

P40200

F-PLACE1002967

35

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).

9.4e-08:95:37

MUS MUSCULUS (MOUSE).

P20490

F-PLACE1003135

40

SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).

1.9e-33:99:50

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q03497

45

F-PLACE1003163

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

9.8e-15:105:38

50

BOS TAURUS (BOVINE).

P07106

F-PLACE1003407

55

CLN5 PROTEIN.

4.2e-109:217:89

HOMO SAPIENS (HUMAN).

O75503

F-PLACE1003428
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
1.0e-36:104:46
HOMO SAPIENS (HUMAN).
P43251

5

F-PLACE1003438
HYPOTHETICAL 104.4 KD PROTEIN C17A5.16 IN CHROMOSOME I.
1.1e-10:148:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
013776

10

F-PLACE1003460
2-HYDROXY-6-KETONONA-2,4-DIENEDIOIC ACID HYDROLASE (EC 3.7.1.-).
0.00028:134:27
ESCHERICHIA COLI.
P77044

15

F-PLACE1003529
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
0.00047:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

25

F-PLACE1003573
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).
0.022:129:25
MUS MUSCULUS (MOUSE).
P20937

30

F-PLACE1003598
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.0017:102:44
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

35

F-PLACE1003644
PROTEIN Q300.
6.7e-05:24:70
MUS MUSCULUS (MOUSE).
Q02722

40

F-PLACE1003737
TOLL PROTEIN PRECURSOR.
7.3e-08:203:27
DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953

45

F-PLACE1003772
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).
3.7e-07:141:32
HOMO SAPIENS (HUMAN).
P81489

50

F-PLACE1003839
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
1.3e-09:201:31

55

MUS MUSCULUS (MOUSE).
P05143

F-PLACE1003845
PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPI-
MERASE).
5.0e-13:103:33
METHANOCOCCUS JANNASCHII.
Q57664

F-PLACE1003852
CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).
2.0e-18:189:29
HOMO SAPIENS (HUMAN).
Q14246

F-PLACE1004028
HYPOTHETICAL 9.7 KD PROTEIN IN PURC-PURL INTERGENIC REGION.
0.97:47:31
BACILLUS SUBTILIS.
P12049

F-PLACE1004078
ADSEVERIN (SCINDERIN) (SC).
5.3e-98:176:90
BOS TAURUS (BOVINE).
Q28046

F-PLACE1004166
CREB-BINDING PROTEIN.
9.6e-08:107:34
HOMO SAPIENS (HUMAN).
Q92793

F-PLACE1004168
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.
6.8e-05:147:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25655

F-PLACE1004199
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
4.2e-05:65:52
HOMO SAPIENS (HUMAN).
P39188

F-PLACE1004279
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.6e-11:166:30
CAENORHABDITIS ELEGANS.
P30638

F-PLACE1004282
HISTONE H1C (CLONE XLHW2).
0.74:73:26
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P15866

EP 1 130 094 A2

- 5 F-PLACE1004305
RAS-RELATED PROTEIN RAC1.
2.3e-23:161:39
DROSOPHILA MELANOGASTER (FRUIT FLY).
P40792
- 10 F-PLACE1004441
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
5.4e-70:156:89
HOMO SAPIENS (HUMAN).
P46091
- 15 F-PLACE1004450
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
3.1e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684
- 20 F-PLACE1004482
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.23:26:30
GALLUS GALLUS (CHICKEN).
P14093
- 25 F-PLACE1004492
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
1.2e-05:150:34
BOS TAURUS (BOVINE).
P02453
- 30 F-PLACE1004519
ENL PROTEIN.
0.68:170:30
HOMO SAPIENS (HUMAN).
Q03111
- 35 F-PLACE1004520
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
3.5e-50:150:74
HOMO SAPIENS (HUMAN).
P11462
- 40 F-PLACE1004630
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
9.1e-31:189:39
HOMO SAPIENS (HUMAN).
P18564
- 50 F-PLACE1004637
MALE SPECIFIC SPERM PROTEIN MST84DA.
0.47:29:44
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01642
- 55 F-PLACE1004648
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
8.4e-05:89:40
MUS MUSCULUS (MOUSE).

P05142

F-PLACE1004816

MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.

1.0e-25:117:46

HOMO SAPIENS (HUMAN).

P55083

F-PLACE1004887

SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.

8.4e-09:195:30

DROSOPHILA ERECTA (FRUIT FLY).

P13730

F-PLACE1005003

PROSTASIN PRECURSOR (EC 3.4.21.-).

1.2e-24:139:40

HOMO SAPIENS (HUMAN).

Q16651

F-PLACE1005005

UBIQUITIN-CONJUGATING ENZYME E2 G2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

2.5e-28:51:84

HOMO SAPIENS (HUMAN).

P56554

F-PLACE1005031

CHLORINE CHANNEL PROTEIN P64.

2.7e-52:142:76

BOS TAURUS (BOVINE).

P35526

F-PLACE1005239

SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55) (FRAGMENT).

0.27:78:26

ORYCTOLAGUS CUNICULUS (RABBIT).

018776

F-PLACE1005250

HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.

0.22:35:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53056

F-PLACE1005383

FIBRILLIN 1 PRECURSOR.

6.7e-09:134:32

MUS MUSCULUS (MOUSE).

Q61554

F-PLACE1005410

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

9.5e-105:204:100

RATTUS NORVEGICUS (RAT).

P38378

F-PLACE1005426

EP 1 130 094 A2

PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
3.2e-33:184:46
HOMO SAPIENS (HUMAN).
Q00888

5

F-PLACE1005519
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
1.2e-23:143:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

10

F-PLACE1005539
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
5.5e-05:94:37
BRASSICA NAPUS (RAPE).
P40603

15

F-PLACE1005544
CELL SURFACE A33 ANTIGEN PRECURSOR.
0.00015:132:31
HOMO SAPIENS (HUMAN).
Q99795

20

F-PLACE1005569
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.00092:122:31
EQUUS CABALLUS (HORSE).
Q28381

25

F-PLACE1005601
TOXIN S4C8.
0.34:32:37
DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).
P25683

30

F-PLACE1005660
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.99:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841

35

F-PLACE1005669
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN).
0.0078:105:37
HOMO SAPIENS (HUMAN).
Q02388

45

F-PLACE1005682
THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9).
2.7e-12:81:41
HOMO SAPIENS (HUMAN).
Q15653

50

F-PLACE1005725
HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.
7.5e-08:142:31
CAENORHABDITIS ELEGANS.
Q11073

55

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- 5 F-PLACE1005736
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
9.0e-11:91:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 10 F-PLACE1005745
ORM1 PROTEIN.
2.2e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 15 F-PLACE1005768
NEUROTOXINS I AND I'PRECURSOR (AAH I AND AAH I').
0.63:13:69
ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION). P01479
- 20 F-PLACE1005815
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
1.8e-12:73:50
HOMO SAPIENS (HUMAN).
P23508
- 25 F-PLACE1005878
CHLORINE CHANNEL PROTEIN P64.
1.6e-49:115:79
BOS TAURUS (BOVINE).
P35526
- 30 F-PLACE1005927
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
3.2e-16:152:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09875
- 35 F-PLACE1006071
LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
4.1e-08:215:26
MUS MUSCULUS (MOUSE).
P02469
- 40 F-PLACE1006073
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
2.1e-05:137:34
NEPHILA CLAVIPES (ORB SPIDER).
P46804
- 50 F-PLACE1006079
HOMEBOX PROTEIN DLX-3.
1.5e-58:144:83
HOMO SAPIENS (HUMAN).
060479
- 55 F-PLACE1006093
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
3.8e-05:72:40
HOMO SAPIENS (HUMAN).
P17600

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F-PLACE1006208
EBNA-2 NUCLEAR PROTEIN.
3.8e-15:28:75
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P12978

5

F-PLACE1006219
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)
(FRAGMENT)
2.0e-09:38:42
KLEBSIELLA PNEUMONIAE.
P45602

10

F-PLACE1006277
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.2e-07:183:29
HOMO SAPIENS (HUMAN).
Q99795

15

F-PLACE1006290
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
8.2e-39:171:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

20

F-PLACE1006443
HYPOTHETICAL 60.0 KD PROTEIN IN IMP1-HLJ1 INTERGENIC REGION.
0.0010:155:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03795

25

F-PLACE1006515
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.046:98:28
MUS MUSCULUS (MOUSE).
P10925

30

F-PLACE1006716
30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC
PROTEIN ADIPOQ).
3.6e-25:177:35
MUS MUSCULUS (MOUSE).
Q60994

40

F-PLACE1006786
PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (BASIC PROTEIN) (WBP) (FRAGMENT).
1.0:19:42
TRITICUM AESTIVUM (WHEAT).
P26913

45

F-PLACE1006809
SLS1 PROTEIN PRECURSOR.
0.0011:37:51
YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
Q99158

50

F-PLACE1006959
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.3e-05:96:41

55

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MUS MUSCULUS (MOUSE).
P05142

5 F-PLACE1007028
EBNA-1 NUCLEAR PROTEIN.
5.9e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-PLACE1007040
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAG-
MENT).
0.68:138:24
HOMO SAPIENS (HUMAN).
15 P02812

F-PLACE1007077
SERINE/THREONINE-PROTEIN KINASE CLA4 (EC 2.7.1.-).
0.73:177:25
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48562

F-PLACE1007081
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
25 3.0e-20:182:39
BOS TAURUS (BOVINE).
Q28107

F-PLACE1007096
30 HYPOTHETICAL SYMPORTER SLL1374.
2.8e-14:162:30
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P74168

35 F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
9.4e-50:120:86
HOMO SAPIENS (HUMAN).
P24390

40 F-PLACE1007591
MEIOTIC RECOMBINATION PROTEIN REC104.
0.68:73:31
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33323

F-PLACE1007626
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.00083:97:34
50 HOMO SAPIENS (HUMAN).
P23246

F-PLACE1007702
55 ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
1.9e-08:87:36
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

F-PLACE1007845
 GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
 1.3e-16:158:40
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P43636

5

F-PLACE1007881
 HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.
 1.2e-11:113:37
 CAENORHABDITIS ELEGANS.
 Q19425

10

F-PLACE1007971
 METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIA AND MT-20-IIIB).
 1.0:32:43
 MYTILUS EDULIS (BLUE MUSSEL).
 P80253

15

F-PLACE1008282
 HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).
 8.1e-87:178:87
 ORYCTOLAGUS CUNICULUS (RABBIT).
 P33279

20

F-PLACE1008297
 MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
 3.6e-17:187:33
 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 P90648

25

F-PLACE1008359
 BEM46 PROTEIN (FRAGMENT).
 4.9e-07:103:33
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 P54069

30

F-PLACE1008469
 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
 0.0018:78:37
 HOMO SAPIENS (HUMAN).
 P21917

40

F-PLACE1008549
 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
 0.0034:89:30
 HOMO SAPIENS (HUMAN).
 Q01543

45

F-PLACE1008657
 ADSEVERIN (SCINDERIN) (SC).
 6.7e-127:257:91
 BOS TAURUS (BOVINE).
 Q28046

50

F-PLACE1008716
 ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).

55

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4.5e-20:66:78
HOMO SAPIENS (HUMAN).
Q10469

5 F-PLACE1008744
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
3.6e-19:221:33
HOMO SAPIENS (HUMAN).
P04003

10 F-PLACE1008984
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-CP).
0.089:61:31
15 GLYCINE MAX (SOYBEAN).
Q42783

F-PLACE1008985
20 SYNAPTOTAGMIN V.
8.6e-09:123:35
HOMO SAPIENS (HUMAN).
000445

F-PLACE1009067
25 HYPOTHETICAL 33.4 KD PROTEIN.
4.3e-09:60:50
HOMO SAPIENS (HUMAN).
Q04323

30 F-PLACE1009196
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).
0.050:23:34
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
P35303

35 F-PLACE1009279
8.6 KD TRANSGLUTAMINASE SUBSTRATE.
1.4e-07:62:35
40 TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).
P81281

F-PLACE1009527
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.037:71:38
45 HOMO SAPIENS (HUMAN).
Q02817

F-PLACE1009546
50 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.9e-07:86:39
MUS MUSCULUS (MOUSE).
P05142

55 F-PLACE1009600
TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H)).
1.7e-08:113:31
PASTEURELLA MULTOCIDA.
P51564

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F-PLACE1009735

TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE1 10) (VMW110) (ALPHA-0 PROTEIN).

2.6e-09:182:35

5 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

F-PLACE1009982

REGULATORY PROTEIN E2.

10 0.99:94:28

HUMAN PAPILLOMAVIRUS TYPE 8.

P06422

F-PLACE1010011

15 DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).

2.8e-20:119:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P17898

20

F-PLACE1010078

ORM1 PROTEIN.

3.4e-20:137:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

25 P53224

F-PLACE1010081

SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).

1.5e-11:147:32

30 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

Q05609

F-PLACE1010251

NEL-LIKE PROTEIN (FRAGMENT).

35 1.8e-10:73:42

HOMO SAPIENS (HUMAN).

Q92832

F-PLACE1010445

40 HYPOTHETICAL BHLF1 PROTEIN.

0.0042:227:33

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03181

45

F-PLACE1010713

PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).

1.5e-77:177:80

MUS MUSCULUS (MOUSE).

070503

50

F-PLACE1010784

P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).

1.7e-18:102:40

GALLUS GALLUS (CHICKEN).

55 P32250

F-PLACE1010827

COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).

2.8e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

5 F-PLACE1010968
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE
PHOSPHOHYDROLASE).
2.3e-06:191:28
10 DROSOPHILA MELANOGASTER (FRUIT FLY).
P16621

F-PLACE1011045
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
6.0e-14:153:34
15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862

F-PLACE1011116
20 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE).
2.3e-06:195:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

25 F-PLACE1011181
MSP1 PROTEIN HOMOLOG.
4.3e-06:93:25
CAENORHABDITIS ELEGANS.
P54815

30 F-PLACE1011236
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
4.1e-17:180:28
CAENORHABDITIS ELEGANS.
35 P30638

F-PLACE1011364
HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II.
2.1e-24:158:41
40 CAENORHABDITIS ELEGANS.
Q09298

F-PLACE1011407
45 ZINC FINGER PROTEIN 140.
3.8e-10:47:74
HOMO SAPIENS (HUMAN).
P52738

F-PLACE1011516
50 HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.6e-13:117:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53073

55 F-PLACE1011708
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
9.9e-22:203:32
DROSOPHILA MELANOGASTER (FRUIT FLY).

P25723

F-PLACE1011824

SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).

1.6e-15:103:36

MUS MUSCULUS (MOUSE).

Q61036

F-PLACE1011978

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.3e-55:188:50

HOMO SAPIENS (HUMAN).

Q03923

F-PLACE2000118

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

2.8e-23:169:43

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-PLACE2000219

MALE SPECIFIC SPERM PROTEIN MST84DA.

0.11:29:41

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01642

F-PLACE3000181

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

9.5e-26:193:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P33450

F-PLACE3000213

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

2.3e-23:191:34

HOMO SAPIENS (HUMAN).

P17927

F-PLACE4000354

E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).

3.2e-25:150:30

ORYCTOLAGUS CUNICULUS (RABBIT).

P27113

F-PLACE4000455

IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).

0.66:52:36

HOMO SAPIENS (HUMAN).

P04433

F-SKNMC1000004

OPTOMOTOR-BLIND PROTEIN (LETHAL(1)OPTOMOTOR-BLIND) (L(1)OMB) (BIFID PROTEIN).

0.079:88:30

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q24432

F-SKNMC1000014
SCO-SPONDIN (FRAGMENT).
0.63:60:36
BOS TAURUS (BOVINE).
P98167

F-SKNMC1000082
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
2.4e-10:93:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53257

F-THYRO1000036
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.72:69:36
MUS MUSCULUS (MOUSE).
P05143

F-THYRO1000061
COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).
0.0068:70:38
BOS TAURUS (BOVINE).
P25508

F-THYRO1000099
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
0.0063:207:28
NEPHILA CLAVIPES (ORB SPIDER).
P46804

F-THYRO1000196
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
1.6e-10:134:32
GALLUS GALLUS (CHICKEN).
P24503

F-THYRO1000400
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
3.9e-28:163:38
MUS MUSCULUS (MOUSE).
P54116

F-THYRO1000580
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
3.3e-15:64:62
MUS MUSCULUS (MOUSE).
Q61751

F-THYRO1000584
EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE)
(135 KD PROTEIN).
1.5e-89:197:72
SUS SCROFA (PIG).
Q28949

F-THYRO1000678
GAP JUNCTION BETA-6 PROTEIN (CONNEXIN 30) (CX30).
7.7e-39:89:87

MUS MUSCULUS (MOUSE).
P70689

F-THYRO1000776
5 HIGH AFFINITY SULPHATE TRANSPORTER 2.
3.0e-25:83:50
STYLOSANTHES HAMATA.
P53392

10 F-THYRO1000795
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).
1.2e-33:227:37
BOS TAURUS (BOVINE).
P22292

15 F-THYRO1000846
CUTICLE COLLAGEN 12 PRECURSOR.
6.7e-09:190:33
CAENORHABDITIS ELEGANS.
20 P20630

F-THYRO1000866
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
0.12:85:31
25 CAENORHABDITIS ELEGANS.
P46580

F-THYRO1000956
30 PROBABLE G PROTEIN-COUPLE1) RECEPTOR APJ.
1.3e-68:165:84
HOMO SAPIENS (HUMAN).
P35414

F-THYRO1000964
35 TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.015:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

40 F-THYRO1000999
CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).
0.28:40:45
MUS MUSCULUS (MOUSE).
P50715

45 F-THYRO1001063
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6; PEPTIDE P-H].
3.5e-05:232:32
50 HOMO SAPIENS (HUMAN).
P04280

F-THYRO1001071
55 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00061:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

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F-THYRO1001102
 TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
 0.25:94:38
 HOMO SAPIENS (HUMAN).
 000268

F-THYRO1001113
 SYNAPTOTAGMIN III (SYTIII).
 2.0e-08:102:35
 MUS MUSCULUS (MOUSE).
 035681

F-THYRO1001128
 GLYCOPROTEIN X PRECURSOR.
 6.8e-07:182:31
 EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
 P28968

F-THYRO1001205
 NEUROGRANIN (NG) (PROTEIN KINASE C SUBSTRATE 7.5 KD PROTEIN) (RC3).
 0.91:33:42
 RATTUS NORVEGICUS (RAT).
 Q04940

F-THYRO1001237
 HYPOTHETICAL PROTEIN IN NIFH2 3 REGION (FRAGMENT).
 4.0e-07:68:38
 METHANOCOCCUS THERMOLITHOTROPHICUS.
 P05410

F-THYRO1001242
 SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
 1.0:104:35
 HOMO SAPIENS (HUMAN).
 P17600

F-THYRO1001266
 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODI-
 UM-GLUCOSE COTRANSPORTER).
 4.3e-09:119:27
 ORYCTOLAGUS CUNICULUS (RABBIT).
 P11170

F-THYRO1001327
 HYPOTHETICAL 23.7 KD PROTEIN IN CYR1-OST1 INTERGENIC REGION.
 1.7e-06:141:24
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P41544

F-THYRO1001456
 HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
 1.1e-11:88:48
 MYCOBACTERIUM TUBERCULOSIS.
 Q10555

F-THYRO1001457
 PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
 2.1e-68:228:59

HOMO SAPIENS (HUMAN).
Q15139

F-THYRO1001471
COLLAGEN 1(X) CHAIN PRECURSOR.
3.9e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125

F-THYRO1001478
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
0.038:162:31
HOMO SAPIENS (HUMAN).
Q03692

F-THYRO1001495
!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!
4.8e-19:50:82
HOMO SAPIENS (HUMAN).
P39193

F-THYRO1001523
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
5.0e-13:66:62
HOMO SAPIENS (HUMAN).
P39195

F-THYRO1001529
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT
2).
1.6e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09925

F-THYRO1001593
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
3.3e-92:225:77
HOMO SAPIENS (HUMAN).
P27448

F-THYRO1001608
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.2e-07:127:35
MUS MUSCULUS (MOUSE).
P05142

F-THYRO1001641
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0039:98:31
NEUROSPORA CRASSA.
Q06712

F-THYRO1001700
INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFER-
ON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE).
3.3e-09:65:43
HOMO SAPIENS (HUMAN).
P19525

F-THYRO1001702
 MYELOID UPREGULATED PROTEIN.
 7.8e-62:161:78
 MUS MUSCULUS (MOUSE).
 035682

F-THYRO1001725
 PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).
 0.00061:82:41
 RATTUS NORVEGICUS (RAT).
 P20468

F-THYRO1001770
 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
 1.0e-20:165:35
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P53974

F-THYRO1001803
 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
 3.6e-07:221:30
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P08640

F-Y79AA1000030
 TRANSCRIPTIONAL ACTIVATOR FE65.
 4.5e-09:43:46
 RATTUS NORVEGICUS (RAT).
 P46933

F-Y79AA1000127
 FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
 1.3e-05:72:43
 HOMO SAPIENS (HUMAN).
 P48023

F-Y79AA1000207
 STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TELEOCALCIN).
 1.0:100:27
 ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
 P18301

F-Y79AA1000226
 HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV.
 2.6e-07:188:28
 CAENORHABDITIS ELEGANS.
 P49049

F-Y79AA1000270
 VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).
 1.6e-102:233:87
 BOS TAURUS (BOVINE).
 P40682

F-Y79AA1000426
 INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).

1.1e-14:149:38

HOMO SAPIENS (HUMAN).

P55103

5

F-Y79AA1000521

MALE SPECIFIC SPERM PROTEIN MST84DD.

0.00079:60:36

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01645

10

F-Y79AA1000750

EBNA-1 NUCLEAR PROTEIN.

2.0e-09:131:38

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

15

P03211

F-Y79AA1000776

CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).

20

0.080:44:40

SUS SCROFA (PIG).

P35323

F-Y79AA1000777

25

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

4.2e-33:204:39

THERMOMONOSPORA CURVATA.

P49695

30

F-Y79AA1000876

PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).

4.6e-16:115:38

BOS TAURUS (BOVINE).

35

P05307

F-Y79AA1000888

TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).

40

2.0e-09:159:35

TREPONEMA PALLIDUM.

083802

F-Y79AA1000959

45

HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23).

8.8e-08:72:38

MUS MUSCULUS (MOUSE).

P09026

50

F-Y79AA1000967

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

1.1e-37:202:42

RATTUS NORVEGICUS (RAT).

Q63450

55

F-Y79AA1001013

SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS : PEPTIDE P-D] (FRAGMENT).

0.038:128:28

EP 1 130 094 A2

HOMO SAPIENS (HUMAN).
P10162

5 F-Y79AA1001056
HYPOTHETICAL 7.1 KD PROTEIN IN TK-VS INTERGENIC REGION.
0.41:42:30
BACTERIOPHAGE T4.
P13307

10 F-Y79AA1001062
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).
9.9e-13:132:38
HOMO SAPIENS (HUMAN).
Q13829

15 F-Y79AA1001090
ANKYRIN HOMOLOG PRECURSOR.
4.0e-19:176:34
CHROMATIUM VINOSUM.
20 Q06527

F-Y79AA1001212
HYPOTHETICAL PROTEIN MJ0110.
0.095:55:34
25 METHANOCOCCUS JANNASCHII.
Q57574

F-Y79AA1001264
HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.
30 3.3e-53:177:55
CAENORHABDITIS ELEGANS.
Q10005

F-Y79AA1001272
35 ACROSIN PRECURSOR (EC 3.4.21.10).
6.3e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038

40 F-Y79AA1001328
DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).
1.3e-08:118:39
RATTUS NORVEGICUS (RAT).
P97677

45 F-Y79AA1001426
BAND 3 ANION TRANSPORT PROTEIN.
1.7e-18:156:32
GALLUS GALLUS (CHICKEN).
50 P15575

F-Y79AA1001427
INDUCIBLE NITRATE REDUCTASE 2 (EC 1.6.6.1) (NR).
1.1e-49:131:51
55 GLYCINE MAX (SOYBEAN).
P39870

F-Y79AA1001430

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RING CANAL PROTEIN (KELCH PROTEIN).

2.5e-24:157:40

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q04652

5

F-Y79AA1001523

TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).

6.2e-15:141:39

10 HOMO SAPIENS (HUMAN).

Q13263

F-Y79AA1001530

TUBULIN BETA-5 CHAIN.

15 8.0e-76:204:76

HOMO SAPIENS (HUMAN).

P04350

F-Y79AA1001592

20 PTB-ASSOCIATED SPLICING FACTOR (PSF).

0.42:104:33

HOMO SAPIENS (HUMAN).

P23246

25 F-Y79AA1001727

AMALGAM PROTEIN PRECURSOR.

1.9e-09:185:28

DROSOPHILA MELANOGASTER (FRUIT FLY).

P15364

30

F-Y79AA1001787

PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).

7.6e-43:210:45

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

35 Q12697

F-Y79AA1001793

CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).

40 0.077:44:40

SUS SCROFA (PIG).

P35323

F-Y79AA1001795

45 HYPOTHETICAL BHLF1 PROTEIN.

0.00014:210:31

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03181

50 F-Y79AA1001799

MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.

2.8e-18:107:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23500

55

F-Y79AA1001803

SECRETOTRANIN III PRECURSOR (SGIII).

1.3e-68:182:76

EP 1 130 094 A2

MUS MUSCULUS (MOUSE).
P47867

5 F-Y79AA1001863
GLYCOPROTEIN J.
0.030:61:32

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480

10 F-Y79AA1002022
WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).
9.8e-08:127:37
HOMO SAPIENS (HUMAN).
P42768

15 F-Y79AA1002058
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.28:56:42
20 HOMO SAPIENS (HUMAN).
P49716

F-Y79AA1002121
25 D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).
0.71:57:36
MUS MUSCULUS (MOUSE).
Q60925

F-Y79AA1002129
30 TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
0.98:158:24
PSEUDOMONAS AERUGINOSA.
P15276

35 F-Y79AA1002213
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
4.7e-39:218:41
CAENORHABDITIS ELEGANS.
Q03567

40 F-Y79AA1002334
HYPOTHETICAL PROTEIN MJ1345.
1.8e-08:164:26
45 METHANOCOCCUS JANNASCHII.
Q58741

F-Y79AA1002373
50 CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).
0.083:44:40
SUS SCROFA (PIG).
P35323

55 F-Y79AA1002376
DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC (DH IC-2).
3.0e-91:214:83
RATTUS NORVEGICUS (RAT).
Q62871

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F-Y79AA1002378
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
1.0e-59:163:74
MUS MUSCULUS (MOUSE).
Q07231

F-Y79AA1002381
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
9.5e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546

Homology search result 6

[0296] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 5'-ends. except EST and STS sequences

Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0297] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020
H.sapiens mitochondrial DNA, complete genome.
6.0e-188:913:97
X93334

F-BNGH41000087
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
7.1e-32:176:99
AL034418

F-BNGH41000091
Homo sapiens potassium channel h-eag.
1.6e-79:687:76
AJ001366

F-HEMBA1000006
S.erythraea second and third ORF's of eryA gene, complete cds.
0.95:243:64
M63677

F-HEMBA1000121
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
5.9e-70:450:89
AL031291

F-HEMBA1000128
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence.
1.0:274:59
Z98549

F-HEMBA1000275

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Herpes simplex virus type 2 (strain HG52), complete genome.
0.036:625:55
Z86099

- 5 F-HEMBA1000300
Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.
1.4e-40:343:80
AC005702
- 10 F-HEMBA1000349
Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.
7.5e-65:451:72
AC005922
- 15 F-HEMBA1000443
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SE-
QUENCE.
8.1e-77:216:95
Z93241
- 20 F-HEMBA1000462
Caenorhabditis elegans cosmid C49H3.
3.7e-06:98:82
U42436
- 25 F-HEMBA1000477
Mus musculus BALB/c putative growth factor GDF7 (Gdf7) gene, partial cds.
9.1e-05:190:65
U08339
- 30 F-HEMBA1000590
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphig-
lycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG
island, complete sequence.
3.0e-102:209:99
AL021578
- 35 F-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.
2.0e-95:460:99
AC004480
- 40 F-HEMBA1000671
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
1.5e-28:259:69
AC006116
- 45 F-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds.
6.5e-126:442:97
AF053470
- 50 F-HEMBA1000732
Homo sapiens clone IMAGE Consortium 302831 latent transforming growth factor-beta binding protein 4 mRNA,
partial cds.
1.7e-45:258:94
AF054502
- 55

F-HEMBA1000745

Streptomyces coelicolor cosmid 3F9.

3.5e-06:360:61

AL023862

5

F-HEMBA1000835

Homo sapiens fibrillin mRNA, complete cds.

1.3e-07:151:69

L13923

10

F-HEMBA1000875

Human Krueppel-type zinc finger protein (ZNF169) gene, partial cds.

2.6e-28:249:81

U28322

15

F-HEMBA1000907

Spermatozopsis similis mRNA for 95 kD basal apparatus-protein.

3.4e-09:599:60

AJ001438

20

F-HEMBA1000940

Homo sapiens connexin46.6 (Cx46.6) gene, complete cds.

1.7e-16:307:66

AF014643

25

F-HEMBA1000962

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

0.00040:497:59

AC004228

30

F-HEMBA1001184

Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds.

8.8e-23:404:67

AF042081

35

F-HEMBA1001221

Human transmembrane protein mRNA, complete cds.

2.4e-42:858:63

U19878

40

F-HEMBA1001228

Human germline oligomeric matrix protein (COMP) mRNA, complete cds.

1.9e-82:470:91

L32137

45

F-HEMBA1001272

Human Ig gamma-2 heavy chain switch region.

0.032:549:60

U39934

50

F-HEMBA1001296

H.sapiens mRNA for PQ-rich protein.

6.9e-07:73:98

Z50194

55

F-HEMBA1001297

Homo sapiens putative transcription factor CA150 mRNA, complete cds.

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9.3e-14:143:81
AF017789

F-HEMBA1001390

Mus musculus polymerase I-transcript release factor mRNA, complete cds.
2.5e-56:464:81
AF036249

F-HEMBA1001563

Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.
3.1e-06:210:68
AL022165

F-HEMBA1001621

Human G protein-coupled receptor APJ gene, complete cds.
2.0e-98:516:95
U03642

F-HEMBA1001878

Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
1.0e-170:810:98
AF090988

F-HEMBA1001886

Human repressor transcriptional factor (ZNF85) mRNA, complete cds.
3.3e-114:849:80
U35376

F-HEMBA1002048

HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.
3.8e-11:244:66
AQ103440

F-HEMBA1002131

Homo sapiens mRNA for KIAA0584 protein, partial cds.
3.5e-44:709:66
AB011156

F-HEMBA1002163

Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
2.3e-28:373:71
AC002489

F-HEMBA1002164

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.
1.3e-127:493:99
AL031427

F-HEMBA1002167

Rattus norvegicus neuroligin I mRNA, complete cds.
8.1e-155:850:91
U22952

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F-HEMBA1002178

Homo sapiens mRNA for KIAA0584 protein, partial cds.

2.6e-46:794:65

AB011156

5

F-HEMBA1002195

Human lysosomal alpha-mannosidase (manB) gene, 5' flanking region and exon 1.

7.7e-35:255:86

U60885

10

F-HEMBA1002227

Homo sapiens mRNA for 80K-L protein, complete cds.

3.8e-137:382:95

D10522

15

F-HEMBA1002239

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.

4.5e-43:452:74

AC003049

20

F-HEMBA1002316

Homo sapiens DNA sequence from PAC 29C18 on chromosome 22.

3.0e-22:609:67

Z97192

25

F-HEMBA1002420

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

4.2e-142:322:98

AC005632

30

F-HEMBA1002421

Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.

1.3e-165:778:98

J04621

35

F-HEMBA1002524

Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.

1.3e-153:313:96

AC004209

40

F-HEMBA1002551

Human potential CENP-C binding target sequence, 0.7 kb clone, partial sequence 2.

6.1e-16:108:97

U57994

45

F-HEMBA1002767

Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.

1.4e-168:798:98

AF038660

50

F-HEMBA1002985

HS_3165_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=16 Row=E, genomic survey sequence.

1.7e-08:127:76

AQ142051

55

F-HEMBA1002992

RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67815, genomic survey sequence.

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2.7e-11:119:86
AQ201833

5 F-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
4.5e-187:873:99
AF034611

10 F-HEMBA1003072
Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.
4.1e-50:515:73
U68380

15 F-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
5.3e-139:671:98
AF049891

20 F-HEMBA1003120
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
3.3e-44:213:73
AC006116

25 F-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds.
5.5e-183:856:98
AF093118

30 F-HEMBA1003294
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SE-
QUENCE.
4.2e-38:558:69
AL031121

35 F-HEMBA1003315
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.
1.2e-61:737:68
AB013390

40 F-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.9e-183:851:99
AF074264

45 F-HEMBA1003399
Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.
8.7e-16:215:74
AC005282

50 F-HEMBA1003487
H.sapiens DNA sequence.
0.0075:158:67
Z22340

55 F-HEMBA1003497
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27O5, WORKING DRAFT SEQUENCE.
1.1e-109:538:98
AL033529

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- 5 F-HEMBA1003530
S.scrofa mRNA for BM88 antigen.
2.8e-47:644:69
X82027
- 10 F-HEMBA1003602
Human (lambda) DNA for immunoglobulin light chain.
2.5e-94:551:91
D86997
- 15 F-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
6.1e-151:777:96
AC006011
- 20 F-HEMBA1003945
Homo sapiens clone 638 unknown mRNA, complete sequence.
1.8e-76:310:93
AF091085
- 25 F-HEMBA1004007
- 30 F-HEMBA1004067
Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S
ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.
8.7e-133:718:94
AL031864
- 35 F-HEMBA1004085
Homo sapiens, clone hRPK.2_A_1, complete sequence.
2.7e-58:256:80
AC006197
- 40 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds.
3.8e-159:779:96
AF064243
- 45 F-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
1.2e-183:863:99
AC005752
- 50 F-HEMBA1004391
H.sapiens gene for neural cell adhesion molecule L1.
0.51:426:59
Z29373
- 55 F-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
3.3e-147:463:93
AC004938
- F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds.
0.00036:230:62
AF065389

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- 5 F-HEMBA1004505
D.melanogaster mRNA for alpha 1,2 mannosidase.
5.5e-17:663:58
X82640
- 10 F-HEMBA1004785
Gallus gallus mRNA for chromobox protein (CHCB3), complete cds.
6.6e-19:322:68
AB005619
- 15 F-HEMBA1004797
Haemonchus contortus GT microsatellite DNA sequence.
3.0e-08:175:71
U84474
- 20 F-HEMBA1004952
Mus musculus recombinant quaking gene sequence.
4.8e-15:398:65
U44942
- 25 F-HEMBA1004971
F-HEMBA1004982
- 30 F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds.
2.5e-65:370:93
AB002308
- 35 F-HEMBA1005084
Mouse transcriptional control element.
0.0024:189:63
M17284
- 40 F-HEMBA1005145
Pseudorabies virus glycoprotein gp50 gene, complete cds.
0.00022:395:60
AF092447
- 45 F-HEMBA1005230
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
2.8e-102:302:94
AC006116
- 50 F-HEMBA1005246
Homo sapiens CAGH44 mRNA, partial cds.
5.0e-29:429:66
U80741
- 55 F-HEMBA1005267
Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.
1.0e-43:320:87
AF042089
- F-HEMBA1005337
Plasmodium falciparum MAL3P6, complete sequence.
4.1e-08:84:89

Z98551

F-HEMBA1005430

5 F-HEMBA1005449
T.aestivum mRNA for a proline-rich protein.
0.00097:385:61
X52472

10 F-HEMBA1005489
Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na⁺-isocitrate dehydrogenase gamma subunit (IDH), and trans-locon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.
15 7.8e-16:405:62
U52111

F-HEMBA1005522
O.cuniculus rACNG mRNA for aorta CNG channel.
20 5.9e-47:344:85
X59668

F-HEMBA1005545
Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.
25 5.1e-173:810:98
U29589

F-HEMBA1005698

30 F-HEMBA1005913
HS_2249_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2249
Col=1 Row=J, genomic survey sequence.
0.17:215:61
AQ072649

35 F-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
7.0e-107:285:93
AC005581

40 F-HEMBA1005945
Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.
1.8e-46:670:65
AF004161

45 F-HEMBA1006016
CIT-HSP-2334L16.TF CIT-HSP Homo Sapiens genomic clone 2334L16, genomic survey sequence.
2.1e-13:246:69
AQ038406

50 F-HEMBA1006171

F-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
55 1.4e-144:416:93
AC005261

F-HEMBA1006299

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F-HEMBA1006311

F-HEMBA1006335

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

9.6e-61:370:91

AL023582

F-HEMBA1006357

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

2.3e-26:389:67

AF005038

F-HEMBA1006430

Caenorhabditis elegans cosmid T12A2.

4.6e-23:283:72

U13019

F-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

1.9e-144:575:98

AF026852

F-HEMBA1006517

F-HEMBA1006544

Homo sapiens suppressor of white-apricot homolog 2 (SWAP2) gene, exons 12 and 13.

2.3e-151:732:97

AF042809

F-HEMBA1006572

HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.

1.9e-45:245:96

AQ103440

F-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

3.6e-127:646:95

AB014587

F-HEMBA1006707

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

1.7e-118:397:98

AL021578

F-HEMBA1006724

H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.

1.4e-53:282:97

Z55440

F-HEMBA1006749

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

3.9e-116:457:98

AL021578

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- 5 F-HEMBA1006770
Xenopus laevis elav-type ribonucleoprotein (etr-1) mRNA, complete cds.
1.6e-53:280:81
U16800
- 10 F-HEMBA1006902
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
4.9e-122:462:98
AL021578
- 15 F-HEMBA1006912
F-HEMBA1006916
Homo sapiens Grb14 mRNA, complete cds.
1.6e-118:651:92
L76687
- 20 F-HEMBA1006960
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.
0.20:298:60
AL033526
- 25 F-HEMBA1007013
Rattus norvegicus repeat element associated with the Rasgrf1 gene.
8.0e-07:531:59
AF056927
- 30 F-HEMBA1007057
Human DNA sequence from clone 522J7 on chromosome 22q13.3. Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs, complete sequence.
0.27:277:64
35 Z98885
- F-HEMBA1007063
F-HEMBA1007226
40 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.
0.00033:488:63
AL031658
- 45 F-HEMBA1007241
Caenorhabditis elegans cosmid T15B7.
0.068:304:59
AF022985
- 50 F-HEMBA1007291
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
6.2e-123:587:98
AC004755
- 55 F-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
1.3e-30:172:97
U56430

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F-HEMBB1000106

Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.
0.033:332:61

AL030995

F-HEMBB1000276

Dictyostelium discoideum gene encoding a novel glycoprotein.
0.00070:440:60

AJ005262

F-HEMBB1000309

Homo sapiens zinc finger protein (MBLL) mRNA, complete cds.
7.6e-34:180:100

AF061261

F-HEMBB1000407

Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces. 0.16:228:64
AC000384

F-HEMBB1000447

Homo sapiens JWA protein mRNA, complete cds.
1.4e-158:750:98

AF070523

F-HEMBB1000542

Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.

4.3e-141:874:89

Z99496

F-HEMBB1000567

Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF.
9.7e-122:572:99

X07868

F-HEMBB1000642

F-HEMBB1000668

Caenorhabditis elegans cosmid K06A5.
0.00041:174:64

AF039038

F-HEMBB1000679

C.familiaris mRNA for TRAM-protein.
6.1e-100:756:80

X63678

F-HEMBB1000881

Danio rerio mRNA for MINDIN2, complete cds.
6.2e-40:581:66

AB006085

F-HEMBB1000905

Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
4.9e-91:209:94

AC005089

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- 5 F-HEMBB1001026
Human p76 mRNA, complete cds.
1.9e-06:410:61
U81006
- 10 F-HEMBB1001048
Human Hpast (HPAST) mRNA, complete cds.
6.8e-55:524:75
AF001434
- 15 F-HEMBB1001200
Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9
unordered pieces.
4.4e-12:794:59
AC004157
- 20 F-HEMBB1001407
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1
ordered pieces.
2.7e-43:281:91
AC004150
- 25 F-HEMBB1001530
HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens
genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.
2.1e-14:95:97
AQ131814
- 30 F-HEMBB1001547
S.cerevisiae chromosome VII reading frame ORF YGL236c.
1.1e-19:550:61
Z72758
- 35 F-HEMBB1001573
Homo sapiens 12p13.3 PAC RPCI5-951N9 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
2.7e-07:467:60
AC004672
- 40 F-HEMBB1001847
H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.r11c.
1.1e-14:94:100
Z64565
- 45 F-HEMBB1001959
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.2e-82:492:90
AL034405
- 50 F-HEMBB1001978
Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.
7.0e-23:239:76
AC005386
- 55 F-HEMBB1002039
Human DNA sequence from cosmid 315B17, between markers DXS366 and DXS87 on chromosome X contains
ESTs.

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3.5e-49:605:71
Z73967

F-HEMBB1002041

5 R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
3.5e-09:501:60
X83546

F-HEMBB1002051

10 Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.
3.1e-95:454:99
AF049703

F-HEMBB1002120

15 F-HEMBB1002162
Homo sapiens genethonin 1 mRNA, complete cds.
7.0e-67:328:99
AF062534

F-HEMBB1002228

20 Homo sapiens unknown mRNA, complete cds.
1.6e-39:208:98
AF047439

F-HEMBB1002245

25 Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds.
3.7e-68:424:87
U26595

F-HEMBB1002302

30 RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.
2.7e-15:101:98
B88081

F-HEMBB1002427

35 Homo sapiens chromosome 9q34, clone 70C11, complete sequence.
2.9e-123:249:90
AC002319

F-HEMBB1002465

40 Mouse short chain acyl-CoA dehydrogenase mRNA, complete cds.
7.9e-18:545:61
L11163

F-HEMBB1002661

45 Drosophila melanogaster; Chromosome 2R; Region 44A1-44A2; P1 clone DS07435, WORKING DRAFT SE-
QUENCE, 2 unordered pieces.
1.9e-07:187:67
50 AC005445

F-HEMBB1002663

F-HEMBB1002693

55 Homo sapiens full length insert cDNA, clone ZD85G07.
2.1e-20:136:93
AF086462

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F-MAMMA1000046

CIT-HSP-2166017.TF CIT-HSP Homo sapiens genomic clone 2166017, genomic survey sequence.

2.0e-60:345:92

B92334

5

F-MAMMA1000102

Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.

3.0e-161:766:98

Z79996

10

F-MAMMA1000106

Rat gene for alpha 1B adrenergic receptor, promoter region and partial cds.

0.0025:247:64

D32045

15

F-MAMMA1000118

Canis familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

6.1e-06:545:60

U73207

20

F-MAMMA1000141

Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.

1.5e-10:151:78

AC004024

25

F-MAMMA1000204

Homo Sapiens mRNA for LGMD2B protein.

2.1e-166:781:98

AJ007670

30

F-MAMMA1000226

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.

2.9e-35:188:100

AC004064

35

F-MAMMA1000403

Human vascular addressin MAdCAM-1 mRNA, complete cds.

0.00043:538:59

U82483

40

F-MAMMA1000449

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.

0.090:514:60

Z97651

45

F-MAMMA1000457

H.sapiens mRNA for NADH-cytochrome b5 reductase.

5.5e-36:469:68

Y09501

50

F-MAMMA1000473

Caenorhabditis elegans cosmid B0491, complete sequence.

0.0052:187:64

Z49907

55

F-MAMMA1000496

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Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
1.2e-81:318:92
AC004997

5 F-MAMMA1000528
P.falciparum complete gene map of plastid-like DNA (IR-B).
0.016:343:58
X95276

10 F-MAMMA1000591
Mus musculus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-T3 mRNA, complete cds.
1.2e-24:493:63
U70538

15 F-MAMMA1000614
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 21 unordered pieces.
7.5e-13:615:60
AC004670

20 F-MAMMA1000652
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.
1.6e-59:451:82
AC004638

25 F-MAMMA1000681
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6.
1.2e-32:636:65
AJ000479

30 F-MAMMA1000706
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0110D16; HTGS phase 1,
WORKING DRAFT SEQUENCE, 7 unordered pieces.
6.8e-06:428:62
35 AC004578

F-MAMMA1000788
HS_3080_A2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080
Col=6 Row=C, genomic survey sequence.
40 4.9e-35:204:94
AQ128409

F-MAMMA1000810
Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.
45 5.8e-06:246:65
AL022098

F-MAMMA1000814
Anadara trapezia (alpha 3.15L) hemoglobin alpha-chain (HBA) gene, exons 2 and 3, intron 2, including hypervar-
50 iable microsatellite polymorphic repeat regions.
1.0e-12:176:75
L25098

F-MAMMA1000881
Rattus norvegicus serum and glucocorticoid-regulated kinase (sgk) mRNA, complete cds.
55 2.8e-07:283:63
L01624

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F-MAMMA1000986

Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.

1.8e-166:306:99

AF001550

5

F-MAMMA1000994

Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.

0.75:260:61

AL021897

10

F-MAMMA1001043

H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2).

0.038:376:60

Z37976

15

F-MAMMA1001066

Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence.

4.4e-15:162:72

AD001527

20

F-MAMMA1001094

Homo sapiens clone 243 unknown mRNA, complete sequence.

6.2e-181:844:99

AF091094

25

F-MAMMA1001141

Cams familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

1.3e-10:602:59

U73207

30

F-MAMMA1001150

M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

7.7e-57:447:67

Z34524

35

F-MAMMA1001237

Rattus norvegicus monocarboxylate transporter MCT3 mRNA, complete cds.

1.5e-08:306:65

AF059258

40

F-MAMMA1001284

HS_3076_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3076 Col=15 Row=K, genomic survey sequence.

5.2e-53:307:93

AQ120674

45

F-MAMMA1001310

1(2)09851 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

0.00072:209:66

AQ025672

50

F-MAMMA1001344

Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete sequence.

5.2e-05:164:67

55

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AF026198

F-MAMMA1001418

Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds.

6.0e-35:622:63

U62966

F-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

5.2e-46:538:74

AC004865

F-MAMMA1001609

Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence. 0.00031:592:57

AC005886

F-MAMMA1001615

H.sapiens CpG island DNA genomic MseI fragment, clone 71h9, reverse read cpg71h9.rt1a.

1.2e-25:146:99

Z62710

F-MAMMA1001623

Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

3.9e-69:471:85

AC006065

F-MAMMA1001634

Human DNA sequence from PAC 93C23 on chromosome X. Contains steroid 5-alpha-reductase pseudogene, ESTs and STS.

2.2e-22:228:79

AL008713

F-MAMMA1001893

HS_3067_B2_H09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=18 Row=P, genomic survey sequence.

2.5e-29:188:93

AQ138065

F-MAMMA1001901

Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS, complete sequence.

2.0e-23:287:71

Z95118

F-MAMMA1001957

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.5e-14:192:66

AC004573

F-MAMMA1001978

Human immunoglobulin S(u) like sequence.

0.60:150:66

X15517

F-MAMMA1002070

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

3.9e-116:250:93

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AC002073

F-MAMMA1002080

Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.

1.1e-59:493:78

AC004807

F-MAMMA1002087

HS-1047-B2-A09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=18 Row=B, genomic survey sequence.

2.1e-31:174:98

B38457

F-MAMMA1002091

Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.

1.6e-156:743:98

AF039916

F-MAMMA1002095

Rat alternatively spliced mRNA.

4.9e-126:691:91

M93017

F-MAMMA1002128

Mus musculus C2C12 unknown mRNA, partial cds.

5.0e-41:353:77

U31629

F-MAMMA1002142

F-MAMMA1002165

Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.

1.2e-34:219:90

AF100780

F-MAMMA1002205

Homo Sapiens Chromosome X clone bWXD691, complete sequence.

8.1e-33:535:67

AC004386

F-MAMMA1002224

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.

1.2e-31:274:82

Z86090

F-MAMMA1002234

Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).

9.8e-145:736:91

X53744

F-MAMMA1002586

Drosophila melanogaster cosmid clone 86E4.

0.0071:306:58

AL021086

F-MAMMA1002633

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.

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3.9e-33:297:79
AL031680

5 F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds.
1.7e-82:801:74
AF001434

10 F-NT2RM1000407
Cloning vector pUC-GM-INT, complete sequence.
9.4e-141:673:98
AF025392

15 F-NT2RM1000462
, complete sequence.
1.5e-86:232:82
AC005300

20 F-NT2RM1000542
Mouse beta-galactosidase (BGAL) gene, complete cds.
4.4e-17:468:62
M57734

25 F-NT2RM1000580
Caenorhabditis elegans cosmid F09E5.
1.6e-08:352:61
U37429

30 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4.
1.1e-94:299:92
Y11306

35 F-NT2RM1000855
Canis familiaris sec61 homologue mRNA, complete cds.
6.6e-110:671:87
M96629

40 F-NT2RM1000858
tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].
2.0e-65:716:70
S70011

45 F-NT2RM1000899
S.pombe chromosome I cosmid c8C9.
0.0010:300:59
Z99168

50 F-NT2RM2000241
Homo sapiens chromosome 12p13.3 clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.
0.99:201:65
AC005844

55 F-NT2RM2000306
Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.
1.1e-142:595:97

AL021878

F-NT2RM2000410

S.gregaria Abd-B gene.

0.076:172:66

X69161

F-NT2RM2000423

Arthrobacter sp. beta-galactosidase gene, complete cds.

4.2e-06:606:57

U78028

F-NT2RM2000497

Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.

1.2e-55:285:81

AC005969

F-NT2RM2000514

F-NT2RM2000565

Caenorhabditis elegans cosmid F28C5, complete sequence.

4.2e-18:539:62

Z68315

F-NT2RM2000582

P.zebra microsatellite locus DNA, 429bp.

0.00015:160:69

X99784

F-NT2RM2000589

Bos taurus myosin X, complete cds.

3.4e-139:817:88

U55042

F-NT2RM2000622

H.sapiens MFH-1 gene.

0.0010:466:57

Y08223

F-NT2RM2000632

Homo sapiens mRNA for TBP-associated factor 170 (TAFII170).

0.0052:331:59

AJ001017

F-NT2RM2000773

Oryctolagus cuniculus serum amyloid A-activating factor SAF-8 mRNA, partial cds.

2.9e-91:496:93

AF076786

F-NT2RM2001126

Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.

1.6e-161:663:99

AF093419

F-NT2RM2001558

Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.

1.2e-164:770:98

AF093408

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F-NT2RM2001626

F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.

4.5e-46:606:68

Z88651

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F-NT2RM2001643

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT775
Col=18 Row=J, genomic survey sequence.

2.5e-06:181:66

B41504

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F-NT2RM2001738

S.capreolus ard2 gene and orf2, orf4 and orf5.

0.41:273:63

Y11036

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F-NT2RM2001767

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.

8.0e-18:130:92

AL034380

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F-NT2RM2001792

Homo sapiens mRNA for serum lectin P35, complete cds.

2.5e-12:244:67

D49353

25

F-NT2RM2001818

F-NT2RM2001902

Drosophila melanogaster mRNA for p21 activated kinase related protein.

7.2e-74:683:75

AJ011578

30

F-NT2RM2001939

Human G protein-coupled receptor GPR-NGA gene, complete cds.

1.4e-140:702:96

U55312

35

F-NT2RM2001941

Human gene for muscarinic acetylcholine receptor HM1.

6.3e-20:488:62

X15263

40

F-NT2RM4000100

Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.

7.7e-25:162:74

AC004827

45

F-NT2RM4000115

F-NT2RM4000198

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F-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds.

7.3e-37:194:98

U12255

55

F-NT2RM4000295

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Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds.
1.6e-05:642:59
AF047717

5 F-NT2RM4000326
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.
1.0e-127:340:92
AJ003147

10 F-NT2RM4000417
Oncorhynchus kisutch microsatellite OKi20 DNA.
0.44:144:66
AF055444

15 F-NT2RM4000444
S.salar mRNA for transport-associated protein Tap2A.
1.7e-27:577:62
Z83328

20 F-NT2RM4000587
Homo sapiens chromosome 19, cosmid R28058, complete sequence.
7.7e-16:388:64
AC005615

25 F-NT2RM4000593

F-NT2RM4000648
M.musculus mRNA for K-glypican.
30 1.4e-50:610:70
X83577

F-NT2RM4000761
Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.
35 4.8e-167:787:98
M10546

F-NT2RM4000965
S.scrofa mRNA for calcium release channel (CRC).
40 0.044:356:60
X62880

F-NT2RM4000997

45 F-NT2RM4001321
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775
Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

50 F-NT2RM4001325
Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds.
6.6e-12:384:64
AB012192

55 F-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
9.7e-155:719:99

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AB014538

F-NT2RM4001735

5 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 483K16, WORKING DRAFT SE-
QUENCE.

1.3e-162:679:96

AL034374

F-NT2RM4001768

10 Human HepG2 partial cDNA, clone hrnd3a07m5.

2.7e-52:271:98

D17020

F-NT2RM4001843

15

F-NT2RM4002352

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.

1.4e-155:761:97

AB009462

20

F-NT2RP1000002

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.7e-06:252:65

M21096

25

F-NT2RP1000050

Human HepG2 partial cDNA, clone hmd3g02m5.

7.1e-18:115:97

D17047

30

F-NT2RP1000181

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.

4.2e-139:427:98

AC004228

35

F-NT2RP1000239

Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.

1.4e-90:524:91

U92989

40

F-NT2RP1000261

Homo sapiens hPMS1 gene, promoter region and exon 1.

2.5e-14:132:85

AB006462

45

F-NT2RP1000271

Homo sapiens DNA-binding protein mRNA, complete cds.

4.3e-139:678:97

AF038951

50

F-NT2RP1000300

Homo sapiens, complete sequence.

0.012:146:69

AC005854

55

F-NT2RP1000325

H.sapiens gene for phosphate carrier.

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4.2e-110:438:98
X77337

5 F-NT2RP1000448
Streptomyces coelicolor cosmid 1A6.
0.79:209:61
AL023496

10 F-NT2RP1000465
Mus musculus nuclear protein NIP45 mRNA, complete cds.
2.2e-29:489:68
U76759

15 F-NT2RP1000468
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.6e-49:306:91
AL034405

20 F-NT2RP1000551
Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.
7.5e-139:742:93
U09585

25 F-NT2RP1000579
Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.
3.6e-140:798:91
L21936

30 F-NT2RP1000613
Sequence 1 from patent US 5589579.
8.1e-10:468:58
I32995

35 F-NT2RP1000679
Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence.
1.3e-112:448:89
AC003688

40 F-NT2RP1000740
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
9.3e-14:211:73
Z60772

45 F-NT2RP1000903
HS_2256_B1_E10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2256
Col=19 Row=J, genomic survey sequence.
9.0e-21:197:84
AQ084622

50 F-NT2RP1000981
F-NT2RP1001004
Danio rerio mRNA for MINDIN2, complete cds.
4.1e-22:472:63
55 AB006085

F-NT2RP1001020
Mus musculus clone OST66, genomic survey sequence.

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1.5e-47:352:81
AF046696

F-NT2RP1001031

CIT-HSP-2330P23.TR CIT-HSP Homo sapiens genomic clone 2330P23, genomic survey sequence.
8.0e-26:145:99
AQ035969

F-NT2RP1001563

Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces. 0.096:405:59
AC004971

F-NT2RP2000092

Human zinc finger protein ZNF136.
1.8e-54:652:70
U09367

F-NT2RP2000178

Streptomyces coelicolor cosmid 3F9.
0.92:217:64
AL023862

F-NT2RP2000240

Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
2.9e-96:534:90
AF001550

F-NT2RP2000394

Gallus gallus p52 pro-apototic protein mRNA, complete cds.
2.9e-19:380:65
AF029071

F-NT2RP2000447

Homo sapiens clone DJ1129D05, complete sequence.
1.3e-109:289:98
AC005630

F-NT2RP2000479

Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudo-gene, ESTs and STSs.
0.0039:219:63
AL008627

F-NT2RP2000514

Homo sapiens roundabout 2 (robo2) mRNA, partial cds.
3.7e-89:461:95
AF040991

F-NT2RP2000533

Mus musculus cornichon mRNA, complete cds.
1.4e-113:677:89
AF022811

F-NT2RP2000610

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
4.3e-25:177:89
AL034405

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F-NT2RP2000616

RPC111-75J11.TK MCI11 Homo sapiens genomic clone R-75J11, genomic survey sequence.

8.4e-34:135:91

AQ268877

5

F-NT2RP2000649

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

1.2e-165:802:97

AF064867

10

F-NT2RP2000663

Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.

1.6e-106:365:97

15

Z73913

F-NT2RP2000694

Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.

4.2e-112:561:96

20

AJ012159

F-NT2RP2000712

HS_3071_A2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=10 Row=G, genomic survey sequence.

7.6e-78:389:97

25

AQ166085

F-NT2RP2000739

Human mRNA for KIAA0326 gene, partial cds.

6.4e-24:574:62

30

AB002324

F-NT2RP2000818

Drosophila melanogaster, chromosome 2R, region 38A5-38B4, BAC clone BACR48M05, complete sequence.

0.00047:304:61

35

AC005719

F-NT2RP2000903

Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.

2.6e-110:541:97

40

AJ012159

F-NT2RP2001200

Homo sapiens mRNA for KIAA0676 protein, partial cds.

3.3e-1 10:540:96

45

AB014576

F-NT2RP2001223

HS-1054-B2-C02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=4 Row=F, genomic survey sequence.

7.2e-10:128:77

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B41982

F-NT2RP2001276

Mouse regulatory protein (npdc-1) mRNA, complete cds.

1.2e-38:296:81

55

L03814

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F-NT2RP2001388
RPCI11-30G23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30G23, genomic survey sequence.
0.32:53:94
B87787

5

F-NT2RP2001469
M.musculus tex292 mRNA (5'region).
4.2e-10:120:83
X80434

10

F-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.
9.0e-140:686:96
L38969

15

F-NT2RP2001495
Human transporter protein (g17) mRNA, complete cds.
1.9e-35:581:64
U49082

20

F-NT2RP2001514
Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
3.7e-22:475:62
AC005115

25

F-NT2RP2001529
Homo sapiens mRNA for ZIP-kinase, complete cds.
4.6e-152:757:96
AB007144

30

F-NT2RP2001538
Sequence 11 from patent US 5624818.
1.4e-88:528:88
I41141

35

F-NT2RP2001562
Homo sapiens GLE1 (GLE1) mRNA, complete cds.
2.3e-117:572:97
AF058922

40

F-NT2RP2001662
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.
6.1e-107:365:91
AL031662

45

F-NT2RP2001755
Sequence 9 from patent US 5750502.
1.5e-53:518:75
AR007441

50

F-NT2RP2001769
A.sativa Aspk11 mRNA.
4.7e-17:537:60
X79992

55

F-NT2RP2001817
Candida albicans SIR2 (SIR2) gene, complete cds.
4.6e-10:285:61

AF045774

F-NT2RP2001878

Mus musculus repeat element upstream of the Rasgrf1/Cdc25Mm gene.

5 5.0e-06:554:60

AF021791

F-NT2RP2001903

M.musculus mRNA for m-calpain.

10 3.1e-06:337:60

Y10139

F-NT2RP2001915

Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.

15 6.8e-28:488:65

AC005670

F-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

20 1.1e-77:148:99

AC005538

F-NT2RP2001948

Sequence 2 from patent US 5541311.

25 0.59:284:57

I24091

F-NT2RP2001956

Feline c-sis proto-oncogene, segment 4.

30 0.99:101:69

M25356

F-NT2RP2002015

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775

35 Col=18 Row=J, genomic survey sequence.

3.0e-06:181:65

B41504

F-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

40 1.3e-108:418:94

AC004050

F-NT2RP2002188

Rattus norvegicus neuroligin 3 mRNA, complete cds.

45 1.0e-125:700:90

U41663

F-NT2RP2002232

50

F-NT2RP2002304

Human FMR1 gene, 5' end.

0.12:93:67

L19476

55

F-NT2RP2002409

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partial cds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1 (rpoE1), and response regulator homolog (frzS) genes, complete cds; and unknown

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genes.

9.0e-10:553:59

AF049107

5 F-NT2RP2002510

Mus musculus (129SV) DNA, unmapped BAC 10817, complete sequence.

4.2e-27:573:62

AC004093

10 F-NT2RP2002527

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

3.2e-110:439:99

AC004228

15

F-NT2RP2002533

Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds.

6.4e-141:726:95

20

AF040709

F-NT2RP2002564

Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.

2.6e-112:403:98

25

AC004941

F-NT2RP2002674

HS_3122_B2_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3122 Col=4 Row=B, genomic survey sequence.

4.8e-13:86:100

30

AQ182907

F-NT2RP2002721

35

F-NT2RP2002824

Arabidopsis thaliana BAC T19D16 genomic sequence.

1.3e-12:135:69

U95973

40

F-NT2RP2002942

Homo sapiens mRNA for KIAA0806 protein, complete cds.

6.1e-145:758:94

AB018349

45

F-NT2RP2002974

Mus musculus mRNA for Six5, partial cds.

8.0e-84:588:82

D83146

50

F-NT2RP2002976

H.sapiens gene for phospholipase C beta 3, exon 14.

0.93:210:61

Z37557

55

F-NT2RP2003042

G.gallus mRNA for lecithin-cholesterol acyltransferase.

9.1e-26:462:65

X91011

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F-NT2RP2003138

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.

3.9e-142:702:96

AL031662

5

F-NT2RP2003179

Homo sapiens mRNA for KIAA0537 protein, complete cds.

3.3e-42:587:70

AB011109

10

F-NT2RP2003210

Mus musculus fatty acid transport protein 4 mRNA, partial cds.

2.6e-112:726:85

AF072759

15

F-NT2RP2003302

Human zinc finger protein ZNF136.

5.5e-63:691:69

U09367

20

F-NT2RP2003369

Homo sapiens chromosome 7q22 sequence, complete sequence.

2.0e-49:249:95

AF053356

25

F-NT2RP2003383

Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds.

1.5e-159:817:95

AF016005

30

F-NT2RP2003390

Homo sapiens SEC63 (SEC63) mRNA, complete cds.

7.0e-115:554:98

AF100141

35

F-NT2RP2003469

Genomic sequence from Human 9q34, complete sequence.

5.6e-38:210:97

AC001644

40

F-NT2RP2003545

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

2.2e-48:579:71

AF024636

45

F-NT2RP2003593

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SEQUENCE.

1.8e-90:326:99

AL021396

50

F-NT2RP2003599

F-NT2RP2003655

M.musculus tex261 mRNA.

5.3e-77:513:85

X81058

55

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F-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein.

1.7e-132:630:98

Y12670

5

F-NT2RP2003931

Homo sapiens chromosome 19, overlapping cosmids R27918 and R33775, complete sequence.

1.3e-114:411:97

AC004447

10

F-NT2RP2003940

Human ZNF43 mRNA.

1.4e-97:693:82

X59244

15

F-NT2RP2003950

Sequence 1 from patent US 5648238.

6.9e-13:143:79

I55887

20

F-NT2RP2004069

F-NT2RP2004108

Human zinc finger protein ZNF136.

1.5e-67:548:78

U09367

25

F-NT2RP2004141

Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.

8.0e-10:487:62

U87960

30

F-NT2RP2004179

Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.

0.56:600:57

AF015416

35

F-NT2RP2004205

Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.

0.32:431:55

AC005356

40

F-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

2.0e-23:252:79

AC000353

45

F-NT2RP2004495

Human transporter protein (g17) mRNA, complete cds.

3.6e-25:497:61

U49082

50

F-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

5.9e-60:203:98

AC001644

55

F-NT2RP2004556

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HS_3022_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022
Col=21 Row=A, genomic survey sequence.

1.3e-51:419:79

AQ119143

5

F-NT2RP2004606

cDNA encoding NIC(Natural Inhibitor of Collagenase).

1.2e-113:617:92

E00985

10

F-NT2RP2004648

Felis catus lysosomal beta-galactosidase (Bgal) mRNA, complete cds.

1.5e-15:403:64

AF006749

15

F-NT2RP2004670

Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.

1.1e-73:493:85

L22557

20

F-NT2RP2004794

Mus musculus mRNA for B-IND1 protein.

5.6e-12:109:86

Z97207

25

F-NT2RP2004837

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.8e-39:352:78

AC006030

30

F-NT2RP2004847

CIT-HSP-2357D24.TR CIT-HSP Homo sapiens genomic clone 2357D24, genomic survey sequence.

2.5e-35:196:96

AQ074738

35

F-NT2RP2005027

Human glucose transporter-like protein-III (GLUT3), complete cds.

2.2e-145:713:96

M20681

40

F-NT2RP2005069

Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.

9.4e-51:200:90

U35245

45

F-NT2RP2005163

Mouse DNA fragment that hybridizes to HSV-1 Smal A fragment.

1.4e-08:231:67

M11041

50

F-NT2RP2005181

Mus musculus cationic amino acid trmsporter (CAT3) mRNA, complete cds.

1.6e-96:575:85

U70859

55

F-NT2RP2005247

Mus musculus ret finger protein mRNA, complete cds.

1.8e-13:310:66

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L46855

F-NT2RP2005378

RPCI11-21D23.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21D23, genomic survey sequence.

3.0e-12:131:80

B85846

F-NT2RP2005391

S.muris mRNA for microneme antigen.

2.5e-10:345:61

Z26947

F-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

1.0e-116:566:97

AB018346

F-NT2RP2005463

F-NT2RP2005514

F-NT2RP2005535

Homo sapiens DNA-binding protein mRNA, complete cds.

2.3e-125:726:90

AF038951

F-NT2RP2005541

CIT-HSP-2386E2.TF.1 CIT-HSP Homo sapiens genomic clone 2386E2, genomic survey sequence.

6.2e-20:152:88

AQ240341

F-NT2RP2005597

D.melanogaster mRNA for rotated abdomen protein.

0.088:270:57

X95956

F-NT2RP2005632

Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.

2.0e-07:207:67

U47276

F-NT2RP2005666

Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.

1.0:328:57

AC005849

F-NT2RP2005774

Human zinc finger protein ZNF136.

4.0e-44:451:74

U09367

F-NT2RP2005878

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

5.1e-16:382:63

AF064635

F-NT2RP2005883

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-

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GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.
1.5e-30:191:95
AL023578

5 F-NT2RP2005887

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
1.8e-50:394:79
AC006030

10 F-NT2RP2005941

Human DNA sequence from cosmid CFAT5, chromosome region 11p13 contains PAX6 exons 1-4, EST and CpG Islands.
9.5e-93:468:96
Z95332

15

F-NT2RP2005994

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
1.6e-139:692:96
AC004050

20

F-NT2RP2006004

CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.
6.6e-39:206:98
AQ080257

25

F-NT2RP2006042

Human mRNA for KIAA0144 gene, complete cds.
1.7e-10:220:69
D63478

30

F-NT2RP2006092

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
3.6e-121:562:82
AC005214

35

F-NT2RP2006099

Human Chromosome 11 pac pDJ392a17, complete sequence.
8.7e-76:383:92
AC000385

40

F-NT2RP2006134

Homo sapiens Chromosome 22q11.2 Cosmid Clone 91c In DGCR Region, complete sequence. 0.055:125:71
AC000091

45

F-NT2RP2006269

D.melanogaster mRNA for rotated abdomen protein.
5.4e-05:357:58
X95956

50

F-NT2RP2006512

Sequence 1 from Patent EP 0285405.
3.7e-102:659:85
I05465

55

F-NT2RP3000011

RPCI11-43E12.TJ RPCI11 Homo sapiens genomic clone R-43E12, genomic survey sequence.
1.8e-10:113:84
AQ195722

EP 1 130 094 A2

F-NT2RP3000022

Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.

6.7e-116:284:99

AL031178

F-NT2RP3000059

R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).

0.0031:511:59

X83546

F-NT2RP3000063

Homo sapiens chromosome 19, fosmid 37502, complete sequence.

0.20:544:57

AC004755

F-NT2RP3000125

HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.

1.0e-21:161:88

AQ101452

F-NT2RP3000148

Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.

5.2e-40:257:77

AC002310

F-NT2RP3000169

Homo sapiens MRS1 mRNA, complete cds.

3.4e-106:501:99

AF093239

F-NT2RP3000171

Mus musculus mRNA for B-IND1 protein.

1.8e-97:571:89

Z97207

F-NT2RP3000172

Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.

2.0e-123:702:86

L22557

F-NT2RP3000201

Homo sapiens mRNA for KIAA0687 protein, partial cds.

9.2e-170:792:98

AB014587

F-NT2RP3000232

HS_3238_B2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=8 Row=H, genomic survey sequence.

9.2e-24:174:88

AQ219879

F-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.

3.3e-171:797:98

AF074264

EP 1 130 094 A2

F-NT2RP3000378

Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.

5.8e-137:774:89

L38621

5

F-NT2RP3000427

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.5e-18:390:65

M21096

10

F-NT2RP3000436

cDNA encoding a human novel protein disulfide isomerase like enzyme,EP52.

4.5e-05:353:59

E13330

15

F-NT2RP3000444

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.

9.7e-75:203:97

AL022315

20

F-NT2RP3000460

Canis familiaris sec61 homologue mRNA, complete cds.

7.1e-131:643:88

M96629

25

F-NT2RP3000481

Homo sapiens RanBP7/importin 7 mRNA, complete cds.

1.7e-162:770:98

AF098799

30

F-NT2RP3000616

Homo sapiens KIAA0405 mRNA, complete cds.

4.7e-31:579:62

AB007865

35

F-NT2RP3000645

Human chromosome 12p13 sequence, complete sequence.

5.9e-07:484:61

U47924

40

F-NT2RP3000652

Human ZNF43 mRNA.

4.4e-131:853:84

X59244

45

F-NT2RP3000676

Homo sapiens mRNA for KIAA0446 protein, complete cds.

2.7e-86:420:98

AB007915

50

F-NT2RP3000677

Human estrogen receptor-related protein (variant ER from breast cancer) mRNA, complete cds.

2.9e-21:125:100

M69296

55

F-NT2RP3000721

HS_2221_A2_C01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221

Col=2 Row=E, genomic survey sequence.

EP 1 130 094 A2

0.94:254:60
AQ253443

F-NT2RP3000789

5 Mus musculus coding region determinant binding protein mRNA, complete cds.
5.4e-139:827:87
AF061569

F-NT2RP3000818

10 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
3.0e-28:218:86
Z97201

F-NT2RP3000820

15 Mus musculus WSB-1 mRNA, complete cds.
1.1e-77:477:87
AF033186

F-NT2RP3000838

20 Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.6e-77:682:79
AB014538

F-NT2RP3000871

25 Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds.
5.8e-07:350:60
AF043431

F-NT2RP3000907

30 Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
1.7e-13:330:62
AC005115

F-NT2RP3000921

35 cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell.
6.8e-68:812:69
E12950

F-NT2RP3001012

40 cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).
2.4e-129:692:92
E12829

F-NT2RP3001044

45 Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
3.7e-60:393:79
AC006030

F-NT2RP3001061

50 F.rubripes GSS sequence, clone 154E17aC12, genomic survey sequence.
1.8e-07:239:62
AL018519

F-NT2RP3001159

55 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
4.4e-24:156:72

AC004770

F-NT2RP3001170

Homo sapiens mRNA for KIAA0784 protein, partial cds.

5 2.3e-181:859:98

AB018327

F-NT2RP3001195

Genomic sequence from Human 9q34, complete sequence.

10 3.8e-53:253:92

AC001644

F-NT2RP3001240

Canis familiaris sec61 homologue mRNA, complete cds.

15 1.4e-133:740:87

M96629

P-NT2RP3001271

Homo sapiens chromosome 19, cosmid F20237, complete sequence.

20 0.082:370:60

AC005775

F-NT2RP3001322

Homo sapiens mRNA for KIAA0566 protein, partial cds.

25 1.9e-38:728:63

AB011138

F-NT2RP3001388

Rattus norvegicus synaptotagmin XI mRNA, complete cds.

30 1.2e-103:701:83

AF000423

F-NT2RP3001542

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

35 8.6e-17:293:65

U73643

F-NT2RP3001560

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

40 7.8e-135:742:91

D67067

F-NT2RP3001592

Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.

45 7.2e-12:188:71

U22398

F-NT2RP3001650

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

50 1.9e-26:374:72

AC005281

F-NT2RP3001685

Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.

55 4.6e-73:284:98

AC004550

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F-NT2RP3001738

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.8e-21:186:67

AC004770

F-NT2RP3001754

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.

5.0e-21:131:96

AL034380

F-NT2RP3001858

Homo sapiens mRNA for KIAA0584 protein, partial cds.

5.9e-39:770:63

AB011156

F-NT2RP3001976

M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.

2.0e-37:536:70

Z30174

F-NT2RP3002015

Homo sapiens huntingtin gene, partial exon.

0.024:175:65

L49359

F-NT2RP3002160

Homo sapiens chromosome 9q34, clone 70C11, complete sequence.

1.6e-95:249:91

AC002319

F-NT2RP3002281

Homo sapiens mRNA for KIAA0765 protein, partial cds.

1.6e-149:713:98

AB018308

F-NT2RP3002286

Mus musculus EGF repeat transmembrane protein mRNA, complete cds.

2.0e-136:756:92

U57368

F-NT2RP3002311

Mouse beta-galactosidase (BGAL) gene, complete cds.

1.0e-29:624:63

M57734

F-NT2RP3002324

Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.

5.7e-122:655:93

Z69890

F-NT2RP3002342

Human transporter protein (g17) mRNA, complete cds.

9.8e-36:565:65

U49082

F-NT2RP3002353

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Streptomyces phaeochromogenes plasmid pJV1, complete sequence.
0.15:466:60
U23762

- 5 F-NT2RP3002409
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.0e-189:897:98
AB018262
- 10 F-NT2RP3002411
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.
7.8e-122:796:84
AF064635
- 15 F-NT2RP3002448
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
4.0e-11:403:64
X83546
- 20 F-NT2RP3002571
Bos taurus mRNA for lyncein.
8.7e-114:652:90
Y17923
- 25 F-NT2RP3002664
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
6.1e-14:211:72
Z60772
- 30 F-NT2RP3002721
Homo sapiens citrate synthase mRNA, complete cds.
7.5e-179:873:96
AF047042
- 35 F-NT2RP3002737
Homo sapiens mRNA for HNSPC, complete cds.
1.4e-42:409:75
D82346
- 40 F-NT2RP3002738
Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.
8.9e-122:812:83
D29766
- 45 F-NT2RP3002790
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
2.2e-15:626:62
U22398
- 50 F-NT2RP3002836
Homo sapiens mRNA for KIAA0463 protein, partial cds.
6.8e-152:717:99
AB007932
- 55 F-NT2RP3002887
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
2.0e-05:491:59
X83546

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F-NT2RP3002900

Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.

7.3e-13:327:66

U26264

F-NT2RP3002958

Mus musculus IgK chain (6S) intron with insertion/deletion mutations.

5.6e-22:403:66

L12153

F-NT2RP3002983

Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.

1.2e-118:339:99

AP000047

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.

7.9e-88:555:88

AF051946

F-NT2RP3003076

Streptomyces coelicolor cosmid 2A11.

0.15:505:59

AL031184

F-NT2RP3003354

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

1.2e-34:625:64

AF005038

F-NT2RP3003448

CIT-HSP-721P7.TV CIT-HSP *Homo sapiens* genomic clone 721P7, genomic survey sequence.

1.2e-16:126:89

B50017

F-NT2RP3003469

Homo sapiens chromosome 19, cosmid F23990, complete sequence.

2.0e-18:126:94

AC005262

F-NT2RP3003473

Homo sapiens chromosome 17, clone hRPK.1003_J_3, complete sequence.

7.1e-68:474:71

AC005181

F-NT2RP3003527

Homo sapiens mRNA for protein kinase Dyrk1B.

1.4e-160:769:98

Y17999

F-NT2RP3003532

Mus musculus cell surface molecule OX-2 mRNA, complete cds.

1.3e-96:712:80

AF004023

F-NT2RP3003535

Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence, complete sequence. 0.027:155:65

AC004313

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F-NT2RP3003559

H.sapiens CpG island DNA genomic Mse1 fragment, clone 171h5, reverse read cpg171h5.rt1a.

3.9e-50:261:97

Z59762

5

F-NT2RP3003614

Mus musculus semaphorin VIa mRNA, complete cds.

1.7e-131:811:86

AF030430

10

F-NT2RP3003729

Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-ordered pieces.

1.4e-97:259:91

15

AC006171

F-NT2RP3003849

F-NT2RP3003874

20

M.musculus mRNA for myosin I heavy chain.

2.9e-151:863:89

X69987

F-NT2RP3003939

25

T24C19TF TAMU Arabidopsis thaliana genomic clone T24C19, genomic survey sequence.

1.4e-19:293:68

B29025

F-NT2RP3003963

30

CIT-HSP-2050C19.TF CIT-HSP Homo sapiens genomic clone 2050C19, genomic survey sequence.

1.3e-16:111:95

B80539

F-NT2RP3004000

35

Homo sapiens klotho gene, exon 1.

0.042:430:60

AB009666

F-NT2RP3004025

40

Human DNA sequence from Fosmid 49D8 on chromosome 22, complete sequence.

0.062:197:65

Z82186

F-NT2RP3004067

45

Human mRNA for KIAA0375 gene, complete cds.

1.7e-33:556:66

AB002373

F-NT2RP3004075

50

jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.

1.5e-12:438:61

B13419

55

F-NT2RP3004083

F-NT2RP3004090

Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

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1.4e-06:469:60
L01060

F-NT2RP30041 19
Human mRNA for KIAA0215 gene, complete cds.
1.3e-72:640:75
D86969

F-NT2RP3004130

F-NT2RP3004133
Pseudomonas aeruginosa phage phi CTX DNA, complete genome.
0.0018:421:60
Y13918

F-NT2RP3004202

F-NT2RP3004294
Xenopus laevis ER1 mRNA, complete cds.
5.0e-77:335:78
AF015454

F-NT2RP3004309
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
9.6e-25:231:65
AC004770

F-NT2RP3004321
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
3.7e-80:279:95
AF015416

F-NT2RP3004345
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
7.2e-12:188:71
U22398

F-NT2RP3004355
HS_3212_A1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=15 Row=E, genomic survey sequence.
0.061:266:65
AQ176625

F-NT2RP3004374
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

F-NT2RP3004406
CIT-HSP-2340N18.TF CIT-HSP Homo sapiens genomic clone 2340N18, genomic survey sequence.
9.9e-74:359:99
AQ058326

F-NT2RP3004481
Mus musculus bassoon gene, exon 6 to 11.
0.0060:528:59

Y17038

F-NT2RP3004552

Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.

5 7.6e-40:731:64

D64009

F-NT2RP3004557

Human Ki nuclear autoantigen mRNA, complete cds.

10 8.1e-120:626:94

U11292

F-NT2RP3004625

Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

15 9.8e-151:710:98

AF082516

F-NT2RP3004640

Bos taurus tuftelin mRNA, complete cds.

20 8.2e-104:565:87

AF105228

F-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds.

25 2.1e-109:524:98

AB007915

F-NT2RP4000108

Human gene for neurofilament subunit NF-L.

30 7.0e-158:862:93

X05608

F-NT2RP4000634

Sequence 11 from patent US 5753446.

35 2.9e-155:828:92

AR008281

F-NT2RP4000962

Mus musculus clone OST66, genomic survey sequence.

40 6.0e-48:352:81

AF046696

F-NT2RP4001001

Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.

45 4.8e-47:360:84

AC005915

F-NT2RP4001009

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

50 5.9e-175:828:98

AF064867

F-NT2RP4001467

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

55 3.3e-159:742:98

X55740

F-NT2RP4001877

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1.7e-27:401:69
AC005637

F-NT2RP4001879

F-NT2RP4002187

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

4.2e-115:777:83
AF064635

F-NT2RP4002451

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.

6.1e-86:452:96
Z98200

F-NT2RP4002715

Homo sapiens clone NH0523H20, complete sequence.

3.6e-59:410:77
AC005041

F-NT2RP4002750

Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.

3.4e-105:586:87
U70859

F-OVARC1000003

B.taurus mRNA for sodium dependent phosphate transporter.

9.0e-125:823:83
X81699

F-OVARC1000090

RPCI11-25E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-25E14, genomic survey sequence.

1.9e-06:151:74
B86784

F-OVARC1000105

S.cerevisiae UBC6 gene.

4.6e-25:525:64
X73234

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds.

1.2e-33:184:98
U95735

F-OVARC1000208

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

1.7e-79:362:91
AC002544

F-OVARC1000255

Porcine protein-tyrosine kinase (syk) mRNA, complete cds.

4.9e-116:424:88
M73237

F-OVARC1000275

Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.

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0.32:314:61
AJ011930

F-OVARC1000298

5 Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.
2.5e-121:306:98
AC005632

F-OVARC1000307

10 Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].
0.017:162:67
X94677

F-OVARC1000313

15 Homo sapiens mRNA for KIAA0573 protein, partial cds.
1.7e-119:585:97
AB011145

F-OVARC1000331

20 Sequence 2 from patent US 5756332.
1.9e-48:290:91
AR009648

F-OVARC1000410

25 Homo sapiens mRNA for angiopoietin-like factor.
4.6e-26:538:62
Y16132

F-OVARC1000439

30 F-OVARC1000467
HS_3008_A2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3008 Col=24 Row=G, genomic survey sequence.
2.0e-11:132:82
35 AQ116995

F-OVARC1000529

40 HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092
Col=22 Row=F, genomic survey sequence.
8.2e-12:115:84
AQ127947

F-OVARC1000553

45 Homo sapiens chromosome 19, cosmid R26894, complete sequence.
6.5e-92:221:96
AC005594

F-OVARC1000775

50 Human chromosome 3p21.1 gene sequence.
6.9e-69:380:95
L13435

F-OVARC1000811

55 Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.
6.7e-77:500:86
AC004235

F-OVARC1000853

EP 1 130 094 A2

HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234
Col=9 Row=K, genomic survey sequence.
4.6e-05:111:71
AQ191345

5

F-OVARC1000873
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
8.2e-42:234:96
AL034418

10

F-OVARC1000916
Sequence 3 from patent US 5674748.
2.0e-55:422:84
I68139

15

F-OVARC1000956
Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.
1.2e-107:540:97
Z69708

20

F-OVARC1000995
H.sapiens genomic DNA (chromosome 3; clone NL1106D).
4.3e-28:166:95
X87478

25

F-OVARC1001030
Human mRNA for KIAA0339 gene, complete cds.
2.1e-10:334:64
AB002337

30

F-OVARC1001049
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.
5.4e-12:420:62
AC004670

35

F-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds.
1.9e-164:761:99
AF048731

40

F-OVARC1001132
Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.
1.5e-89:328:75
AP000038

45

F-OVARC1001163
Caenorhabditis elegans cosmid F40E10, complete sequence.
3.8e-26:337:71
Z69792

50

F-OVARC1001222
CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.
1.2e-08:171:70
B57734

55

F-OVARC1001260

F-OVARC1001336

B.taurus mRNA for sodium dependent phosphate transporter.

5 5.4e-83:622:80

X81699

F-OVARC1001338

HS_2181_B2_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181

10 Col=22 Row=J, genomic survey sequence.

2.3e-17:144:86

AQ022764

F-OVARC1001569

15 Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.

2.9e-06:241:63

AF100904

F-OVARC1001570

20 Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.

1.6e-10:235:64

AJ011929

F-OVARC1001596

25 Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.

2.2e-45:498:73

AC005951

F-OVARC1001607

30 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.

1.7e-38:323:80

U15128

F-OVARC1001725

35 Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.

3.5e-172:821:98

AF064800

F-OVARC1001727

40 Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.

2.2e-132:633:98

AL031132

F-OVARC1001807

45 Human TR3 orphan receptor mRNA, complete cds.

7.1e-90:566:87

L13740

F-OVARC 1001833

50 Rattus norvegicus cis-Golgi matrix protein GM130 mRNA, complete cds.

5.2e-46:364:79

U35022

F-OVARC1001952

55 Homo sapiens FGFR-4 gene.

1.7e-14:392:62

Y13901

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F-OVARC1001991
Human Chromosome 11 Cosmid cSRL34e5, complete sequence.
2.3e-06:298:64
U73643

5

F-OVARC1002058
, complete sequence.
1.3e-108:617:92
AC005500

10

F-OVARC1002178
Herpes simplex virus type 2 (strain HG52), complete genome.
0.43:234:63
Z86099

15

F-PLACE1000033
Mus musculus otogelin mRNA, complete cds.
5.9e-18:579:59
U96411

20

F-PLACE1000231
Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.
1.1e-18:273:68
AF037272

25

F-PLACE1000258
Human KRAB zinc finger protein (ZNP177) mRNA, complete cds.
1.2e-13:241:70
U37263

30

F-PLACE1000442
Human zinc finger protein ZNF136.
2.3e-87:774:76
U09367

35

F-PLACE1000560
Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.
4.1e-107:318:96
AC005368

40

F-PLACE1000740
Rat notch 2 mRNA.
1.1e-37:399:74
M93661

45

F-PLACE1000907
RPCI11-73M20.TJ RPCI11 Homo sapiens genomic clone R-73M20, genomic survey sequence.
3.5e-21:147:92
AQ269030

50

F-PLACE1000912

F-PLACE1000914
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.8e-74:206:93
AC002093

55

F-PLACE1000927

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Cowpox virus strain GRI-90 DNA (49 kb fragment).
6.8e-75:683:74
Y15035

- 5 F-PLACE1000986
RPCI11-75H23.TK RPCI11 Homo sapiens genomic clone R-75H23, genomic survey sequence.
1.0:316:57
AQ268409
- 10 F-PLACE1001016
Human dihydropyridine-sensitive L-type calcium channel alpha-1 subunit (CACNL1A3) mRNA, complete cds.
0.28:432:59
L33798
- 15 F-PLACE1001100
RPCI11-32N5.TK RPCI-11 Homo sapiens genomic clone RPCI-11-32N5, genomic survey sequence.
0.48:145:64
AQ047336
- 20 F-PLACE1001114
Lysobacter enzymogenes beta-lactamase gene sequence.
0.033:349:60
M97392
- 25 F-PLACE1001123
F.rubripes GSS sequence, clone 084A20aC12, genomic survey sequence.
9.7e-05:138:64
AL015804
- 30 F-PLACE1001183
Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.
0.15:576:59
AC005091
- 35 F-PLACE1001229
F.rubripes GSS sequence, clone 144D13aC10, genomic survey sequence.
2.2e-21:271:70
AL017986
- 40 F-PLACE1001231
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
6.4e-102:677:84
AF026554
- 45 F-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds.
1.3e-130:636:97
AB018262
- 50 F-PLACE1001401
CIT-HSP-2323H22.TR CIT-HSP Homo sapiens genomic clone 2323H22, genomic survey sequence.
6.4e-13:165:76
AQ028562
- 55 F-PLACE1001407
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
2.4e-28:228:85
AL023582

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F-PLACE1001464

Human placental cDNA coding for 5 nucleotidase (EC 3.1.3.5).

5.0e-151:742:96

X55740

5

F-PLACE1001500

CIT-HSP-2368L16.TR CIT-HSP Homo sapiens genomic clone 2368L16, genomic survey sequence.

1.1e-25:150:97

AQ078655

10

F-PLACE1001516

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.

1.2e-139:676:98

AC002425

15

F-PLACE1001536

Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.

1.7e-142:513:97

AC004387

20

F-PLACE1001564

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SE-
QUENCE.

2.9e-104:373:89

AL033377

25

F-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K⁺ channel alpha subunit (KCNS3) mRNA, complete cds.

1.3e-123:585:98

AF043472

30

F-PLACE1001788

Homo sapiens mRNA for HYA22, complete cds.

9.9e-21:234:75

D88153

35

F-PLACE1001795

Drosophila melanogaster; Chromosome 3L; Region 83F1-83F2; P1 clone DS07437, WORKING DRAFT SE-
QUENCE, 3 unordered pieces.

1.4e-05:218:64

AC005985

40

F-PLACE1001836

Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence.

4.9e-79:577:82

AC004022

45

F-PLACE1001918

Arabidopsis thaliana BAC T19D16 genomic sequence.

3.7e-24:417:63

U95973

50

F-PLACE1001949

S.cerevisiae chromosome XV reading frame ORF YOR291w.

3.6e-16:255:70

Z75199

55

F-PLACE1002080

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Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.
7.5e-129:622:98
AF039691

5 F-PLACE1002095
Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.
2.3e-48:551:71
AC004219

10 F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
8.3e-161:764:98
AF095791

15 F-PLACE1002329
Sequence 12 from Patent WO 9000403.
6.9e-05:380:63
I09634

20 F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds.
2.8e-17:190:77
AF055917

25 F-PLACE1002374
Human mRNA for pro-cathepsin L(major excreted protein MEP).
6.2e-162:716:94
X12451

30 F-PLACE 1002518
HS_3091_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3091
Col=15 Row=K, genomic survey sequence.
3.2e-74:316:94
AQ123005

35 F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.6e-171:819:98
AB018262

40 F-PLACE1002726
CIT-HSP-2369G10.TR CIT-HSP Homo sapiens genomic clone 2369G10, genomic survey sequence.
4.8e-18:135:88
AQ075115

45 F-PLACE1002905
Drosophila melanogaster DNA sequence (P1 DS00906 (D99)), complete sequence.
3.7e-06:235:66
AC004154

50 F-PLACE1002911
Bovine herpesvirus 1 complete genome.
0.93:264:63
AJ004801

55 F-PLACE1002967
Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds.
0.0041:302:60

L35848

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

4.7e-49:450:75

AF024636

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

4.7e-152:722:98

AF069301

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

6.3e-141:682:97

AF068227

F-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2, ESTs, GSSs,, complete sequence.

1.2e-116:286:100

AL032821

F-PLACE1003438

Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.

0.13:468:60

AF092918

F-PLACE1003460

HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=9 Row=K, genomic survey sequence.

5.8e-05:111:71

AQ191345

F-PLACE1003529

Homo sapiens clone DJ0981O07, complete sequence.

5.8e-134:457:97

AC006017

F-PLACE1003573

Sequence 2 from patent US 5792648.

0.93:186:62

AR022348

F-PLACE1003598

Mus musculus mismatch repair protein (MSH6) gene, exon 1.

3.3e-07:311:63

AF031085

F-PLACE1003644

Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.

1.8e-06:138:74

AC001234

F-PLACE1003737

Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.

1.4e-165:791:98

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AC005859

F-PLACE1003772

Human p300/CBP-associated factor (P/CAF) mRNA, complete cds.

5 2.2e-07:448:61

U57317

F-PLACE1003839

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.

10 2.0e-106:525:97

AC004131

F-PLACE1003845

Caenorhabditis elegans cosmid D2096.

15 9.8e-26:386:69

U40800

F-PLACE1003852

Homo sapiens mRNA for KIAA0758 protein, partial cds.

20 7.4e-171:814:98

AB018301

F-PLACE1004028

25 F-PLACE1004078

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

2.0e-116:274:98

AC005281

30 F-PLACE1004166

HS_3223_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=17 Row=O, genomic survey sequence.

0.77:304:58

AQ193346

35

F-PLACE1004168

F-PLACE1004199

CIT-HSP-2328F14.TR CIT-HSP Homo sapiens genomic clone 2328F14, genomic survey sequence.

40 9.4e-16:186:76

AQ042262

F-PLACE1004279

Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.

45 1.2e-18:456:62

AF057039

F-PLACE1004282

50 F-PLACE1004305

Homo sapiens mRNA for KIAA0740 protein, complete cds.

2.7e-121:612:96

AB018283

55 F-PLACE1004441

Human G protein-coupled receptor (GPR1) gene, complete cds.

2.4e-104:537:95

U13666

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F-PLACE1004450

Pleuronectes americanus aminopeptidase N (ampN) mRNA, complete cds.

3.1e-20:601:60

AF012465

F-PLACE1004482

HS_3032_B1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=F, genomic survey sequence.

1.1e-86:423:98

AQ129106

F-PLACE1004492

Human DNA sequence from PAC 434P1 on chromosome 22. Contains inward rectifier potassium channel 4, (potassium channel, inwardly rectifying, subfamily J, member 4) (hippocampal inward rectifier) (HIR) (HRK1) (HIRK2) (KIR2.3), ESTs similar to lumen protein retaining receptor 2 (KDEL receptor 2), DEAD-box protein P72, ESTs, CpG islands.

0.17:180:67

Z97056

F-PLACE1004519

Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.

1.1e-75:432:84

AL021808

F-PLACE1004520

Human pregnancy-specific beta-1-glycoprotein mRNA PSG95, complete cds.

4.1e-109:606:92

M34715

F-PLACE1004630

Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds.

6.2e-138:749:92

AB008375

F-PLACE1004637

HS-1061-B1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 783 Col=19 Row=J, genomic survey sequence.

0.013:92:75

B45487

F-PLACE1004648

F-PLACE1004816

Homo sapiens mRNA for Hakata antigen, complete cds.

3.8e-98:590:90

D88587

F-PLACE1004887

Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

1.2e-06:469:60

L01060

F-PLACE1005003

Human SNC19 mRNA sequence.

4.8e-20:472:63

U20428

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F-PLACE1005005

Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.

7.8e-143:650:97

5 AJ011930

F-PLACE1005031

Bovine chlorine channel protein (p64) mRNA, complete cds.

7.1e-62:463:83

10 L16547

F-PLACE1005239

Homo sapiens mRNA for HIRIP3 protein, clone pH4-31.

2.2e-14:115:85

15 AJ223349

F-PLACE1005250

Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.

3.3e-40:370:77

20 U50734

F-PLACE1005383

Homo sapiens UP50 mRNA, complete cds.

2.7e-126:633:96

25 AF093118

F-PLACE1005410

Rattus rattus sec61 homologue mRNA, complete cds.

1.9e-115:771:85

30 M96630

F-PLACE1005426

Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.

7.2e-113:391:96

35 AC005392

F-PLACE1005519

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

1.0e-53:521:74

40 AF024636

F-PLACE1005539

c-erbB=proto-oncogene {exon 1, promoter} [chickens, Genomic, 700 nt].

3.6e-05:434:62

45 S66408

F-PLACE1005544

Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.

3.3e-56:575:74

50 U89915

F-PLACE1005569

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

1.1e-118:381:96

55 AL034397

F-PLACE1005601

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

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3.9e-143:697:98
AC002073

F-PLACE1005660

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F-PLACE1005669
Fruit fly (*D.melanogaster*) Glued mRNA, complete cds.
3.4e-14:275:66
J02932

10

F-PLACE1005682
Mus musculus Ankhzn mRNA, complete cds.
0.75:347:57
AB011370

15

F-PLACE1005725
Homo sapiens huntingtin (HD) gene, exon 1.
1.4e-06:425:62
L27350

20

F-PLACE1005736

F-PLACE1005745
HS_3039_B1_F12_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3039
Col=23 Row=L, genomic survey sequence.
1.0:283:59
AQ155068

25

F-PLACE1005768
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
1.5e-141:719:96
Z82185

30

F-PLACE1005815
Sequence 1 from patent US 5571905.
0.088:199:62
I28535

35

F-PLACE1005878
Bovine chlorine channel protein (p64) mRNA, complete cds.
2.5e-54:394:84
L16547

40

F-PLACE1005927
HS_3138_B2_B03_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3138
Col=6 Row=D, genomic survey sequence.
8.0e-32:162:95
AQ183333

45

F-PLACE1006071
1.6e-180:877:96
AF028816

50

F-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds.
1.7e-94:464:98
AB009598

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F-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5.2e-107:423:96

AF028233

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F-PLACE1006093

jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.

0.00018:316:60

10

B13419

F-PLACE1006208

Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.

1.4e-12:421:64

15

L14320

F-PLACE1006219

Caenorhabditis elegans cosmid D2096.

6.4e-25:386:69

20

U40800

F-PLACE1006277

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

7.2e-135:381:97

25

AL034397

F-PLACE1006290

Caenorhabditis elegans cosmid F09E5.

1.4e-08:354:61

30

U37429

F-PLACE1006443

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

2.9e-80:168:95

35

AC002093

F-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds.

4.2e-140:655:99

40

AB011148

F-PLACE1006716

Human DNA sequence from PAC 151B14 on chromosome 22q12-qter contains somatostatin receptor subtype 3 (SSTR3), tRNA, ESTs, CpG island and STS.

2.2e-51:621:70

45

Z86000

F-PLACE1006786

CITBI-E1-2502A9.TR CITBI-E1 Homo sapiens genomic clone 2502A9, genomic survey sequence.

0.43:237:64

50

AQ264473

F-PLACE1006809

HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.

2.1e-14:95:97

55

AQ131814

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F-PLACE1006959

HS_3247_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=5 Row=J, genomic survey sequence.

1.1e-09:199:70

AQ220414

F-PLACE1007028

Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.

2.0e-24:658:62

AC005950

F-PLACE1007040

Mus musculus neuronal intermediate filament protein (alpha-internexin) gene, complete cds.

8.8e-09:585:62

L27220

F-PLACE1007077

F-PLACE1007081

RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.

2.3e-42:228:97

AQ016433

F-PLACE1007096

F-PLACE1007296

Human mRNA for a presumptive KDEL receptor.

1.3e-71:542:83

X55885

F-PLACE1007591

Homo sapiens full length insert cDNA clone YP44A02.

1.1e-18:141:90

AF085890

F-PLACE1007626

Homo sapiens unknown mRNA, complete cds.

7.8e-104:516:97

AF047439

F-PLACE1007702

Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.

7.5e-50:439:77

AC002348

F-PLACE1007845

Caenorhabditis elegans cosmid F09E5.

4.4e-08:355:62

U37429

F-PLACE1007881

CITBI-E1-2517N6.TF CITBI-E1 Homo sapiens genomic clone 2517N6, genomic survey sequence.

1.4e-14:104:95

AQ279407

F-PLACE1007971

HS_3237_B2_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237

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Col=18 Row=L, genomic survey sequence.
1.2e-12:169:76
AQ206052

- 5 F-PLACE1008282
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.
4.5e-101:192:100
AC005995
- 10 F-PLACE1008297
Mycoplasma genitalium random genomic clone hg1, partial cds.
0.099:193:60
U02109
- 15 F-PLACE1008359
Homo sapiens DNA for (CGG)_n trinucleotide repeat region, isolate CL16-1 (Chr.16).
0.53:185:65
AJ001218
- 20 F-PLACE1008469
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.2e-93:213:98
AC002093
- 25 F-PLACE1008549
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.
5.7e-144:693:98
AF049703
- 30 F-PLACE1008657
Bovine mRNA for adseverin, complete cds.
5.6e-140:782:90
D26549
- 35 F-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
1.1e-133:648:97
U15128
- 40 F-PLACE1008744
Sequence 1 from patent US 5691147.
8.4e-91:475:95
I76197
- 45 F-PLACE1008984
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.
4.2e-103:493:99
AL031427
- 50 F-PLACE1008985
Mus musculus synaptotagmin VIII mRNA, partial cds.
1.1e-23:289:72
U20107
- 55 F-PLACE1009067
H.sapiens CpG island DNA genomic Mse1 fragment, clone 52e12, forward read cpg52e12.ft1a.
1.2e-28:164:96

Z61442

F-PLACE1009196

- 5 F-PLACE1009279
H.sapiens mRNA for serine protease.
6.0e-10:327:64
Y07921
- 10 F-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds.
2.0e-19:125:96
U82613
- 15 F-PLACE1009546
S.lividans mercury resistance operon.
0.56:358:59
X65467
- 20 F-PLACE1009600
Mouse mRNA for tetracycline transporter-like protein, complete cds.
2.1e-128:718:91
D88315
- 25 F-PLACE1009735
Homo sapiens clone NH0523H20, complete sequence.
2.9e-128:613:99
AC005041
- 30 F-PLACE1009982
- F-PLACE1010011
, complete sequence.
2.1e-26:234:83
- 35 AC005409
- F-PLACE1010078
Saccharomyces cerevisiae chromosome XII cosmid 8300.
0.066:273:58
- 40 U19028
- F-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
7.0e-150:733:97
- 45 AF027706
- F-PLACE1010251
Sequence 1 from patent US 5665588.
0.0012:309:62
- 50 I64695
- F-PLACE1010445
Herpes simplex virus type 2 (strain HG52), complete genome.
9.4e-07:511:58
- 55 Z86099
- F-PLACE1010713
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

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- 2.1e-89:612:83
AF064635
- 5 F-PLACE1010784
Sequence 1 from patent US 5686597.
2.5e-103:505:98
I73723
- 10 F-PLACE1010827
Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.
7.3e-13:327:66
U26264
- 15 F-PLACE1010968
O.cuniculus mRNA for titin.
0.44:165:64
X64696
- 20 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.8e-127:595:99
AF094516
- 25 F-PLACE1011116
HS_2033_A2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033
Col=10 Row=I, genomic survey sequence.
8.3e-29:192:92
AQ229784
- 30 F-PLACE1011181
H.sapiens CpG island DNA genomic Mse1 fragment, clone 99f2, reverse read cpg99f2.rt1a.
4.8e-35:200:95
Z64239
- 35 F-PLACE1011236
Mus musculus mRNA for RST, complete cds.
4.5e-54:717:66
AB005451
- 40 F-PLACE1011364
Homo sapiens protein kinase/endoribonulcease (IRE1) mRNA, complete cds.
0.13:502:57
AF059198
- 45 F-PLACE1011407
M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.
7.2e-15:313:68
Z30174
- 50 F-PLACE1011516
Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SE-
QUENCE, 4 unordered pieces.
1.8e-16:317:66
AC005720
- 55 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
1.8e-143:722:96

AF034611

F-PLACE1011824

Human Ste20-like kinase (MST2) mRNA, complete cds.

5.0e-100:561:92

U26424

F-PLACE 101 1978

Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.

9.6e-76:722:74

M27877

F-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

5.2e-112:568:95

AL022578

F-PLACE2000219

Homo sapiens Down Syndrome critical region, partial sequence.

0.0059:144:71

AF015262

F-PLACE3000181

Sequence 102 from patent US 5643781.

4.1e-127:745:90

I51041

F-PLACE3000213

F-PLACE4000354

HS_3071_A2_B06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071

Col=12 Row=C, genomic survey sequence.

4.4e-12:335:64

AQ137396

F-PLACE4000455

Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS.

9.5e-118:563:98

M63896

F-SKNMC1000004

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.9e-141:292:98

AC005632

F-SKNMC1000014

CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.

0.89:136:67

AQ075724

F-SKNMC1000082

H.sapiens CpG island DNA genomic MseI fragment, clone 26g3, reverse read cpg26g3.rt1b.

5.6e-06:60:98

265216

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F-THYRO1000036

F-THYRO1000061

Homo sapiens chromosome 19, cosmid R28991, complete sequence.

5 2.4e-105:425:94

AC004623

F-THYRO1000099

Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.

10 0.35:609:57

U87960

F-THYRO1000196

Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.

15 5.1e-125:475:98

AF016272

F-THYRO1000400

Mycobacterium tuberculosis sequence from clone y423.

20 1.0:264:59

AD000014

F-THYRO1000580

HS_3216_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216

25 Col=17 Row=O, genomic survey sequence.

2.8e-25:157:96

AQ184086

F-THYRO1000584

Boar mRNA for 135kDa protein, complete cds.

30 2.0e-104:787:80

D28521

F-THYRO1000678

M.musculus Cx30 gene.

35 6.9e-41:285:85

Z70023

F-THYRO1000776

Drosophila melanogaster DNA sequence (P1 DS08948 (D168)), complete sequence.

40 2.7e-10:389:59

AC004288

F-THYRO1000795

Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier.

45 1.2e-107:736:83

AJ223355

F-THYRO1000846

CITBI-E1-2505H6.TR CITBI-E1 Homo sapiens genomic clone 2505H6, genomic survey sequence.

50 0.00025:351:61

AQ260270

F-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds.

55 3.3e-91:529:89

AF015913

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F-THYRO1000956

Human G protein-coupled receptor APJ gene, complete cds.

3.8e-148:724:97

U03642

5

F-THYRO1000964

Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.

5.0e-37:714:64

AF091624

10

F-THYRO1000999

CITBI-E1-2508B3.TF CITBI-E1 Homo sapiens genomic clone 2508B3, genomic survey sequence.

1.2e-06:280:62

AQ261426

15

F-THYRO1001063

H.sapiens (xs174) mRNA, 300bp.

1.6e-41:298:85

Z36825

20

F-THYRO1001071

Human mRNA for KIAA0154 gene, partial cds.

7.4e-16:197:73

D63876

25

F-THYRO1001102

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

3.5e-10:128:83

AC004997

30

F-THYRO1001113

Homo sapiens mRNA for LGMD2B protein.

8.8e-52:684:68

AJ007670

35

F-THYRO1001128

Homo sapiens chromosome 9q34, clone 63G10, complete sequence.

1.2e-141:227:97

AC002096

40

F-THYRO1001205

F-THYRO1001237

Mus musculus interleukin-2 (Il-2) gene, 5'end.

0.77:78:74

L07576

45

F-THYRO1001242

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

5.1e-127:721:90

D67067

50

F-THYRO1001266

Human sodium iodide symporter mRNA, complete cds.

2.7e-41:806:62

U66088

55

F-THYRO1001327

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Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

3.1e-117:374:96

5 AL021578

F-THYRO1001456

F-THYRO1001457

10 M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

1.8e-57:491:69

Z34524

F-THYRO1001471

15 Sequence 52 from Patent WO9712992.

0.00019:546:58

A62364

F-THYRO1001478

20

F-THYRO1001495

Homo sapiens clone DJ1163L11, complete sequence.

4.4e-20:222:76

AC005230

25

F-THYRO1001523

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F17, WORKING DRAFT SEQUENCE.

8.8e-21:538:62

30

Z83845

F-THYRO1001529

M.musculus mRNA for serine palmitoyltransferase subunit B.

5.8e-32:448:66

35

X95642

F-THYRO1001593

Homo sapiens chromosome 19, cosmid R31237, complete sequence.

5.8e-91:213:98

40

AC005581

F-THYRO1001608

Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.

45

0.0028:335:65

AE000662

F-THYRO1001641

Leishmania major chromosome 3 clone L6290 strain Friedlin, WORKING DRAFT SEQUENCE, 2 ordered pieces.

50

0.92:378:61

AC005928

F-THYRO1001700

HS_3220_A1_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=15 Row=C, genomic survey sequence.

55

1.0e-49:265:96

AQ184388

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F-THYRO1001702

Mus musculus mRNA for myeloid associated differentiation protein.

1.4e-70:502:82

AJ001616

5

F-THYRO1001725

F.rubripes GSS sequence, clone 133B16aE1, genomic survey sequence.

3.8e-06:249:65

AL004967

10

F-THYRO1001770

S.cerevisiae chromosome II reading frame ORF YBR059c.

1.5e-07:320:62

Z35928

15

F-THYRO1001803

Homo sapiens chromosome 10 clone CRI-JC2019 map 10q22.1-10q22.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.

1.2e-38:234:94

AC006108

20

F-Y79AA1000030

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

9.9e-92:389:98

AC005214

25

F-Y79AA1000127

Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.

9.2e-131:359:100

AP000034

30

F-Y79AA1000207

Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.

2.2e-151:302:98

AC005562

35

F-Y79AA1000226

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.1e-50:549:67

AC004573

40

F-Y79AA1000270

Bos taurus vacuolar H⁺ ATPase subunit Ac45 mRNA, complete cds.

6.4e-111:771:83

U10039

45

F-Y79AA1000426

Mus musculus activin beta E subunit mRNA, complete cds.

2.4e-87:703:76

U96386

50

F-Y79AA1000521

Homo sapiens LERK-6 (EPLG6) gene, exon 1.

0.0092:148:68

U92893

55

F-Y79AA1000750

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

9.0e-07:143:74
AC002544

F-Y79AA1000776

5

F-Y79AA1000777

Podospora anserina beta transducin-like protein (het-e1) gene, complete cds.
6.6e-17:760:59
L28125

10

F-Y79AA1000876

Homo sapiens long form transcription factor C-MAF (c-maf) mRNA, complete cds.
3.3e-10:323:66
AF055377

15

F-Y79AA1000888

Streptomyces coelicolor cosmid 8A6.
3.1e-06:665:59
AL031013

20

F-Y79AA1000959

Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.
1.6e-52:277:96
AF093420

25

F-Y79AA1000967

Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
2.9e-131:752:86
L22557

30

F-Y79AA1001013

F-Y79AA1001056

Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
1.2e-85:676:79
U50734

35

F-Y79AA1001062

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.
8.6e-17:293:65
U73643

40

F-Y79AA1001090

Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.
1.9e-05:223:63
AC004596

45

F-Y79AA1001212

Homo sapiens SL15 protein mRNA, complete cds.
4.7e-162:763:98
AF038961

50

F-Y79AA1001264

Drosophila melanogaster DNA sequence (P1s DS00764 (D273) and DS00501 (D274)), complete sequence.
1.2e-32:599:63
AC005269

55

F-Y79AA1001272

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Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.
1.2e-11:356:67
AJ009613

5 F-Y79AA1001328
Rattus norvegicus Delta 3 mRNA, complete cds.
2.1e-51:443:76
AF084576

10 F-Y79AA1001426
HS_3146_A1_A10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146
Col=19 Row=A, genomic survey sequence.
9.0e-23:106:91
AQ141090

15 F-Y79AA1001427
Bovine cytochrome b5 reductase mRNA, partial cds.
1.4e-55:670:70
M83104

20 F-Y79AA1001430
Homo sapiens mRNA for KIAA0469 protein, complete cds.
8.6e-123:577:99
AB007938

25 F-Y79AA1001523
Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds.
3.3e-91:496:93
AF009353

30 F-Y79AA1001530
Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.
1.8e-126:764:89
AL030996

35 F-Y79AA1001592
40 HS_3219_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219
Col=24 Row=I, genomic survey sequence.
5.2e-36:234:89
AQ180547

45 F-Y79AA1001727

F-Y79AA1001787
S.pombe chromosome III cosmid c1672.
8.8e-11:409:58
50 AL031324

F-Y79AA1001793
Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.
0.12:131:70
55 AL025355

F-Y79AA1001795
Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11

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- to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.
1.2e-140:672:98
AL031228
- 5
- 10 F-Y79AA1001799
S.pombe chromosome I cosmid c8C9.
0.00031:300:60
Z99168
- 15 F-Y79AA1001803
Mus musculus secretogranin III (SgIII) mRNA, complete cds.
4.6e-101:516:82
U02982
- 20 F-Y79AA1001863
Homo sapiens DNA, anonymous heat-stable fragment RP5-6A.
5.2e-85:410:99
AB012170
- 25 F-Y79AA1002022
CIT-HSP-2053H1.TF CIT-HSP Homo sapiens genomic clone 2053H1, genomic survey sequence.
4.3e-20:130:95
B68526
- 30 F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence.
5.3e-153:740:98
AF052149
- 35 F-Y79AA1002121

F-Y79AA1002129
Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
5.5e-12:565:61
40 L14320
- F-Y79AA1002213
Rattus norvegicus brain specific Na+dependent inorganic phosphate cotransporter mRNA, complete cds.
4.0e-12:434:60
45 U07609
- F-Y79AA1002334
F.rubripes GSS sequence, clone 174E24aB10, genomic survey sequence.
3.0e-10:171:72
50 AL019366
- F-Y79AA1002373
Rattus norvegicus Smad8 mRNA, complete cds.
0.96:420:61
55 AF012347
- F-Y79AA1002376
Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.

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1.1e-132:805:88
U39045

F-Y79AA1002378

Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
1.9e-64:521:78
D10630

F-Y79AA1002381

O.sativa mRNA for cdc2+/CDC28-related protein kinase.
3.3e-21:431:60
X58194

Homology search result 7

[0298] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 3'-ends. except EST and STS sequences.

Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0299] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone. Data were not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000006

R-HEMBA1000121

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
2.2e-43:355:80
AL031291

R-HEMBA1000128

Homo sapiens chromosome X, PAC 671D9, complete sequence.
0.99:389:60
AF031078

R-HEMBA1000275

Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG
island.
3.4e-10:212:66
Z93023

R-HEMBA1000300

{Alu RNA transcript, clone NE461} [human, embryonal carcinoma cells, NTera2D1 pluripotent cells, Other RNA,
282 nt].
4.6e-42:246:89
S42653

R-nnnnnnnnnnnnn

Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.
1.0e-71:192:95
AC005922

R-HEMBA1000462

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Homo sapiens clone 243 unknown mRNA, complete sequence.
8.3e-90:313:94
AF091094

5 R-HEMBA1000477
Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 8/11.
0.22:377:60
AB020865

10 R-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial.
8.0e-101:547:93
AJ007581

15 R-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.
0.95:186:62
20 AC004480

R-HEMBA1000671
RPC11-65E1.TJ RPC11 Homo sapiens genomic clone R-65E1, genomic survey sequence.
2.1e-09:165:73
25 AQ237194

R-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds.
1.2e-117:575:97
30 AF053470

R-HEMBA1000732
Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.
1.4e-108:581:93
35 Y13622

R-nnnnnnnnnnnnnnn

40 R-HEMBA1000875
Homo sapiens chromosome 17, clone hRPK.1090_M_7, complete sequence.
0.044:253:64
AC005274

45 R-HEMBA1000940
***ALU WARNING: Human Alu-J subfamily consensus sequence.
1.9e-33:222:82
U14567

50 R-HEMBA1000962

R-HEMBA1001184
Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.00044:466:58
55 AC004688

R-HEMBA1001221
Sequence 1 from patent US 5633147.

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7.1e-11:232:65
I43819

R-HEMBA1001228

5 Human germline oligomeric matrix protein (COMP) mRNA, complete cds.
7.8e-89:358:96
L32137

R-HEMBA1001272

10 nbxb0003bDO1r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003G00r, genomic survey sequence.
0.00014:201:64
AQ050116

R-HEMBA1001296

15 Homo sapiens PAC clone DJ1168D11 from 7p21-p22, complete sequence.
0.13:440:58
AC004614

R-HEMBA1001297

20 Homo sapiens putative transcription factor CA150 mRNA, complete cds.
5.0e-92:466:96
AF017789

R-HEMBA1001390

25 CIT-HSP-2314K10.TR CIT-HSP Homo sapiens genomic clone 2314K10, genomic survey sequence.
3.4e-43:196:85
AQ027191

R-HEMBA1001563

30 H.sapiens villin gene, exon 1.
2.1e-43:342:81
X71058

R-HEMBA1001621

35 Human G protein-coupled receptor APJ gene, complete cds.
1.2e-41:288:87
U03642

R-HEMBA1001878

40 Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
2.0e-79:434:93
AF090988

R-HEMBA1001886

45 Human zinc finger protein (ZNF141) mRNA, complete cds.
1.8e-59:530:80
L15309

R-HEMBA1002048

50 Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.
0.36:322:61
AC005355

R-HEMBA1002131

55 Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.
0.22:233:61
AL031730

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R-HEMBA1002163

Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.

1.1e-16:275:69

AC002489

5

R-HEMBA1002167

Rattus norvegicus neuroligin I mRNA, complete cds.

8.7e-23:193:84

U22952

10

R-HEMBA1002178

R-HEMBA1002195

Homo sapiens DHPS gene, exons 8 to 9.

1.4e-19:114:100

AJ001704

15

R-HEMBA1002227

Homo sapiens mRNA for 80K-L protein, complete cds.

6.1e-115:567:97

D10522

20

R-HEMBA1002316

Homo sapiens mRNA for putative GTP-binding protein.

1.5e-18:161:85

Y14391

25

R-HEMBA1002420

Caenorhabditis elegans cosmid C27A7, complete sequence.

0.88:214:62

Z81041

30

R-HEMBA1002421

Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.

6.0e-90:443:97

J04621

35

R-HEMBA1002524

Human MHC Class I region proline rich protein mRNA, complete cds.

3.2e-110:551:96

U63336

40

R-HEMBA1002551

Mouse Bac 276o8, WORKING DRAFT SEQUENCE, 25 unordered pieces.

7.0e-06:397:61

AC003022

45

R-HEMBA1002767

Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.

4.2e-110:568:96

AC005038

50

R-HEMBA1002985

Homo sapiens chromosome 17, clone hRPK.15_K_2, complete sequence.

3.4e-23:184:86

AC005901

55

R-HEMBA1003047

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Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.

5.0e-114:571:96

AF034611

5 R-HEMBA1003072
HS-1014-B1-F12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 789
Col=23 Row=L, genomic survey sequence.
1.5e-62:340:94
B32084

10 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
3.8e-116:575:97
AF049891

15 R-HEMBA1003120
HS_3220_A1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=7 Row=K, genomic survey sequence.
3.6e-61:354:92
20 AQ184345

R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds.
1.3e-42:258:93
25 AF093118

R-HEMBA1003294
HS_3220_A1_D03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=5 Row=G, genomic survey sequence.
30 0.0095:204:63
AQ190655

R-HEMBA1003315
Sus scrofa DNA for LH beta, exons 1, 2, 3, complete cds.
35 6.6e-24:163:79
D00579

R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
40 2.6e-115:557:98
AF074264

R-HEMBA1003399
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.
45 1.8e-63:166:100
AC004971

R-HEMBA1003487

50 R-HEMBA1003497
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27O5, WORKING DRAFT SEQUENCE.
1.4e-119:592:97
AL033529

55 R-HEMBA1003530

R-HEMBA1003602
Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.

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9.4e-79:468:91
AC002041

5 R-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
2.0e-118:586:98
AC006011

10 R-HEMBA1003945
Human calcineurin B mRNA, complete cds.
8.9e-82:410:97
M30773

15 R-HEMBA1004007
Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.
6.7e-56:404:75
AC004851

20 R-HEMBA1004085
G.gallus microsatellite DNA (LEI0311 (= EC12A05)).
0.66:144:65
Z95196

25 R-nnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds.
2.1e-115:569:97
AF064243

30 R-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
3.8e-98:478:98
AC005752

35 R-HEMBA1004391
Plasmodium falciparum MAL3P8, complete sequence.
0.29:126:65
AL034560

40 R-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
8.4e-52:308:78
AC004938

45 R-HEMBA1004454
CIT-HSP-2337122.TF CIT-HSP Homo sapiens genomic clone 2337122, genomic survey sequence.
0.78:59:77
AQ038475

50 R-HEMBA1004505

R-HEMBA1004785

R-HEMBA1004797

55 R-HEMBA1004952
Mus musculus diabetic embryopathy (Dep-1) mRNA.
3.4e-39:327:82
AF032130

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R-HEMBA1004971

Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.

0.00040:251:66

AC005099

5

R-HEMBA1004982

Strongyloides fulleborni 18S ribosomal RNA and 5.8S ribosomal RNA genes, partial sequence, and internal transcribed spacer 1, complete sequence.

0.092:191:63

10

U43581

R-HEMBA1005070

Human mRNA for KIAA0310 gene, complete cds.

1.2e-94:381:91

15

AB002308

R-HEMBA1005084

R-HEMBA1005145

20

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.

5.7e-58:283:84

AJ003147

25

R-HEMBA1005230

CIT-HSP-2333N15.TR CIT-HSP Homo sapiens genomic clone 2333N15, genomic survey sequence.

5.5e-31:363:73

AQ040189

30

R-HEMBA1005246

Homo sapiens full length insert cDNA clone YX52E07.

1.6e-11:173:72

AF086040

35

R-HEMBA1005267

Sequence 1 from patent US 5618695.

2.4e-73:536:81

I40055

40

R-HEMBA1005337

Caenorhabditis elegans cosmid K07D4.

0.16:157:63

AF077534

45

R-HEMBA1005430

R-HEMBA1005449

R-HEMBA1005489

50

Anopheles rangeli NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial product, partial cds.

0.020:271:61

U35272

55

R-HEMBA1005522

R-HEMBA1005545

Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.

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1.8e-115:579:96
U29589

5 R-HEMBA1005698
0.0065:223:65
AG004952

10 R-HEMBA1005913
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
3.7e-15:272:68
AC003037

15 R-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
9.4e-55:502:76
AC005581

20 R-HEMBA1005945
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SE-
QUENCE.
0.45:245:62
AL034410

25 R-HEMBA1006016
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
3.5e-25:415:66
AC005562

30 R-HEMBA1006171
Human DNA sequence from PAC 433M19 on chromosome Xq26.3-Xq27.1. Contains ESTs, STSs and polymorphic
CA repeat.
1.0:176:64
Z95703

35 R-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
2.8e-118:592:96
AC005261

40 R-HEMBA1006299

R-HEMBA1006311

45 R-HEMBA1006335
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
6.1e-111:578:96
AL023582

50 R-HEMBA1006357
Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.
4.8e-11:174:74
AC004469

55 R-HEMBA1006430
Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.
8.7e-45:402:79
AC004086

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R-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

1.7e-105:537:96

AF026852

5

R-HEMBA1006517

345A19.TV CIT978SKA1 Homo sapiens genomic clone A-345A19, genomic survey sequence.

1.5e-44:176:88

B15409

10

R-HEMBA1006544

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

2.5e-66:310:83

AC004997

15

R-HEMBA1006572

Homo sapiens reduced folate carrier (RFC1) gene, exons 1a, 1c and 1b.

0.028:255:64

U92868

20

R-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

7.3e-1 11:570:94

AB014587

25

R-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial.

5.1e-78:389:97

AJ007581

30

R-HEMBA1006724

HS_2052_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=15 Row=F, genomic survey sequence.

2.6e-46:309:88

AQ305998

35

R-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial.

3.2e-88:472:94

AJ007581

40

R-HEMBA1006770

Homo sapiens CAGH4 mRNA, partial cds.

6.5e-25:145:82

U80746

45

R-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial.

9.3e-112:540:98

AJ007581

50

R-HEMBA1006912

***ALU WARNING: Human Alu-Sc subfamily consensus sequence.

6.6e-48:279:92

U14571

55

R-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds.

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1.8e-114:346:99
L76687

5 R-HEMBA1006960
Homo sapiens chromosome 19, cosmid F16403, complete sequence.
0.78:203:62
AC005777

10 R-HEMBA1007013
Human mRNA for DNA-binding protein TAXREB302, complete cds.
6.3e-31:163:100
D28468

15 R-HEMBA1007057
CIT-HSP-517F5.TP CIT-HSP Homo sapiens genomic clone 517F5, genomic survey sequence.
1.0:128:67
B49904

20 R-HEMBA1007063
Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.
5.0e-43:300:88
AL022069

25 R-HEMBA1007241
HIV-1 RNA V3 region (patient Y, sample Y1, clone 05).
0.74:148:66
Z47529

30 R-HEMBA1007291
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
3.6e-36:300:80
AC004755

35 R-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
7.3e-15:148:80
U56430

40 R-HEMBA1000106
Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.
8.0e-05:313:60
L40609

45 R-HEMBA1000276
HS_3048_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=14 Row=E, genomic survey sequence.
0.91:234:58
AQ099411

50 R-HEMBA1000309

R-HEMBA1000407
Mus musculus clone OST5976, genomic survey sequence.
55 6.4e-28:226:81
AF046768

R-HEMBA1000447

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Homo sapiens JWA protein mRNA, complete cds.
1.7e-107:533:97
AF070523

5 R-HEMBB1000542

Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.
4.4e-72:547:80
AF084259

10 R-HEMBB1000567

Human insulin-like growth factor (IGF-II) gene, exon 1 of 4.
4.3e-60:368:88
M13970

15 R-HEMBB1000642

Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.
2.9e-42:431:75
Z84483

20 R-HEMBB1000668

CITBI-E1-2508D15.TR CITBI-E1 Homo sapiens genomic clone 2508D15, genomic survey sequence.
2.5e-40:249:91
AQ261535

25 R-HEMBB1000679

HS_3061_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061
Col=5 Row=E, genomic survey sequence.
1.8e-48:257:96
AQ127602

30

R-HEMBB1000881

CIT-HSP-2350020.TR CIT-HSP Homo sapiens genomic clone 2350O20, genomic survey sequence.
0.0072:248:61
AQ062620

35

R-HEMBB1000905

Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
2.5e-104:547:94
AC005089

40

R-HEMBB1001026

R-HEMBB1001048

45

R-HEMBB1001200

P.falciparum complete gene map of plastid-like DNA (IR-A).
1.5e-11:521:59
X95275

50

R-HEMBB1001407

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.
3.0e-29:308:77
AL033529

55

R-HEMBB1001530

Homo sapiens chromosome 19, cosmid R30538, complete sequence.
0.040:373:63
AC005943

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R-HEMBB1001547

Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.

0.027:291:62

AJ235270

5

R-HEMBB1001573

CIT-HSP-2307C1.TR CIT-HSP Homo sapiens genomic clone 2307C1, genomic survey sequence.

1.3e-13:90:98

AQ020395

10

R-HEMBB1001847

Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence.

3.4e-27:147:80

AF064864

15

R-HEMBB1001959

Homo sapiens clone 24781 mRNA sequence.

4.4e-103:504:97

AF070640

20

R-HEMBB1001978

CIT-HSP-2328G6.TF CIT-HSP Homo sapiens genomic clone 2328G6, genomic survey sequence.

7.9e-29:220:86

AQ040310

25

R-HEMBB1002039

Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.

2.7e-37:550:68

AC005014

30

R-HEMBB1002041

Sequence 1 from patent US 5633147.

2.7e-23:322:70

I43819

35

R-HEMBB1002051

Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.

9.2e-35:302:79

AC004825

40

R-HEMBB1002120

Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.

6.0e-05:479:59

AC003106

45

R-HEMBB1002162

Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.

3.7e-30:238:84

AL031289

50

R-HEMBB1002228

Homo sapiens BAC clone NH0436H22 from 2, complete sequence.

6.6e-57:274:86

AC005234

55

R-HEMBB1002245

Sequence 25 from patent US 5747660.

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4.8e-30:361:73
AR005295

R-HEMBB1002302

5 Methanococcus jannaschii section 84 of 150 of the complete genome.
0.00019:362:59
U67542

R-HEMBB1002427

10 Genomic sequence from Human 9q34, complete sequence.
3.9e-105:533:96
AC001643

R-HEMBB1002465

15 Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.
2.9e-05:335:62
AE001382

R-HEMBB1002661

20 R-HEMBB1002663
***ALU WARNING: Human Alu-Sq subfamily consensus sequence.
8.3e-43:268:89
U14573

R-HEMBB1002693

25 Human BAC clone RG126M09 from 7q21-q22, complete sequence.
2.4e-24:220:76
AC002067

R-MAMMA1000046

30 Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.
0.032:402:57
AC005505

R-MAMMA1000102

40 Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.
2.0e-84:428:96
Z79996

R-MAMMA1000106

45 Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.
0.095:138:66
AP000031

R-MAMMA1000118

R-MAMMA1000141

50 Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.
9.0e-91:480:95
AC004024

R-MAMMA1000204

55 Homo sapiens mRNA for LGMD2B protein.
1.5e-107:544:96
AJ007670

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R-MAMMA1000226

H.sapiens VASP gene, exons 4 to 13.

0.99:244:63

X98534

5

R-MAMMA1000403

CIT-HSP-2372A15.TF CIT-HSP Homo sapiens genomic clone 2372A15, genomic survey sequence.

8.0e-38:187:81

AQ112406

10

R-MAMMA1000449

Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.

1.2e-41:422:76

AC004491

15

R-MAMMA1000457

Homo sapiens clone 638 unknown mRNA, complete sequence.

7.4e-116:570:97

AF091084

20

R-MAMMA1000473

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.

9.6e-09:136:77

AC004131

25

R-MAMMA1000496

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

2.6e-48:272:93

AC004997

30

R-MAMMA1000528

Human BAC clone RG114A06 from 7q31, complete sequence.

1.8e-13:109:80

AC002542

35

R-MAMMA1000591

Human cosmid g1572c264, complete sequence.

1.6e-22:329:71

AC000359

40

R-MAMMA1000614

R-MAMMA1000652

H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28A10.

0.81:158:65

Z84499

45

R-MAMMA1000681

Homo sapiens full length insert cDNA clone YY85D04.

1.0e-107:560:94

AF088014

50

R-MAMMA1000706

Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.

1.1e-46:232:100

AF067223

55

R-MAMMA1000788

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Bos taurus P14 (p14) mRNA, complete cds.
3.8e-72:493:84
AF037349

5 R-MAMMA1000810
Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.
5.0e-37:318:79
AC003002

10 R-MAMMA1000814
Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.
7.7e-15:140:85
AC003071

15 R-MAMMA1000881
Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.
8.8e-46:457:75
20 AL031311

R-MAMMA1000986
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
7.7e-44:343:82
25 AF001550

R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds.
3.6e-108:552:96
30 AB003184

R-MAMMA1001043

35 R-MAMMA1001066
Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.
1.3e-42:302:82
AC006120

40 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence.
5.4e-115:567:97
AF091094

45 R-MAMMA1001141
HS_3059_B1_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3059 Col=11 Row=P, genomic survey sequence.
1.3e-68:388:92
AQ214896

50 R-MAMMA1001150
H.sapiens mRNA for protein kinase C mu.
5.4e-20:340:66
X75756

55 R-MAMMA1001237
Mouse DNA fragment that hybridizes to HSV- 1 SmaI A fragment.
0.15:222:65
M11041

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R-MAMMA1001284

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.

1.2e-33:344:76

AL034423

R-MAMMA1001310

Human Bruton agammaglobulinemia (BTK) gene, exons 10-12.

1.8e-39:332:80

L31565

R-MAMMA1001418

Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.

4.4e-42:411:76

U07563

R-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

2.3e-10:196:73

AC004865

R-MAMMA1001609

HS-1054-B2-H01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=2 Row=P, genomic survey sequence.

1.6e-34:170:79

B42016

R-MAMMA1001615

R-MAMMA1001623

Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

8.8e-21:180:82

AC006065

R-MAMMA1001634

Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.

2.6e-40:283:86

AC005695

R-MAMMA1001893

Homo sapiens clone DJ0782K24, WORKING DRAFT SEQUENCE, 16 unordered pieces.

0.73:132:67

AC006003

R-MAMMA1001901

Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.

4.0e-43:288:77

Z93023

R-MAMMA1001957

Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.

1.2e-41:298:86

AC005212

R-MAMMA1001978

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- R-MAMMA1002070
Homo sapiens clone DJ400N23, WORKING DRAFT SEQUENCE, 10 unordered pieces.
2.1e-104:530:97
AC005003
- 5
- R-MAMMA1002080 rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].
5.9e-47:449:76
S72304
- 10
- R-MAMMA1002087
Human Cosmid g1572c037 from 7q31.3, complete sequence.
1.7e-11:120:83
AC000125
- 15
- R-MAMMA1002095
Rat alternatively spliced mRNA.
5.3e-30:289:74
M93018
- 20
- R-MAMMA1002128
- R-MAMMA1002142
- R-MAMMA1002165
- 25
- Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.
1.1e-28:350:72
AC005871
- R-MAMMA1002205
- 30
- Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.
1.2e-42:282:75
Z83843
- 35
- R-MAMMA1002224
Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAll project).
0.99:210:60
AL022224
- 40
- R-MAMMA1002234
Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).
1.7e-61:310:81
X53744
- 45
- R-MAMMA1002586
Streptomyces collinus coenzyme B12-dependent mutase (meaA) gene, complete cds.
0.99:348:60
AF008569
- 50
- R-MAMMA1002633
Homo sapiens, clone hRPK. 1_A_1, complete sequence.
2.6e-13:381:64
AC006196
- 55
- R-MAMMA1003126
- R-NT2RM4000100
Plasmodium falciparum MAL3P2, complete sequence.

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0.00047:296:61
AL034558

5 R-NT2RM4000115
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SE-
QUENCE.

0.079:270:64
AL031746

10 R-NT2RM4000198
Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-
ordered pieces.

7.7e-24:244:78
AC006171

15 R-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds.
1.7e-93:440:100
U12255

20 R-NT2RM4000295
, complete sequence.
0.89:351:58
AC005663

25 R-NT2RM4000326
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterra-
nean Fever gene disease.

2.3e-112:602:94
AJ003147

30 R-NT2RM4000417
Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.
0.78:229:62
Z82170

R-NT2RM4000444

R-NT2RM4000587

40 R-NT2RM4000593

R-NT2RM4000648
0.010:260:61
AG005508

45 R-NT2RM4000761
H.sapiens mitochondrial genome (consensus sequence).
3.2e-95:476:97
X62996

R-NT2RM4000965

R-NT2RM4000997

55 R-NT2RM4001321
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-bind-
ing Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

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6.0e-19:282:73
AL031277

R-NT2RM4001325

R-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.9e-111:553:96
AB014538

R-NT2RM4001735
Homo sapiens clone 23904 mRNA sequence.
4.6e-106:553:94
AF052129

R-NT2RM4001768
Human HepG2 3'region Mbol cDNA, clone hmd3c03m3.
4.1e-29:187:91
D17194

R-NT2RM4001843
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.95:366:58
AC005828

R-NT2RM4002352
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.
5.5e-108:557:95
AB009462

R-NT2RP2000092
HS_3070_B1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070
Col=7 Row=D, genomic survey sequence.
1.1e-23:247:77
AQ120714

R-NT2RP2000178
E.amylovora lon gene.
1.1e-15:422:62
X77706

R-NT2RP2000240
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.
0.00010:260:62
AC004480

R-NT2RP2000394
HS_3211_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211
Col=12 Row=N, genomic survey sequence.
1.1e-61:316:97
AQ174850

R-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
8.7e-67:357:94
AC005630

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R-NT2RP2000479

Homo sapiens chromosome 17, clone 193h18, complete sequence.

5.7e-51:551:73

AC002546

5

R-NT2RP2000514

P.falciparum parasite antigen reactive with the parasite inhibitory mouse monoclonal antibody (mMAb) 43E5, clone #366, partial cds.

2.1e-08:192:68

10

M21323

R-NT2RP2000533

Mus musculus cornichon mRNA, complete cds.

3.5e-59:243:82

15

AF022811

R-NT2RP2000616

Human DNA sequence from clone 694E4 on chromosome 22 Contains exon similar to phosphatidylserine decarboxylase, EST, GSS, complete sequence.

20

0.0064:105:67

AL031255

R-NT2RP2000649

Homo sapiens mRNA for Hs Ste24p, complete cds.

25

1.4e-65:326:98

AB016068

R-NT2RP2000663

Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.

30

7.9e-110:555:96

Z73913

R-NT2RP2000712

Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.

35

9.8e-32:308:78

AC006001

R-NT2RP2000739

Bos taurus TATA box binding protein (TBP) gene, partial cds.

40

0.19:128:68

L47974

R-NT2RP2000818

Caenorhabditis elegans cosmid C48D5, complete sequence.

45

0.010:429:58

Z36237

R-NT2RP2000903

H.sapiens 5T4 gene for 5T4 Oncofetal antigen.

50

4.0e-99:505:96

Z29083

R-NT2RP2001200

Homo sapiens mRNA for KIAA0676 protein, partial cds.

55

2.0e-57:306:95

AB014576

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R-NT2RP2001223

R-NT2RP2001276

Mouse regulatory protein (npdc-1) mRNA, complete cds.

5.8e-14:353:65

L03814

R-NT2RP2001388

Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.

1.7e-31:291:77

AC004971

R-NT2RP2001469

M.musculus tex292 mRNA (3'region).

3.7e-26:188:89

X80433

R-NT2RP2001480

Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.

6.6e-83:426:95

L38969

R-NT2RP2001495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

6.3e-43:238:96

S77359

R-NT2RP2001514

Homo sapiens cyclin K (CPR4) mRNA, complete cds.

6.6e-06:57:100

AF060515

R-NT2RP2001538

Mus musculus transcriptional regulatory protein (mSin3) gene, complete cds.

6.9e-12:179:75

L36831

R-NT2RP2001562

Human PAC clone DJ0800B09 from 7q11.23-q21, complete sequence.

0.074:257:61

AC004028

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence.

3.2e-94:485:95

AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds.

1.3e-103:576:92

AB018305

R-NT2RP2001769

CIT-HSP-2376O23.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.

1.5e-74:381:96

AQ111163

R-NT2RP2001817

EP 1 130 094 A2

HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=18 Row=B, genomic survey sequence.

3.9e-60:430:84

AQ243047

5

R-NT2RP2001878

Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.

10

0.018:148:67

Z83821

R-NT2RP2001903

Human Not1 linking clone from chromosome 1q32.

15

0.99:160:63

U36769

R-NT2RP2001915

20

R-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

6.5e-86:295:98

AC005538

25

R-NT2RP2001948

Homo sapiens chromosome 19, cosmid R33590, complete sequence.

2.3e-79:440:91

AC005620

30

R-NT2RP2001956

R-NT2RP2002015

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

35

1.1e-16:254:72

AL031277

R-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

40

5.8e-105:550:95

AC004050

R-NT2RP2002188

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.

45

0.47:212:62

AL034555

R-NT2RP2002232

50

R-nnnnnnnnnnnnn

Human mRNA for KIAA0383 gene, partial cds.

2.5e-100:511:96

AB002381

55

R-NT2RP2002409

S.pombe chromosome I cosmid c17H9.

1.0:241:63

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Z98597

R-NT2RP2002510

Homo sapiens chromosome 19, cosmid F19847, complete sequence.

1.6e-38:307:81

AC005952

R-NT2RP2002527

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.5e-18:165:83

AC004770

R-NT2RP2002533

Homo sapiens alpha 2 delta calcium channel subunit isoform II mRNA, complete cds.

9.7e-116:580:96

AF042793

R-NT2RP2002564

Homo sapiens clone DJ0800G07, complete sequence.

3.8e-110:580:94

AC004890

R-NT2RP2002674

Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.

1.0:244:60

AE001374

R-NT2RP2002721

Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.

1.2e-10:221:73

AC003962

R-NT2RP2002824

Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.

3.0e-07:108:77

D17237

R-NT2RP2002942

Human DNA sequence from clone 88D7 on chromosome Xq25-26.3 Contains F9 (coagulation factor IX (plasma thromboplastic component, Christmas disease, haemophilia B)), dbl oncogene. EST, STS, GSS, complete sequence.

2.0e-37:491:71

AL033403

R-NT2RP2002974

H.sapiens DMAHP gene.

4.0e-118:585:97

X84813

R-NT2RP2002976

CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.

8.4e-45:233:98

AQ059444

R-NT2RP2003042

R-NT2RP2003179

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R-NT2RP2003210

R-NT2RP2003302

Human DNA sequence from 4PTCL, Huntington's Disease Region, chromosome 4p16.3.

1.5e-24:255:78

Z95704

R-NT2RP2003369

Homo sapiens chromosome 7q22 sequence, complete sequence.

3.1e-95:514:92

AF053356

R-NT2RP2003383

Homo sapiens mRNA for KIAA0458 protein, complete cds.

3.9e-111:549:97

AB007927

R-NT2RP2003390

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.

4.9e-102:413:99

AL024507

R-NT2RP2003469

Genomic sequence from Human 9q34, complete sequence.

1.4e-35:376:74

AC001644

R-NT2RP2003545

Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.

1.5e-09:503:61

AL034557

R-NT2RP2003593

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SEQUENCE.

7.8e-81:433:93

AL021396

R-NT2RP2003599

HS_3240_A1_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3240 Col=7 Row=E, genomic survey sequence.

0.091:341:58

AQ206348

R-NT2RP2003655

Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.

2.0e-08:249:69

AC004819

R-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein.

1.7e-110:549:96

Y12670

R-NT2RP2003931

Human mRNA for KIAA0365 gene, partial cds.

5.4e-112:571:96

EP 1 130 094 A2

AB002363

R-NT2RP2003940

Human Chromosome 11 pac pDJ1173a5, complete sequence.

2.4e-20:353:70

AC000378

R-NT2RP2003950

Homo sapiens clone 24778 unknown mRNA.

1.5e-96:494:95

AF070572

R-NT2RP2004069

Human DNA sequence from clone 618F1 on chromosome Xq25 Contains part of gene similar to DOC4, CA repeat, GSS, complete sequence.

2.6e-50:539:75

AL023878

R-NT2RP2004108

RPCII1-91F9.TV RPCI11 Homo sapiens genomic clone R-91F9, genomic survey sequence. 0.00013:281:63

AQ283338

R-NT2RP2004141

cSRL-115f11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-115f11, genomic survey sequence.

2.3e-05:239:64

B00539

R-NT2RP2004179

Genomic sequence from Human 9q34, complete sequence.

0.43:130:68

AC002322

R-NT2RP2004205

Homo sapiens chromosome 7q22 sequence, complete sequence.

1.4e-42:324:83

AF053356

R-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

5.5e-35:285:84

AC000353

R-NT2RP2004495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

3.4e-44:238:97

S77359

R-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

7.4e-113:572:96

AC001644

R-NT2RP2004556

CIT-HSP-2306F6.TF CIT-HSP Homo sapiens genomic clone 2306F6, genomic survey sequence.

8.1e-99:514:95

AQ019229

EP 1 130 094 A2

R-NT2RP2004606 cDNA encoding NIC(Natural Inhibitor of Collagenase).
8.2e-116:576:96
E00985

5 R-NT2RP2004648
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.98:369:57
AC005828

10 R-NT2RP2004670
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
4.5e-43:592:69
L22557

15 R-NT2RP2004794

R-NT2RP2004837
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
20 AC001232

R-NT2RP2004847
Homo sapiens full length insert cDNA clone YY87C09.
1.0e-68:333:100
25 AF086055

R-NT2RP2005027
Human glucose transporter-like protein-III (GLUT3), complete cds.
7.8e-103:508:97
30 M20681

R-NT2RP2005069
Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.
3.8e-42:463:73
35 U35245

R-NT2RP2005163
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
7.4e-44:233:96
40 AQ059444

R-NT2RP2005181
Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.
7.6e-53:567:73
45 AB000113

R-NT2RP2005247
Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell
Park Cancer Center) complete sequence.
50 5.8e-38:341:76
AC002357

R-NT2RP2005378
Homo sapiens full length insert cDNA clone YW25A12.
55 0.13:152:66
AF086029

R-NT2RP2005391

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HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3056 Col=5 Row=E, genomic survey sequence.

1.1e-14:140:84

AQ134064

5

R-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

8.2e-100:526:94

AB018346

10

R-NT2RP2005463

R-NT2RP2005514

15

R-NT2RP2005535

Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.

1.9e-11:488:62

AC003973

20

R-NT2RP2005541

CIT-HSP-2034G23.TF CIT-HSP Homo sapiens genomic clone 2034G23, genomic survey sequence.

2.7e-61:311:98

B74709

25

R-NT2RP2005597

R-nnnnnnnnnnnnn

{FRA16A, folate-sensitive fragile site} [human, Genomic, 160 nt].

0.92:104:65

30

S70397

R-NT2RP2005666

R-NT2RP2005774

Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence.

2.2e-94:440:96

AF035364

40

R-NT2RP2005878

Homo sapiens chromosome 19, cosmid F17987, complete sequence.

1.3e-32:340:76

AC004790

45

R-NT2RP2005883

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.

1.3e-117:581:97

AL023578

50

R-NT2RP2005887

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces

2.5e-61:367:90

AC001232

55

R-nnnnnnnnnnnnn

Human paired box gene (PAX6) homologue, complete cds.

5.0e-115:578:96

M93650

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R-NT2RP2005994

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

2.4e-116:594:96

AC004050

5

R-NT2RP2006004

Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.

1.8e-45:264:93

U42975

10

R-NT2RP2006042

T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.

0.42:111:70

B78148

15

R-NT2RP2006092

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

1.7e-73:385:95

AC005214

20

R-NT2RP2006099

Homo sapiens PAC clone DJ0903G02, complete sequence.

1.3e-27:335:74

AC004924

25

R-NT2RP2006134

Homo sapiens chromosome 4 clone B139M23 map 4q25, complete sequence.

1.0:143:63

AC004045

30

R-NT2RP2006269

Phreatamoeba balamuthi UBI3 sequence, putative polyubiquitin gene.

0.82:153:63

AJ000657

35

R-NT2RP2006512

Homo sapiens clone 23904 mRNA sequence.

4.6e-106:531:96

AF052129

40

R-NT2RP3000011

HS_2196_A2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196

Col=16 Row=I, genomic survey sequence.

1.3e-36:292:83

AQ210450

45

R-NT2RP3000022

Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-15, complete sequence.

0.28:248:60

Z98550

50

R-NT2RP3000059

Homo sapiens chick ovalbumin upstream promoter transcription factor II (COUP-TFII) mRNA, partial cds.

0.047:393:61

M62760

55

R-NT2RP3000063

HS_3190_B2_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone

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Plate=3190 Col=20 Row=H, genomic survey sequence.
0.88:232:63
AQ172428

- 5 R-nnnnnnnnnnnnn
RPCI11-35A1.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-35A1, genomic survey sequence.
3.8e-29:159:99
AQ045699
- 10 R-NT2RP3000148
Homo sapiens full length insert cDNA clone ZE03A07.
2.8e-112:574:95
AF086510
- 15 R-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds.
4.4e-110:551:96
AF093239
- 20 R-NT2RP3000171

R-NT2RP3000172
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
1.3e-40:554:70
- 25 L22557

R-NT2RP3000201
Homo sapiens BAC clone NH0353P23 from 2, complete sequence.
6.4e-96:478:97
- 30 AC005035

R-NT2RP3000232
Plasmodium falciparum MAL3P2, complete sequence.
0.93:262:61
- 35 AL034558

R-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.4e-109:546:97
- 40 AF074264

R-NT2RP3000378
Mus musculus mSin3A (sin3A) mRNA, complete cds.
3.0e-27:411:72
- 45 U22394

R-NT2RP3000436
Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.
1.1e-06:440:57
- 50 AE001398

R-NT2RP3000444
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 889J22, WORKING DRAFT SEQUENCE.
5.9e-105:543:95
- 55 AL031406

R-NT2RP3000460
Canis familiaris sec61 homologue mRNA, complete cds.

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2.8e-12:292:68
M96629

5 R-NT2RP3000481
WORKING DRAFT SEQUENCE, 8 unordered pieces.
0.99:160:65
AC005992

10 R-NT2RP3000616
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.00087:412:57
AC005308

15 R-NT2RP3000645

R-NT2RP3000652
Homo sapiens DNA from chromosome 19, cosmid R32532, complete sequence.
1.9e-44:539:74
20 AC004004

R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds.
3.1e-103:542:94
25 AB007915

R-NT2RP3000677
Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.
0.067:235:61
30 AB020872

R-NT2RP3000721
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
4.0e-45:233:98
35 AQ059444

R-NT2RP3000789

40 R-NT2RP3000818
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
5.7e-95:510:93
Z97201

45 R-NT2RP3000820
RPC11-77B13.TJ RPC11 Homo sapiens genomic clone R-77B13, genomic survey sequence.
2.1e-50:266:96
AQ283547

50 R-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds.
4.6e-99:522:94
AB014538

55 R-NT2RP3000871
Homo sapiens clone DJ0703P08, WORKING DRAFT SEQUENCE, 23 unordered pieces.
0.68:249:61
AC005481

EP 1 130 094 A2

- 5 R-NT2RP3000907
X.laevis oocyte repetitive sequence (XLOREP) mRNA.
2.9e-30:386:69
X65290
- 10 R-NT2RP3000921
HS_2026_A1_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026
Col=11 Row=C, genomic survey sequence.
2.2e-54:311:92
AQ232644
- 15 R-NT2RP3001012
Rattus norvegicus mRNA for TIP120, complete cds.
9.2e-63:456:83
D87671
- 20 R-NT2RP3001044
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
AC001232
- 25 R-NT2RP3001061
Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7
unordered pieces.
0.17:357:61
AC005506
- 30 R-NT2RP3001159
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
8.8e-111:561:96
AC004228
- 35 R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds.
8.8e-117:561:98
AB018327
- 40 R-NT2RP3001195
Genomic sequence from Human 9q34, complete sequence.
1.4e-35:376:74
AC001644
- 45 R-NT2RP3001240
Canis familiaris sec61 homologue mRNA, complete cds.
2.8e-12:292:68
M96629
- 50 R-NT2RP3001271
Homo sapiens chromosome 19, BAC CIT-B-470f8 (BC330812), complete sequence.
7.9e-17:260:71
AC006115
- 55 R-NT2RP3001322
Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.
0.035:451:60
Z97629

EP 1 130 094 A2

5 R-NT2RP3001542
Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8
unordered pieces.
4.1e-08:500:61
AC004153

10 R-NT2RP3001560
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
1.0e-30:523:65
D67067

15 R-NT2RP3001592

R-NT2RP3001685
Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome
C oxidase gene, EST, CpG island, complete sequence.
2.4e-30:147:85
AL024474

20 R-NT2RP3001738
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
9.2e-107:553:95
AC004228

25 R-NT2RP3001754
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.
2.0e-67:345:97
AL034380

30 R-NT2RP3001858

R-NT2RP3001976
Homo sapiens chromosome 9, clone hRPK.467_F_21, complete sequence.
35 4.4e-14:302:62
AC006239

R-NT2RP3002015
Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.
40 6.2e-65:492:82
AC004832

R-NT2RP3002160
Genomic sequence from Human 9q34, complete sequence.
45 2.1e-82:431:95
AC001643

R-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds.
50 1.1e-81:446:93
AB018308

R-NT2RP3002286
Mus musculus EGF repeat transmembrane protein mRNA, complete cds.
55 1.0e-80:378:90
U57368

R-NT2RP3002311

EP 1 130 094 A2

Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.57:366:58
AC005828

5 R-NT2RP3002324
H.sapiens gene for nitric oxide synthase (promoter region).
1.6e-30:337:72
Z49251

10 R-NT2RP3002342
transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].
6.5e-45:238:98
S77359

15 R-NT2RP3002353
Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence. 0.00015:164:70
AC002044

20 NNNNNNNNNNNNNNNN
Homo sapiens mRNA for KIAA0788 protein, partial cds.
4.5e-98:493:96
AB018331

25 NNNNNNNNNNNNNNNN

R-NT2RP3002448
S.cerevisiae DNA for ori 2.
0.52:91:71
X59535

30 /
R-NT2RP3002571

R-NT2RP3002664
Homo sapiens full length insert cDNA clone ZC48G09.
35 9.9e-103:522:96
AF086209

R-NT2RP3002721

40 R-NT2RP3002737

R-NT2RP3002738
Sequence 4 from patent US 5541109.
2.9e-22:171:74
45 I24014

R-NT2RP3002790

50 R-NT2RP3002836
Bos taurus retina specific RGS protein (RET-RGS1) mRNA, complete cds.
2.3e-34:384:75
U89254

55 R-NT2RP3002887
Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.
1.6e-05:435:62
AF051726

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R-NT2RP3002900

Homo sapiens mRNA from chromosome 5q21-22, clone:A3-B.

1.3e-116:569:97

AB002451

R-NT2RP3002958

Homo sapiens clone 23851 mRNA sequence.

2.0e-117:575:98

AF035313

R-NT2RP3002983

Homo sapiens genomic DNA, chromosome 21q11.1, segment 17/28, WORKING DRAFT SEQUENCE.

5.1e-59:295:99

AP000046

R-NT2RP3003000

Homo sapiens clone 24597 mRNA sequence.

6. |e-109:562:95

AF070604

R-NT2RP3003076

R-NT2BP3003354

Human protocadherin 42 mRNA, complete cds for abbreviated PC42.

0.87:208:61

L11370

R-NT2RP3003448

High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.

1.3e-41:287:80

AC005840

R-NT2RP3003469

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

2.1e-18:223:77

AL031277

R-NT2RP3003473

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SE-
QUENCE.

1.5e-54:294:96

Z99716

R-NT2RP3003527

Homo sapiens mRNA for protein kinase Dyrk1B.

5.1e-91:445:97

Y17999

R-NT2RP3003532

Mus musculus cell surface molecule OX-2 mRNA, complete cds.

1.2e-30:529:67

AF004023

R-oooooooooooo

Homo sapiens PAC clone DJ0531G15 from 7p21, complete sequence.

0.13:294:61

AC004739

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R-NT2RP3003559

CIT-HSP-2307F17.TR CIT-HSP Homo sapiens genomic clone 2307F17, genomic survey sequence.

1.4e-15:342:68

AQ016972

5

R-NT2RP3003614

Homo sapiens chromosome 19, cosmid F21967, complete sequence.

0.013:174:64

AC005256

10

R-NT2RP3003729

R-NT2RP3003849

Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 6 unordered pieces.

8.9e-106:557:94

AC002320

15

R-NT2RP3003874

Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.

1.6e-55:302:94

AJ001381

20

R-NT2RP3003963

cSRL-66f9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-66f9, genomic survey sequence.

0.028:78:76

B05608

25

R-NT2RP3004000

Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 861 nt, segment 7 of 7].

0.87:212:62

S45012

30

R-NT2RP3004025

Homo sapiens chromosome 19, cosmid F17987, complete sequence.

0.71:197:62

AC004790

35

R-NT2RP3004075

R-NT2RP3004083

Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5.

0.27:375:59

Z97340

40

R-NT2RP3004090

CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.

2.2e-40:243:91

B99962

45

R-NT2RP3004119

Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.

8.3e-42:475:73

AC004953

50

R-NT2RP3004130

R-NT2RP3004133

55

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CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
0.00037:194:64
AQ022229

5 R-NT2RP3004202
Homo sapiens BAC clone GS285F21 from 7q21-q22, complete sequence.
0.65:209:62
AC004012

10 R-NT2RP3004294

R-NT2RP3004309
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.
15 7.4e-99:500:96
AC004228

R-NT2RP3004321
Human chromosome 11 168h3 cosmid, complete sequence.
20 1.7e-105:540:96
U73637

R-NT2RP3004345
Human BAC clone RG016J04 from 7q21, complete sequence.
25 0.00033:348:61
AC002064

R-NT2RP3004355
Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.
30 0.0029:180:66
AC004709

R-NT2RP3004374
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
35 4.3e-18:223:77
AL031277

40 R-NT2RP3004406
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-70, complete sequence.
1.0:201:62
AL010239

45 R-NT2RP3004481

R-NT2RP3004552
Human germline immunoglobulin lambda light chain pseudogene (VII.1).
1.0:165:63
50 X57825

R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
8.2e-49:352:84
55 AF082516

R-NT2RP3004640
Homo sapiens full length insert cDNA clone ZC45E05.

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1.2e-96:471:98
AF086205

5 R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds.
1.5e-109:555:96
AB007915

10 R-NT2RP4000108
Mouse neurofilament protein (NF-L) gene, 3' flank.
1.0e-09:344:63
M55424

15 R-NT2RP4000634
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
1.6e-16:267:71
AC003037

20 R-NT2RP4000962
Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).
0.026:176:67
AL021069

25 R-NT2RP4001001
Drosophila melanogaster Oregon-R mitochondrial A+T region.
0.00026:354:61
U11584

30 R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds.
1.6e-82:408:98
AB016068

35 R-NT2RP4001467
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).
1.8e-111:545:97
X55740

40 R-NT2RP4001877
Yeast (S.cerevisiae) mitochondrial cob gene, intron 4.
0.19:384:59
J01469

45 R-NT2RP4001879
Homo sapiens full length insert cDNA clone ZD76G10.
4.4e-107:548:94
AF086408

50 R-NT2RP4002187
RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.
7.1e-37:240:89
AQ238297

55 R-NT2RP4002451
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.
5.8e-111:575:96
Z98200

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R-NT2RP4002715

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.

2.5e-61:367:90

AC001232

5

R-NT2RP4002750

Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.

1.2e-52:527:74

AB000113

10

R-OVARC1000003

Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.

2.3e-10:140:77

AC004909

15

R-OVARC1000090

Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SE-
QUENCE.

2.8e-59:323:78

20

DB4394

R-OVARC1000105

H.sapiens gene for ribosomal protein L38.

2.7e-12:83:100

25

Z26876

R-OVARC1000137

R-OVARC1000208

30

Homo sapiens PAC clone DJ0817I18 from 7p11.2p13, complete sequence.

2.7e-52:464:79

AC004901

R-OVARC1000255

35

H.sapiens syk mRNA for protein-tyrosine kinase.

1.9e-105:511:98

Z29630

R-OVARC1000275

40

R-OVARC1000298

Plasmodium falciparum carbamoyl phosphate synthetase II gene, complete cds.

0.66:364:59

L32150

45

R-OVARC1000307

R-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds.

50

1.6e-96:534:93

AB011145

R-OVARC1000331

Sequence 2 from patent US 5763589.

55

8.1e-66:335:97

AR012692

R-OVARC1000410

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Homo sapiens clone 23767 and 23782 mRNA sequences.

1.0e-88:462:94

AF007150

5

R-OVARC1000439

E.coli fanG and fanH genes.

0.99:424:58

Y00531

10

R-OVARC1000467

HS_3235_A2_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=24 Row=A, genomic survey sequence.

9.2e-09:125:76

AQ206826

15

R-OVARC1000529

R-OVARC1000553

Homo sapiens chromosome 19, cosmid R26894, complete sequence.

20

2.0e-84:437:96

AC005594

R-OVARC1000775

CIT-HSP-2060P5.TF CIT-HSP Homo sapiens genomic clone 2060P5, genomic survey sequence. 0.29:223:63

25

B70025

R-OVARC1000811

Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.

2.8e-89:438:98

30

AC004235

R-OVARC1000853

RPCI11-16C11.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16C11, genomic survey sequence.

5.3e-53:317:92

35

B76661

R-OVARC1000873

Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.

40

1.2e-102:511:97

AL034418

R-OVARC1000916

H.sapiens PISSLRE mRNA.

45

5.8e-111:588:94

X78342

R-OVARC1000956

Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.

50

2.7e-89:478:94

Z69708

R-OVARC1000995

Human DNA sequence from clone 885E17 on chromosome 1p33-34.1. Contains STSs and GSSs and genomic marker D1S1302, complete sequence.

55

9.5e-46:325:84

AL031294

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- 5 R-OVARC1001030
Homo sapiens neuroendocrine-specific protein C (NSP) mRNA, complete cds.
1.2e-05:197:63
L10335
- R-OVARC1001049
- R-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds.
10 4.3e-105:569:94
AF048731
- R-OVARC1001132
Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.
15 2.2e- 111:569:96
AP000038
- R-OVARC1001163
Sus scrofa MHC SLA class III steroid 21-hydroxylase (CYP21) gene, complete cds, ORF human-like gene, last 5
20 exons.
0.010:349:60
M83939
- R-OVARC1001222
25 Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived
ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.
0.58:184:60
U28972
- R-OVARC1001260
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
30 1.1e-10:140:78
AC004909
- R-OVARC1001336
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
35 2.3e-10:140:77
AC004909
- R-OVARC1001338
- R-OVARC1001569
- R-OVARC1001570
- R-OVARC1001596
Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
45 5.9e-47:361:83
AC005951
- R-OVARC1001607
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
50 3.3e-112:559:96
U15128
- R-OVARC1001725
Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
55 3.9e-56:318:95

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AF064800

R-OVARC1001727

Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.
6.1e-101:533:94
AL031132

R-OVARC1001807

Human TR3 orphan receptor mRNA, complete cds.
2.8e-87:426:97
L13740

R-OVARC1001833

Mouse fork head related protein (HNF-3beta) mRNA, complete cds.
1.1e-21:263:76
L10409

R-OVARC1001991

H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 301e3, reverse read 301e3.r.
0.90:151:59
Z79826

R-OVARC1002058

Homo sapiens full length insert cDNA clone ZD58C02.
1.9e-105:547:95
AF088043

R-OVARC1002178

Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.
0.26:429:58
AL031053

R-PLACE1000033

Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.098:467:59
AC004688

R-PLACE1000231

Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.
0.91:141:64
AC003083

R-PLACE1000258

Human DNA sequence from clone 710L4 on chromosome Xq11.2-12 Contains part of a gene similar to myotubularin-related protein, EST, STS and GSS, complete sequence.
3.8e-53:524:75
AL034408

R-PLACE1000442

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence.
3.0e-07:413:62
AB016873

R-PLACE1000560

Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.
6.3e-59:323:94

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AC005368

R-PLACE1000740
H.sapiens PEX gene.
0.0065:202:63
Y10196

R-PLACE1000912

R-PLACE1000914
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
3.4e-68:452:86
AC002093

R-PLACE1000927
Cowpox virus strain GRI-90 DNA (49 kb fragment).
1.8e-46:432:76
Y15035

R-PLACE1000986
HS_2037_A2_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=12 Row=C, genomic survey sequence.
0.087:48:89
AQ232754

R-PLACE1001016
M.fascicularis gene for apolipoprotein A-IV.
0.016:226:61
X68361

R-PLACE1001100
Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear in-
hibitor of protein phosphatase-1, ESTs, and a CA repeat.
3.4e-37:320:80
AL020997

R-PLACE1001114
RPC111-5C23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5C23, genomic survey sequence.
9.2e-44:173:85
B49180

R-PLACE1001123

R-PLACE1001183
Plasmodium falciparum MAL3P8, complete sequence.
0.47:217:63
AL034560

R-PLACE1001229
Mitochondrion Culex torrentium A+T rich mitochondrial control region.
3.3e-09:356:63
U69573

R-PLACE1001231
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
1.2e-09:186:72
AF026554

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R-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds.

2.0e-51:265:98

AB018262

R-PLACE1001401

Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.

0.0073:203:60

AF033929

R-PLACE1001407

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

5.8e-70:360:96

AL023582

R-PLACE1001464

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

3.1e-90:457:96

X55740

R-PLACE1001500

Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.

1.0:232:62

AC004929

R-PLACE1001516

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.

1.9e-26:168:88

AC002425

R-PLACE1001536

Human Chromosome X clone bWXD187, complete sequence.

6.5e-61:310:98

AC004383

R-PLACE1001564

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.

2.9e-100:504:97

AL033377

R-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K⁺ channel alpha subunit (KCNS3) mRNA, complete cds.

3.8e-1 17:578:97

AF043472

R-PLACE1001788

Sequence 9 from Patent WO9722695.

1.9e-05:91:82

A63556

R-PLACE1001795

R-PLACE1001836

, complete sequence.

4.1e-14:269:69

AC005406

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R-PLACE1001918

Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.

7.3e-25:151:95

D17237

5

R-PLACE1001949

Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR1S1). Contains ESTs, an STS and GSSs, complete sequence.

10

0.54:165:63

Z94056

R-PLACE1002080

Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.

15

3.7e-60:289:95

AC004150

R-PLACE1002095

Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-52, complete sequence.

20

0.00052:422:59

AL008982

R-PLACE1002153

Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.

25

4.6e-100:514:95

AF095791

R-PLACE1002329

Homo sapiens chromosome 19, cosmid R31855, complete sequence.

30

1.3e-46:257:95

AC005782

R-PLACE1002355

HS_2057_B1_D01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2057 Col=1 Row=H, genomic survey sequence.

35

0.089:132:65

AQ245227

R-PLACE1002374

Human mRNA for pro-cathepsin L (major excreted protein MEP).

40

2.6e-101:501:97

X12451

R-PLACE1002518

HS_2176_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=8 Row=G, genomic survey sequence.

45

1.7e-43:221:100

AQ014851

R-PLACE1002547

Homo sapiens mRNA for KIAA0719 protein, complete cds.

50

2.0e-53:276:97

AB018262

R-PLACE1002726

Human DNA-binding protein ABP/ZF mRNA, complete cds.

55

1.1e-37:212:94

U82613

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R-PLACE1002905

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SE-
QUENCE.

1.2e-42:302:86

AL034417

R-PLACE1002911

R-PLACE1002967

Homo sapiens chromosome 16, BAC clone 461A8, complete sequence.

2.3e-39:310:82

AC006111

R-PLACE1003135

Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.

2.2e-07:418:60

AL034557

R-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

4.7e-110:547:96

AF069301

R-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

1.7e-47:287:91

AF068227

R-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2,
ESTs, GSSs,, complete sequence.

1.1e-75:268:98

AL032821

R-PLACE1003438

R-PLACE1003460

HS_3026_B1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026
Col=15 Row=B, genomic survey sequence.

0.30:100:69

AQ093523

R-nnnnnnnnnnnnn

Homo sapiens clone DJ0981007, complete sequence.

3.3e-46:135:98

AC006017

R-PLACE1003573

HS_3079_B2_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079
Col=4 Row=B, genomic survey sequence.

1.1e-49:261:96

AQ121751

R-PLACE1003598

R-PLACE1003644

Caenorhabditis elegans cosmid F52H3, complete sequence.

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0.38:345:62
Z66512

R-PLACE1003737

5 Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.
1.9e-77:406:96
AC005859

R-PLACE1003772

10 Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.
2.2e-29:454:70
AL020997

R-PLACE1003839

15 Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
3.0e-52:272:97
AC004131

R-PLACE1003845

20 HS_3219_A1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=19 Row=A, genomic survey sequence.
1.5e-13:231:70
AQ181482

R-PLACE1003852

25 Homo sapiens mRNA for KIAA0758 protein, partial cds.
6.8e-86:439:96
AB018301

R-PLACE1004028

R-PLACE1004078

30 Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
5.0e-36:310:80
AC006064

R-PLACE1004166

40 Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.
0.95:224:62
U19361

R-nnnnnnnnnnnnn

45 Fugu rubripes GSS sequence, clone 076D01bH10, genomic survey sequence.
3.0e-08:107:77
AL026605

R-PLACE1004199

50 Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.
0.0028:157:67
M98538

R-PLACE1004279

55 Human DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3. Contains histone H2A/d, H2B/d, H2A.i, H1.5, H3.F, H4.k, H3/j genes, histone pH2b.i and hypothetical protein A4 pseudogenes, histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene, olfactory receptor OL1 like gene, ESTs STSs and predicted CpG islands.

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0.00065:228:58
Z98744

R-PLACE1004282

R-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds.
2.0e-77:377:99
AB018283

R-PLACE1004441
RPCI11-76P13.TV RPCI11 Homo sapiens genomic clone R-76P13, genomic survey sequence.
1.8e-73:370:97
AQ281810

R-PLACE1004450
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.
0.87:269:59
AB012242

R-PLACE1004482
Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete cds.
5.2e-33:356:75
AF009513

R-PLACE1004492
Mus musculus mRNA for Doc2, partial cds.
4.1e-28:268:77
D50000

R-PLACE1004519
Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.
1.8e-14:330:67
AL021808

R-PLACE1004520
Human pregnancy specific beta-1-glycoprotein 1 (PSG1) gene.
1.4e-73:397:93
M93705

R-PLACE1004630

R-PLACE1004637
Human Chromosome 11 Cosmid cSRL16b6, complete sequence.
5.5e-108:625:91
U73638

R-PLACE1004648

R-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds.
5.6e-103:586:90
D88587

R-PLACE1004887
CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.

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1.2e-31:177:97
B99962

5 R-PLACE1005003
Mus musculus clone OST13719, genomic survey sequence.
0.0043:159:64
AF046703

10 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.
2.1e-56:299:95
AF032456

15 R-PLACE1005031
Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.
1.0:155:65
AC005821

20 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).
4.4e-85:450:93
AJ223351

25 R-PLACE1005250
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
7.7e-19:232:73
U50734

30 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds.
2.0e-77:471:88
AF093118

35 R-PLACE1005410
Canis familiaris sec61 homologue mRNA, complete cds.
6.4e-12:132:82
M96629

40 R-PLACE1005426
Human pregnancy specific beta-1-glycoprotein 4 (PSG4) mRNA, complete cds.
2.3e-109:574:94
M94891

45 R-PLACE1005519
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
4.1e-08:426:61
AL034557

50 R-PLACE1005539

R-PLACE1005544
Homo sapiens chromosome 19, cosmid F20887, complete sequence.
1.0e-17:202:73
55 AC005578

R-PLACE1005569
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

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3.8e-89:470:95
AL034397

R-PLACE 1005601
Homo Sapiens angiotensin II receptor gene, complete cds.
8.0e-52:301:90
L48211

R-PLACE1005660

R-PLACE1005669
Mitochondrion Culex torrentium A+T rich mitochondrial control region.
9.5e-09:338:63
U69573

R-PLACE1005682
Caenorhabditis elegans cosmid M70.
0.012:226:62
AF047661

R-PLACE1005725
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48E1, WORKING DRAFT SE-
QUENCE.
0.42:435:59
Z92856

R-PLACE1005736
Rattus norvegicus DD6A4-1 mRNA, partial sequence.
9.0e-21:282:73
AF034237

R-PLACE1005745
RPC11-88L20.TJ RPC11 Homo sapiens genomic clone R-88L20, genomic survey sequence.
2.4e-62:310:99
AQ281511

R-PLACE1005768
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
5.6e-94:511:93
Z82185

R-PLACE1005815
Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.
9.0e-55:586:73
AC002310

R-PLACE1005878

R-PLACE1005927

R-PLACE1006071
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
1.6e-76:410:95
AQ022149

R-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds.
2.2e-97:513:93

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AB009598

R-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5.4e-57:333:91

AF028233

R-PLACE1006093

R-nnnnnnnnnnnnn

Caenorhabditis elegans mRNA for GAP-2-7, partial cds.

1.9e-08:251:60

AB011283

R-PLACE1006219

HS_3219_A1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219

Col=19 Row=A, genomic survey sequence.

3.1e-12:228:69

AQ181482

R-PLACE1006277

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

7.8e-96:557:91

AL034397

R-PLACE1006290

Bacillus whitei clone pWH/CugI satellite DNA.

0.37:209:62

U90159

R-PLACE1006443

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

8.9e-76:451:91

AC002093

R-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds.

2.1e-76:413:94

AB011148

R-PLACE1006716

M.musculus gene encoding prostaglandin D synthase, putative.

1.0:199:59

Y10138

R-PLACE1006786

HS_2037_A2_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037

Col=12 Row=C, genomic survey sequence.

0.33:47:91

AQ232754

R-PLACE1006809

Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.

0.67:241:59

U52112

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R-PLACE1006959

R-PLACE1007028

5 R-PLACE1007040
Rabbit angiotensin-converting enzyme (ACE-P) gene, 5' end.
0.0037:208:65
M58579

10 R-PLACE1007077
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
3.0e-76:411:94
AQ022149

15 R-PLACE1007081
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
1.9e-06:88:84
AQ016433

20 R-PLACE1007096
H.sapiens DMD gene microsatellite (147-200bp).
1.0:142:59
X77677

25 R-PLACE1007296

R-PLACE1007591
Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.
30 1.6e-11:203:66
AL023574

R-PLACE1007626
Homo sapiens unknown mRNA, complete cds.
35 4.9e-29:183:91
AF047439

R-PLACE1007702
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
40 2.3e-75:445:90
AC002348

R-PLACE1007845
CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
45 0.00045:194:64
AQ022229

R-PLACE1007881
CITBI-E1-2503C21.TF CITBI-E1 Homo sapiens genomic clone 2503C21, genomic survey sequence.
50 0.43:104:69
AQ263355

R-PLACE1007971

55 R-PLACE1008282
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.
7.7e-73:396:94
AC005995

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R-PLACE1008297

N.frontalis enolase gene, promotor region.

1.2e-08:457:57

X81451

R-PLACE1008359

Plasmodium falciparum MAL3P1, complete sequence.

0.00044:443:56

Z97348

R-PLACE1008469

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

4.4e-78:536:84

AC002093

R-PLACE1008549

Mus musculus E74-like factor 5 (Elf5) mRNA, complete cds.

3.4e-30:256:75

AF049702

R-PLACE1008657

Homo sapiens BAC clone GS067A24 from 7q21.q21.2, complete sequence.

1.9e-40:320:82

AC005009

R-PLACE1008716

Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.

8.2e-118:591:96

U15128

R-PLACE1008744

Sequence 1 from patent US 5691147.

3.le-108:559:94

I76197

R-PLACE1008984

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.

1.6e-102:503:96

AL031427

R-PLACE1008985

Mus musculus synaptotagmin VIII mRNA, partial cds.

9.7e-29:255:77

U20107

R-PLACE1009067

R-PLACE1009196

Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SE-
QUENCE.

0.0094:206:65

Z92854

R-PLACE1009279

Homo sapiens serine protease (PRSS11) mRNA, partial cds.

2.4e-26:553:62

AF097709

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R-PLACE1009527

Human DNA-binding protein ABP/ZF mRNA, complete cds.

7.9e-91:497:91

U82613

R-PLACE1009546

Human PAC clone DJ218B13 from Xq23, complete sequence.

0.29:147:64

AC002072

R-PLACE1009600

Mouse mRNA for tetracycline transporter-like protein, complete cds.

6.1e-81:466:90

D88315

R-PLACE1009735

Homo sapiens clone NH0523H20, complete sequence.

2.0e-74:268:99

AC005041

R-nnnnnnnnnnnnn

Homo sapiens DNA sequence from PAC 833B2 on chromosome Xq26.1-27.2. Contains an EST, complete sequence.

1.9e-05:255:65

AL023800

R-PLACE1010011

, complete sequence.

2.9e-77:174:100

AC005409

R-PLACE1010078

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING DRAFT SEQUENCE.

1.0:108:65

Z84465

R-PLACE1010081

Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.

9.2e-105:560:93

AF027706

R-PLACE1010251

Plasmodium falciparum MAL3P4, complete sequence.

5.0e-07:468:58

AL008970

R-PLACE1010445

Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.

1.2e-49:303:90

AF077058

R-PLACE1010713

RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.

7.4e-11:114:80

AQ238297

R-PLACE1010784

Capra hircus strain Saanen, genomic survey sequence.

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7.4e-24:182:87
AF083406

R-PLACE1010827

5 nbxb0026K23f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026K23f, genomic survey sequence.
1.0:252:61
AQ271546

R-PLACE1010968

10 Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.0038:295:57
AC005308

R-PLACE1011045

15 Homo sapiens E1-like protein mRNA, complete cds.
1.6e-90:453:96
AF094516

R-PLACE1011116

20 Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds.
4.6e-72:385:94
AF006621

R-PLACE1011236

25 *** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0289H06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.98:142:65
AC004580

R-PLACE1011364

R-PLACE1011407

35 Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some
similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1).
Contains GSSs, complete sequence.
9.1e-27:293:74
AL031575

R-PLACE1011516

40 Fugu rubripes GSS sequence, clone 190N14aC12, genomic survey sequence.
1.0:96:68
AL030602

R-PLACE1011708

45 Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
2.4e-91:521:91
AF034611

R-PLACE1011824

50 Figure 6. DNA sequence of three 3'apoB VNTR alleles.
2.2e-06:264:65
M23046

R-PLACE1011978

55 Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.
4.8e-50:553:69
M27877

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R-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

3.9e-107:567:94

AL022578

R-PLACE2000219

Homo sapiens clone RG132J19, complete sequence.

4.7e-39:317:82

AC005163

R-PLACE3000181

Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8.

3.9e-81:441:94

L11369

R-PLACE3000213

Sequence 1 from patent US 5691147.

1.5e-109:559:95

I76197

R-PLACE4000354

Sequence 1 from patent US 5691147.

2.7e-106:548:95

I76197

R-PLACE4000455

Arabidopsis thaliana genomic DNA chromosome 3, P1 clone: MEBS, complete sequence.

9.3e-07:357:60

AB019230

R-THYRO1000036

Sequence 11 from patent US 5773248.

4.0e-99:527:93

AR014074

R-THYRO1000061

Homo sapiens chromosome 19, cosmid R34382, complete sequence.

7.3e-90:460:96

AC005329

R-THYRO1000099

R-THYRO1000196

Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.

1.1e-104:530:96

AF016272

R-THYRO1000400

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.

1.0:308:61

AC004685

R-THYRO1000580

Human Kox26 mRNA for zinc finger protein, partial.

0.11:105:67

X52357

R-THYRO1000584

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.

1.4e-14:241:68

AC004480

R-THYRO1000678

Belonogaster petiolata 16S ribosomal RNA gene, mitochondrial gene for mitochondrial rRNA, partial sequence.

0.049:150:64

AF066910

R-THYRO1000776

CITBI-E1-2505N5.TF.1 CITBI-E1 Homo sapiens genomic clone 2505N5, genomic survey sequence.

0.38:179:63

AQ241670

R-THYRO1000795

R-THYRO1000846

Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.

3.6e-06:425:61

AF029779

R-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds.

4.0e-42:251:92

AF015913

R-THYRO1000956

R-THYRO1000964

Human Chromosome 11 Cosmid cSRL186g7, complete sequence.

0.18:292:61

U73627

R-THYRO1000999

CIT-HSP-2288E24.TR CIT-HSP Homo sapiens genomic clone 2288E24, genomic survey sequence.

3.6e-18:292:71

AQ002356

R-THYRO1001063

Homo sapiens chromosome 16 BAC clone CIT987SK-381E11 complete sequence.

1.5e-27:292:76

AF001552

R-THYRO1001071

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.

1.7e-105:513:98

Z83844

R-THYRO1001102

Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.

3.2e-62:429:86

AC004832

R-THYRO1001113

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Caenorhabditis elegans cosmid C25F9, complete sequence.
0.026:338:58
Z81476

5 R-THYRO1001128
Homo sapiens chromosome 9q34, clone 63G10, complete sequence.
5.3e-12:132:79
AC002096

10 R-THYRO1001205
Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.
1.9e-60:251:85
AC004987

15 R-THYRO1001237

R-THYRO1001242
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
1.5e-45:525:75
20 D67067

R-THYRO1001266
H.sapiens DNA containing a polymorphic (CA)_n repeat (436bp).
6.0e-05:258:67
25 X65457

R-THYRO1001327
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
2.8e-104:541:95
30 AL021578

35 R-THYRO1001456

R-THYRO1001457
H.sapiens mRNA for protein kinase C mu.
2.9e-23:391:66
40 X75756

R-THYRO1001471
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence.
0.39:271:61
45 AC004787

R-THYRO1001478

R-THYRO1001495
Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
2.8e-88:446:88
50 AC006006

R-THYRO1001523
CIT-HSP-2333F9.TF CIT-HSP Homo sapiens genomic clone 2333F9, genomic survey sequence.
1.4e-05:126:71
55 AQ039390

R-THYRO1001529

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5
R-THYRO1001593
Homo sapiens chromosome 19, cosmid R33632, complete sequence.
3.7e-100:514:96
AC005781

10
R-THYRO1001608
Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.
2.3e-40:369:79
AC004845

15
R-THYRO1001641
Homo sapiens clone 24448 unknown mRNA, partial cds.
3.4e-110:562:96
AF070638

20
R-THYRO1001700

R-THYRO1001702
Mus musculus mRNA for myeloid associated differentiation protein.
1.1e-11:367:66
AJ001616

25
R-THYRO1001725
Homo sapiens, clone hRPK.1_A_1, complete sequence.
9.1e-12:329:65
AC006196

30
R-THYRO1001770
Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence..
0.12:339:59
AC004879

35
R-THYRO1001803

R-Y79AA1000030
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
2.0e-98:515:95
AC005214

40
R-Y79AA1000127
Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.
3.2e-115:551:99
AP000034

45
R-Y79AA1000207
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
1.8e-38:282:85
AC005562

50
R-Y79AA1000226
Homo sapiens full length insert cDNA YN52F10.
4.8e-09:104:85
AF075033

55
R-Y79AA1000270
Human mRNA for ORF, Xq terminal portion.
1.0e-105:564:93
D16469

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- 5 R-Y79AA1000426
Rattus norvegicus activin beta E mRNA, complete cds.
6.1e-50:562:72
AF089825
- 10 R-Y79AA1000521
Rattus norvegicus steroid sulfatase (Sts) mRNA, complete cds.
0.48:233:62
U37138
- 15 R-Y79AA1000750
Human DNA from cosmid f23280 from chromosome 19q13.2, genomic sequence.
6.8e-07:320:60
L47334
- 20 R-Y79AA1000776
R-Y79AA1000777
Homo sapiens full length insert cDNA clone ZD93D10.
2.9e-110:574:95
AF088072
- 25 R-Y79AA1000876
Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.
0.0096:105:71
U73520
- 30 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.
1.0e-78:453:92
AF093420
- 35 R-Y79AA1000967
Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.
2.3e-43:263:84
L22557
- 40 R-Y79AA1001013
R-Y79AA1001056
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
1.5e-22:269:73
U50734
- 45 R-Y79AA1001062
D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.
1.1e-07:494:57
X54011
- 50 R-Y79AA1001090
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.
1.2e-26:269:77
AC002300
- 55 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds.
5.7e-82:407:97
AF038961

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R-Y79AA1001264

HS_2195_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195
Col=14 Row=A, genomic survey sequence.

3.4e-07:101:82

AQ191092

R-Y79AA1001272

Hansenula wingei mitochondrial DNA, complete sequence.

2.1e-05:435:60

D31785

R-Y79AA1001328

Rattus norvegicus Delta 3 mRNA, complete cds.

1.0e-29:356:72

AF084576

R-Y79AA1001426

R-Y79AA1001430

Homo sapiens mRNA for KIAA0469 protein, complete cds.

6.2e-111:555:96

AB007938

R-Y79AA1001523

Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.

3.7e-71:259:90

Z84480

R-Y79AA1001530

Human beta-tubulin gene (5-beta) with ten Alu family members.

2.6e-56:301:96

X00734

R-Y79AA1001592

HS_2175_A2_B11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175
Col=22 Row=C, genomic survey sequence.

1.0:237:59

AQ307634

R-Y79AA1001727

R-Y79AA1001787

Homo sapiens mRNA for putative ATPase, partial.

7.2e-80:405:97

AJ009947

R-Y79AA1001795

Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.

4.2e-110:555:97

AL031228

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R-Y79AA1001799

R-Y79AA1001803

Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.

6.2e-60:499:77

U02983

R-Y79AA1001863

Human DNA sequence from PAC 365E2 on chromosome 6p22.3-24.1. Contains EST and STS.

1.4e-45:261:75

AL009177

R-Y79AA1002022

H.sapiens mRNA for basement membrane heparan sulfate proteoglycan.

1.0:311:61

X62515

R-nnnnnnnnnnnnn

Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence.

1.0:208:62

AE001381

R-nnnnnnnnnnnnn

Homo sapiens DNA, trinucleotide repeats region, clone CAG83.

0.17:132:67

AB018494

R-Y79AA1002213

Human DNA sequence from PAC 340G1 on chromosome 6 contains STS.

5.6e-46:490:73

Z84719

R-Y79AA1002334

Japanese Quail (C.coturnix) troponin T isoform mRNA, clone cC501.

0.96:210:63

M26599

R-Y79AA1002373

Human BAC clone RG126M09 from 7q21-q22, complete sequence.

9.7e-82:544:85

AC002067

R-Y79AA1002376

Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.

1.9e-111:546:97

M10546

R-Y79AA1002378

Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.

1.5e-33:244:74

D10630

R-Y79AA1002381

Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.

0.0046:177:68

Z95152

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Homology search result 8.

[0300] The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 5'-ends.

5
Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
10 the Accession No. of the top hit data.

[0301] Data were not shown for the clones in which the P-value was higher than 1.

15 F-BNGH41000020
ESTs
6.6e-72:412:92
Hs.153375:AI287812

20 F-BNGH41000087
Homo sapiens mRNA for MIFR-1, complete cds
0.027:499:57
Hs.58269:AB010962

25 F-BNGH41000091
Homo sapiens voltage-gated potassium channel eag (EAG) mRNA, complete cds
5.2e-81:687:76
Hs.158305:AJ001366

30 F-HEMBA1000006
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cere-
visiae]
2.0e-25:167:91
Hs.9252:R53360

35 F-HEMBA1000121
ESTs, Moderately similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis
elegans]
3.0e-34:180:98
Hs.149509:N24022

40 F-HEMBA1000128
EST
0.00069:177:62
Hs.158854:AI377837

45 F-HEMBA1000275
Human modulator recognition factor I (MRF-1) mRNA, 3'end
0.012:508:58
Hs.920:M62324

50 F-HEMBA1000300
Human mRNA for KIAA0355 gene, complete cds
1.6e-46:402:78
Hs.153014:AB002353

55 F-HEMBA1000349
EST
6.7e-08:65:95

	Hs.54372:N80032
	F-HEMBA1000443
	ESTs
5	6.1e-23:278:76
	Hs.69492:AA116026
	F-HEMBA1000462
10	F-HEMBA1000477
	ESTs
	6.9e-78:414:94
	Hs.152861:AA287444
15	F-HEMBA1000590
	Homo sapiens mRNA for matrilin-4, partial
	7.3e-95:482:96
	Hs.129361:AJ007581
20	F-HEMBA1000634
	ESTs
	1.3e-38:246:86
	Hs.6145:W26640
25	F-HEMBA1000671
	Zinc finger protein 140 (clone pHZ-39)
	2.4e-53:469:68
	Hs.154205:U09368
30	F-HEMBA1000713
	Homo sapiens 10kD protein (BC10) mRNA, complete cds
	2.1e-127:442:97
	Hs.5300:AF053470
35	F-HEMBA1000732
	Homo sapiens latent transforming growth factor-beta binding protein 4S mRNA, complete cds
	1.0e-45:258:94
	Hs.85087:AF051344
40	F-HEMBA1000745
	Human cardiotrophin-1 (CTF1) mRNA, complete cds
	1.1e-07:316:61
	Hs.25537:U43030
45	F-HEMBA1000835
	ESTs
	4.2e-11:188:72
	Hs.116265:A1184988
50	F-HEMBA1000875
	Zinc finger protein 133 (clone pHZ-13)
	1.5e-27:169:93
	Hs.78434:U09366
55	F-HEMBA1000907
	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
	1.3e-06:545:60
	Hs.143551:AF048693

F-HEMBA1000940

Homo sapiens connexin46.6 (Cx46.6) gene, complete cds

4.1e-18:307:66

Hs.100072:AF014643

5

F-HEMBA1000962

Homo sapiens mRNA for MEGF8, partial cds

0.0018:391:62

Hs.158200:AB011541

10

F-HEMBA1001184

Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds

2.7e-24:404:67

Hs.14368:AF042081

15

F-HEMBA1001221

Human transmembrane protein mRNA, complete cds

7.7e-44:858:63

Hs.78531:U19878

20

F-HEMBA1001228

Human germline oligomeric matrix protein (COMP) mRNA, complete cds

2.2e-85:463:93

Hs.1584:AC003107

25

F-HEMBA1001272

Antidiuretic hormone receptor

0.064:616:57

Hs.2524:L22206

30

F-HEMBA1001296

Homo sapiens delta-catenin mRNA, complete cds

0.031:410:59

Hs.80220:U96136

35

F-HEMBA1001297

Homo sapiens putative transcription factor CA150 mRNA, complete cds

3.0e-15:143:81

Hs.13063:AF017789

40

F-HEMBA1001390

ESTs, Highly similar to polymerase I-transcript release factor [M.musculus]

1.6e-49:297:91

Hs.25581:AI246284

45

F-HEMBA1001563

ESTs

4.9e-12:160:74

Hs.162813:AA524616

50

F-HEMBA1001621

Human P2U nucleotide receptor mRNA, complete cds

0.00098:314:61

Hs.339:U07225

55

F-HEMBA1001878

Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds

3.4e-172:810:98

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Hs.10290:AF090988

F-HEMBA1001886

Human repressor transcriptional factor (ZNF85) mRNA, complete cds

1.1e-115:849:80

Hs.37138:U35376

F-HEMBA1002048

Homo sapiens mRNA for APC 2 protein, complete cds

0.96:266:62

Hs.20912:AB012162

F-HEMBA1002131

Homo sapiens mRNA for KIAA0584 protein, partial cds

1.1e-45:709:66

Hs.106794:AB011156

F-HEMBA1002163

ASPARTYL-TRNA SYNTHETASE

0.026:568:58

Hs.80758:J05032

F-HEMBA1002164

Pregnancy-associated plasma protein A

0.0049:274:60

Hs.158229:U28727

F-HEMBA1002167

F-HEMBA1002178

Homo sapiens mRNA for KIAA0584 protein, partial cds

8.3e-48:794:65

Hs.106794:AB011156

F-HEMBA1002195

EST

2.0e-05:177:70

Hs.145935:AI275921

F-HEMBA1002227

Myristoylated alanine-rich C-kinase substrate

1.2e-138:382:95

Hs.75607:D10522

F-HEMBA1002239

Homo sapiens mRNA, chromosome I specific transcript KIAA0488

1.2e-47:570:71

Hs.67619:AB007957

F-HEMBA1002316

EST

1.8e-28:246:79

Hs.136950:AA825638

F-HEMBA1002420

Homo sapiens GABA-B receptor mRNA, complete cds

1.7e-05:303:63

Hs.12307:AF056085

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F-HEMBA1002421

Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)

4.3e-167:778:98

Hs.1501:J04621

5

F-HEMBA1002524

Human MHC Class I region proline rich protein mRNA, complete cds

8.5e-128:751:89

Hs.41548:U63336

10

F-HEMBA1002551

ESTs

2.4e-25:207:84

Hs.158172:N24325

15

F-HEMBA1002767

Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds

4.4e-170:798:98

Hs.19154:AF038660

20

F-HEMBA1002985

ESTs

2.6e-09:124:76

Hs.118620:T60326

25

F-HEMBA1002992

ESTs

2.4e-21:121:97

Hs.143571:AI089396

30

F-HEMBA1003047

Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds

1.5e-188:873:99

Hs.148318:AF034611

35

F-HEMBA1003072

ESTs

1.2e-33:387:71

Hs.59628:W91959

40

F-HEMBA1003101

Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds

1.7e-140:671:98

Hs.26350:AF049891

45

F-HEMBA1003120

Zinc finger protein 91 (HPF7, HTF10)

1.0e-24:143:76

Hs.8597:L11672

50

F-HEMBA1003230

Homo sapiens UP50 mRNA, complete cds

1.8e-184:856:98

Hs.11494:AF093118

55

F-HEMBA1003294

Human antiseecretory factor-1 mRNA, complete cds

5.1e-45:324:83

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Hs.148495:AF050199

F-HEMBA1003315

Homo sapiens mRNA for TIP49, complete cds

4.2e-19:377:64

Hs.155541:AF070735

F-HEMBA1003392

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds

9.2e-185:851:99

Hs.23672:AF074264

F-HEMBA1003399

H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase

0.00042:297:61

Hs.118929:X79568

F-HEMBA1003487

Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds

0.0011:237:63

Hs.88145:AF030339

F-HEMBA1003497

ESTs, Weakly similar to similar to zinc finger 5 protein from Gallus gallus, U51640 [H.sapiens]

2.5e-09:303:63

Hs.143723:H86048

F-HEMBA1003530

Homo sapiens mRNA for ephrin-A2

0.024:396:60

Hs.158306:AJ007292

F-HEMBA1003602

Homo sapiens DNA from chromosome 19, cosmid R29144

0.0072:663:57

Hs.155647:AC004221

F-HEMBA1003732

ESTs

1.0e-106:494:100

Hs.157568:AI356515

F-HEMBA1003945

Homo sapiens clone 638 unknown nRNA, complete sequence

5.9e-78:310:93

Hs.159515:AF091085

F-HEMBA1004007

PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC

0.56:165:64

Hs.115742:AF077754

F-HEMBA1004067

Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]

0.048:581:58

Hs.83190:U29344

F-HEMBA1004085

ESTs

1.7e-15:92:98

Hs.98138:AI183561

- 5 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds
1.2e-159:779:96
Hs.66392:AF064244
- 10 F-HEMBA1004250
Human mRNA for KIAA0327 protein, complete cds
2.1e-23:676:59
Hs.149323:AB002325
- 15 F-HEMBA1004391
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR
0.43:157:63
Hs.1757:U52112
- 20 F-HEMBA1004444
H.sapiens mRNA for gp25L2 protein
1.5e-54:544:73
Hs.159569:X90872
- 25 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds
1.1e-05:230:62
Hs.20709:AF065389
- 30 F-HEMBA1004505
ESTs
9.1e-61:345:93
Hs.4814:AA631254
- 35 F-HEMBA1004785
Homo sapiens Polycomb 2 homolog (hPc2) mRNA, complete cds
3.7e-18:294:65
Hs.123085:AF013956
- 40 F-HEMBA1004797
ESTs
3.9e-06:107:73
Hs.42302:AI032142
- 45 F-HEMBA1004952
Human cardiotrophin-1 (CTF1) mRNA, complete cds
0.00021:175:68
Hs.25537:U43030
- 50 F-HEMBA1004971

F-HEMBA1004982
Human metabotropic glutamate receptor 8 mRNA, complete cds
0.31:288:60
- 55 F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds

7.9e-67:370:93
Hs.5716:AB002308

5 F-HEMBA1005084
Homo sapiens mRNA for KIAA0612 protein, partial cds
0.00022:400:59
Hs.112499:AB014512

10 F-HEMBA1005145
Lymphocyte-activation gene 3
3.4e-05:480:59
Hs.74011:X51985

15 F-HEMBA1005230
ESTs
2.3e-103:481:99
Hs.135112:AI090827

20 F-HEMBA1005246
Homo sapiens ALR mRNA, complete cds
2.0e-05:220:62
Hs.153638:AF010403

25 F-HEMBA1005267
ESTs
5.6e-16:305:64
Hs.125699:AA868017

30 F-HEMBA1005337
EST
2.1e-59:304:97
Hs.48956:N64339

35 F-HEMBA1005430
ESTs
6.9e-19:333:65
Hs.116567:AI332643

40 F-HEMBA1005449
Human plectin (PLEC1) mRNA, complete cds
0.026:576:56
Hs.79706:U53204

45 F-HEMBA1005489
Homo sapiens mRNA for KIAA0291 gene, partial cds
0.14:551:59
Hs.104717:AB006629

50 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR
1.8e-12:298:64
Hs.36989:M13232

55 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
2.6e-143:672:98
Hs.7138:U29589

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F-HEMBA1005698
 ESTs
 1.8e-124:611:97
 Hs.144441:AI338335
 5 F-HEMBA1005913

 F-HEMBA1005929
 H.sapiens mRNA for serine/threonine protein kinase EMK
 10 1.5e-86:847:72
 Hs.157199:X97630

 F-HEMBA1005945
 ESTs, Weakly similar to F17E5.2 [C.elegans]
 15 4.2e-26:159:92
 Hs.126571:AI038963

 F-HEMBA1006016
 ESTs
 20 1.3e-22:145:93
 Hs.33728:H97503

 F-HEMBA1006171

 25 F-HEMBA1006276
 Homo sapiens KIAA0412 mRNA, partial cds
 5.1e-19:371:65
 Hs.6200:AB007872

 30 F-HEMBA1006299

 F-HEMBA1006311

 F-HEMBA1006335
 35 ESTs
 0.00021:327:62
 Hs.146044:AI089998

 F-HEMBA1006357
 40 Homo sapiens secretory carrier mernbrane protein (SCAMP2) mRNA, complete cds
 7.4e-28:389:67
 Hs.10761:AF005038

 F-HEMBA1006430
 45 ESTs
 9.7e-92:463:95
 Hs.143702:AI084062

 F-HEMBA1006482
 50 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
 6.2e-146:575:98
 Hs.14511:AF026852

 F-HEMBA1006517
 55 ESTs
 3.6e-63:381:87
 Hs.11611:W21919

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F-HEMBA1006544

Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds

2.0e-50:503:76

Hs.43543:AF042800

5

F-HEMBA1006572

Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit

0.031:611:57

Hs.96253:U79666

10

F-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds

1.2e-128:646:95

Hs.3628:AB014587

15

F-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial

1.7e-101:476:98

Hs.129361:AJ007581

20

F-HEMBA1006724

ESTs

8.3e-86:450:95

Hs.10056:AA210796

25

F-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial

6.1e-97:457:98

Hs.129361:AJ007581

30

F-HEMBA1006770

ESTs, Highly similar to BRAIN PROTEIN F41 [Mus musculus]

1.6e-31:237:85

Hs.31612:H41366

35

F-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial

9.4e-113:541:97

Hs.129361:AJ007581

40

F-HEMBA1006912

ESTs

1.4e-94:460:97

Hs.88672:AA279956

45

F-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds

5.2e-120:651:92

Hs.83070:L76687

50

F-HEMBA1006960

Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds

0.011:628:57

Hs.159234:U89995

55

F-HEMBA1007013

ESTs

2.6e-05:139:69

Hs.113817:AA702497

F-HEMBA1007057

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds

5 7.5e-12:389:64

Hs.143641:AB009462

F-HEMBA1007063

10 F-HEMBA1007226

ESTs

1.8e-35:202:94

Hs.105140:N32669

15 F-HEMBA1007241

ESTs, Weakly similar to No definition line found [C.elegans]

4.1e-27:361:67

Hs.114062:AI421699

20 F-HEMBA1007291

ESTs

0.96:114:69

Hs.121411:AA770241

25 F-HEMBA1007332

ESTs, Weakly similar to hTAFII100 [H.sapiens]

2.5e-81:405:97

Hs.3727:AA205887

30 F-HEMBA1000106

ESTs

2.2e-76:393:96

Hs.151874:AI023405

35 F-HEMBA1000276

EST

0.81:239:63

Hs.149811:AI286277

40 F-HEMBA1000309

Homo sapiens zinc finger protein (MBLL) mRNA, complete cds

2.4e-35:180:100

Hs.44806:AF061261

45 F-HEMBA1000407

Cyclin-dependent kinase inhibitor 1C (p57, Kip2)

0.026:218:65

Hs.106070:U22398

50 F-HEMBA1000447

Homo sapiens JWA protein mRNA, complete cds

4.6e-160:750:98

Hs.92384:AF070523

55 F-HEMBA1000542

ESTs, Weakly similar to C01H6.7 [C.elegans]

6.8e-07:130:77

Hs.18171:AA524327

5 F-HEMBB1000567
ESTs
8.8e-13:271:71
Hs.19934:AA455673

F-HEMBB1000642

10 F-HEMBB1000668
EST
0.83:192:58
Hs.126372:AA912193

15 F-HEMBB1000679
H.sapiens mRNA for TRAMP protein
4.1e-96:727:80
Hs.4147:X63679

20 F-HEMBB1000881
Homo sapiens chromosome 4p homeobox mRNA sequence
2.2e-06:512:60
Hs.104134:M99587

25 F-HEMBB1000905
Homo sapiens mRNA for voltage gated potassium channel
0.93:337:58
Hs.4975:Y15065

30 F-HEMBB1001026
Human p76 mRNA, complete cds
6.1e-08:410:61
Hs.28757:U81006

35 F-HEMBB1001048
Human Hpast (HPAST) mRNA, complete cds
2.1e-56:524:75
Hs.155119:AF001434

40 F-HEMBB 1001200
EST
0.10:300:61
Hs.161647:AA133367

45 F-HEMBB1001407
Homo sapiens PRKY exon 1 and joined CDS
2.6e-40:271:81
Hs.56336:Y15801

50 F-HEMBB1001530
ESTs
1.2e-98:477:98
Hs.135208:AI093908

55 F-HEMBB1001547
F-HEMBB1001573
EST
2.2e-06:115:75
Hs.138275:R43976

5
F-HEMBB1001847
ESTs
5.3e-79:389:98
Hs.16141:W56079

10
F-HEMBB1001959
Homo sapiens clone 24781 mRNA sequence
1.0e-58:322:93
Hs.108112:AF070640

15
F-HEMBB1001978
EST
4.7e-23:245:74
Hs.136356:AA493225

20
F-HEMBB1002039
EST
2.3e-25:345:70
Hs.128248:AA972858

25
F-HEMBB1002041
Human plectin (PLEC1) mRNA, complete cds
2.2e-08:477:60
Hs.79706:U53204

30
F-HEMBB1002051
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
9.9e-97:454:99
Hs.159267:AF049703

35
F-HEMBB1002120
ESTs
7.6e-10:68:100
Hs.146335:AI262660

40
F-HEMBB1002162
Homo sapiens genethonin 1 mRNA, complete cds
2.2e-68:328:99
Hs.109590:AF062534

45
F-HEMBB1002228
Homo sapiens unknown mRNA, complete cds
5.3e-41:208:98
Hs.11441:AF047439

50
F-HEMBB1002245
Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds
5.6e-05:299:63
Hs.92614:M62302

55
F-HEMBB1002302
F-HEMBB1002427
Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds
0.84:108:68
Hs.8786:AB014680

EP 1 130 094 A2

5	F-HEMBB1002465 ESTs, Highly similar to ACYL-COA DEHYDROGENASE [Bacillus subtilis] 3.2e-18:159:84 Hs.14791:AA741056
10	F-HEMBB1002661 ESTs 0.023:424:55 Hs.154029:AI380603
	F-HEMBB1002663
	F-HEMBB1002693
15	F-MAMMA1000046 Human mRNA for tryptophan hydroxylase (EC 1.14.16.4) 3.2e-43:454:74 Hs.144563:AF057280
20	F-MAMMA1000102 Homo sapiens mRNA for cathepsin V, complete cds 0.70:222:65 Hs.87417:AB001928
25	F-MAMMA1000106 Homo sapiens mRNA for KIAA0754 protein, partial cds 0.00076:331:61 Hs.159183:AB018297
30	F-MAMMA1000118 B94 PROTEIN 1.5e-07:511:61 Hs.75522:M92357
35	F-MAMMA1000141 ESTs 2.3e-18:268:73 Hs.155334:AA827904
40	F-MAMMA1000204 Homo sapiens dysferlin mRNA, complete cds 2.5e-167:781:98 Hs.143897:AF075575
45	F-MAMMA1000226 Human involucrin mRNA 0.0010:414:61 Hs.157091:M13903
50	F-MAMMA1000403 ESTs 2.0e-24:163:90 Hs.44281:AI342377
55	F-MAMMA1000449 ESTs 0.99:211:60 Hs.143715:AI167929

5 F-MAMMA1000457
NADH-CYTOCHROME B5 REDUCTASE
7.7e-37:551:66
Hs.75666:M28713

10 F-MAMMA1000473

F-MAMMA1000496
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
1.1e-107:543:96
Hs.8003:AC004997

15 F-MAMMA1000528
EST
0.22:227:59
Hs.161400:AI423879

20 F-MAMMA1000591
H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
3.3e-23:470:62
Hs.55823:X92689

25 F-MAMMA1000614
H.sapiens mRNA for CCAAT/enhancer binding protein alpha
1.9e-06:492:61
Hs.76171:Y11525

30 F-MAMMA1000652
Homo sapiens mRNA, chromosome I specific transcript KIAA0487
1.5e-61:449:75
Hs.92381:AB007956

35 F-MAMMA1000681
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
4.0e-34:636:65
Hs.159543:AJ000479

40 F-MAMMA1000706
COAGULATION FACTOR VII PRECURSOR
9.7e-16:378:65
Hs.36989:M13232

45 F-MAMMA1000788
ESTs, Weakly similar to M01E11.2 [C.elegans]
3.4e-118:571:97
Hs.78389:AI191127

50 F-MAMMA1000810
EST
0.065:211:61
Hs.116798:AA633813

55 F-MAMMA1000814
EST
3.1e-08:224:66
Hs.141620:N63316

F-MAMMA1000881

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- Homo sapiens sgk gene
3.5e-08:165:69
Hs.159640:AJ000512
- 5 F-MAMMA1000986
Homo sapiens clone 24796 mRNA sequence
2.3e-115:320:99
Hs.27191:AF070596
- 10 F-MAMMA1000994
Human HOX4C mRNA for a homeobox protein
0.050:178:64
Hs.74061:X59372
- 15 F-MAMMA1001043
Latent transforming growth factor beta binding protein 2
0.0013:376:60
Hs.83337:Z37976
- 20 F-MAMMA1001066
ESTs
1.1e-18:128:77
Hs.114031:AA700958
- 25 F-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
2.0e-182:844:99
Hs.20423:AF091094
- 30 F-MAMMA1001141
Homo sapiens achaete scute homologous protein (ASH1) mRNA, complete cds
6.1e-07:492:58
Hs.1619:L08424
- 35 F-MAMMA1001150
Protein kinase C, mu
8.3e-51:691:67
Hs.2891:X75756
- 40 F-MAMMA1001237
Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds
8.2e-08:386:60
Hs.85838:U81800
- 45 F-MAMMA1001284
ESTs
1.1e-91:452:97
Hs.114756:AI279440
- 50 F-MAMMA1001310
Homo sapiens mRNA for KIAA0708 protein, partial cds
0.014:512:57
Hs.117177:AB014608
- 55 F-MAMMA1001344
ESTs, Weakly similar to No definition line found [C.elegans]
8.3e-80:406:96
Hs.121619:AI188389

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F-MAMMA1001418

Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds

1.9e-36:622:63

Hs.97207:U62966

5

F-MAMMA1001532

Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds

2.1e-33:282:68

Hs.158174:U66561

10

F-MAMMA1001609

Insulin-like growth factor-binding protein 4

0.00026:596:57

Hs.1516:U20982

15

F-MAMMA1001615

Homo sapiens DNA from chromosome 19, cosmid R29144

1.1e-05:504:59

Hs.155647:AC004221

20

F-MAMMA1001623

Excision repair protein ERCC6

1.2e-38:274:86

Hs.99924:L04791

25

F-MAMMA1001634

ESTs

1.5e-26:176:90

Hs.16187:AI139901

30

F-MAMMA1001893

Cyclin-dependent kinase inhibitor 1C (p57, Kip2)

0.00030:170:68

Hs.106070:U22398

35

F-MAMMA1001901

ESTs

1.5e-36:201:76

Hs.161660:AA167744

40

F-MAMMA1001957

Prostaglandin I₂ (prostacyclin) receptor (IP)

0.041:277:61

Hs.393:D38128

45

F-MAMMA1001978

EST

4.0e-43:359:81

Hs.136494:AA587773

50

F-MAMMA1002070

Human PAC clone DJ515N1 from 22q11.2-q22

5.1e-135:652:97

Hs.26670:AC002073

55

F-MAMMA1002080

Calcium channel, voltage-dependent, L type, alpha 1C subunit

0.0019:574:57

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Hs.89925:L04569

F-MAMMA1002087

Human mRNA for KIAA0009 gene, complete cds

0.71:228:63

Hs.79972:D13634

F-MAMMA1002091

Homo sapiens CD39L2 (CD39L2) mRNA, complete cds

5.2e-158:743:98

Hs.12330:AF039916

F-MAMMA1002095

Homo sapiens mRNA for KIAA0703 protein, complete cds

4.9e-55:657:68

Hs.6168:AB014603

F-MAMMA1002128

Human leucine zipper on the D14S46E locus mRNA, complete cds

0.77:449:59

Hs.89606:M95925

F-MAMMA1002142

F-MAMMA1002165

Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds

1.2e-35:182:98

Hs.139340:AF083500

F-MAMMA1002205

ESTs

4.7e-32:385:71

Hs.46158:AI160121

F-MAMMA1002224

TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT

1.3e-34:248:85

Hs.3006:X63468

F-MAMMA1002234

ESTs

1.1e-100:501:97

Hs.158161:AA312511

F-MAMMA1002586

Human mRNA for KIAA0183 gene, partial cds

0.00041:388:61

Hs.76666:D80005

F-MAMMA1002633

Landsteiner-Wiener blood group glycoprotein

1.1e-37:477:71

Hs.108287:L27670

F-MAMMA1003126

Human Hpast (HPAST) mRNA, complete cds

4.1e-84:801:74

Hs.155119:AF001434

5 F-NT2RM1000407
ESTs
4.1e-19:132:92
Hs.133484:D80522

10 F-NT2RM1000462

10 F-NT2RM1000542
Beta-galactosidase (GLB1)
1.3e-17:436:61
Hs.79222:M34423

15 F-NT2RM1000580
ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
6.2e-51:254:98
Hs.132096:AA314601

20 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4
3.5e-96:299:92
Hs.154485:Y11306

25 F-NT2RM1000855
Hydroxysteroid (11-beta) dehydrogenase 2
0.021:178:67
Hs.1376:U26726

30 F-NT2RM1000858

30 F-NT2RM1000899
Homo sapiens BAC clone RG119C02 from 7p15
0.037:222:63
Hs.22900:AC004520

35 F-NT2RM2000241
ESTs
2.9e-31:166:97
Hs.156175:AI334328

40 F-NT2RM2000306

45 F-NT2RM2000410
ESTs
3.2e-12:81:97
Hs.72116:AA151564

50 F-NT2RM2000423
Beta-galactosidase (GLB1)
0.074:163:63
Hs.79222:M34423

55 F-NT2RM2000497
ESTs, Weakly similar to CHL1 protein [H.sapiens]
3.7e-21:121:97
Hs.97515:AA435715

F-NT2RM2000514

F-NT2RM2000565

F-NT2RM2000582

EST

1.7e-42:218:98

Hs.160262:AI146610

F-NT2RM2000589

F-NT2RM2000622

Androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)

0.00018:409:62

Hs.99915:M23263

F-NT2RM2000632

Homo sapiens TBP-associated factor 172 (TAF-172) mRNA, complete cds

0.00017:331:59

Hs.14244:AF038362

F-NT2RM2000773

Human zinc finger protein (MAZ) mRNA

7.2e-47:274:91

Hs.7647:M94046

F-NT2RM2001126

Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds

5.1e-163:663:99

Hs.21301:AF093419

F-NT2RM2001558

Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds

3.9e-166:770:98

Hs.98397:AF093408

F-NT2RM2001626

Human mRNA for KIAA0231 gene, partial cds

2.8e-40:562:67

Hs.7938:D86984

F-NT2RM2001643

ESTs

7.9e-112:548:97

Hs.12610:W56112

F-NT2RM2001738

FACTOR VIII INTRON 22 PROTEIN

0.32:452:59

Hs.83363:M34677

F-NT2RM2001767

Homo sapiens mRNA for B120, complete cds

5.0e-24:131:100

Hs.123090:AB001895

F-NT2RM2001792

Homo sapiens mRNA for serum lectin P35, complete cds

8.2e-14:244:67

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Hs.54517:D63160

F-NT2RM2001818

EST

5 0.051:152:61

Hs.157619:AI357718

F-NT2RM2001902

Human p21-activated protein kinase (Pak1) gene, complete cds

10 4.4e-39:568:66

Hs.62402:U24152

F-NT2RM2001939

Human G protein-coupled receptor GPR-NGA gene, complete cds

15 4.2e-141:664:98

Hs.92458:U55312

F-NT2RM2001941

Dopamine receptor D4

20 1.3e-14:547:61

Hs.99922:L12398

F-NT2RM4000100

Human involucrin mRNA

25 1.1e-09:487:62

Hs.157091:M13903

F-NT2RM4000115

30 F-NT2RM4000198

ESTs

9.3e-101:496:98

Hs.128676:AA464413

35 F-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds

2.4e-38: 194:98

Hs.110804:U12255

40 F-NT2RM4000295

Homo sapiens SOX22 protein (SOX22) mRNA, complete cds

1.7e-06:479:60

Hs.43627:U35612

45 F-NT2RM4000326

Phosphorylase kinase, gamma 2 (testis)

0.95:204:63

Hs.87452:M31606

50 F-NT2RM4000417

H.sapiens Syt V gene (genomic and cDNA sequence)

0.97:143:67

Hs.23179:X96783

55 F-NT2RM4000444

Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)

0.45:194:64

Hs.90319:Z21507

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F-NT2RM4000587
 Human proto-oncogene (FRAT1) gene, complete cds
 3.8e-05:495:60
 Hs.143005:U58975
 5 F-NT2RM4000593

 F-NT2RM4000648
 Homo sapiens glypican-4 (GPC4) mRNA, complete cds
 10 1.0e-50:610:70
 Hs.58367:AF030186

 F-NT2RM4000761
 EST
 15 0.89:53:79
 Hs.161967:AA494423

 F-NT2RM4000965
 H.sapiens mRNA for PHAPI2b protein
 20 0.18:148:68
 Hs.84264:U70439

 F-NT2RM4000997

 25 F-NT2RM4001321
 ESTs
 1.8e-94:467:97
 Hs.12610:W56112

 30 F-NT2RM4001325
 Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds
 2.1e-13:384:64
 Hs.158304:AB012192

 35 F-NT2RM4001377
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 3.1e-156:719:99
 Hs.77864:AB014538

 40 F-NT2RM4001735

 F-NT2RM4001768
 ESTs
 0.00012:123:68
 45 Hs.128045:AA970231

 F-NT2RM4001843

 F-NT2RM4002352
 50 Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
 4.4e-157:761:97
 Hs.143641:AB009462

 F-NT2RP1000002
 55 EST
 0.00023:170:68
 Hs.135504:AI091717

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F-NT2RP1000050
 Histidine-rich calcium binding protein
 0.0047:257:61
 Hs.1480:M60052
 5

F-NT2RP1000181
 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
 6.9e-99:510:94
 Hs.132898:AC004770
 10

F-NT2RP1000239
 ESTs
 1.7e-34:240:67
 Hs.33020:N31946
 15

F-NT2RP1000261
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
 9.1e-92:484:94
 Hs.7870:AI078137
 20

F-NT2RP1000271
 Homo sapiens DNA-binding protein mRNA, complete cds
 1.4e-140:678:97
 Hs.137582:AF038951
 25

F-NT2RP1000300
 Human endosome-associated protein (EEA1) mRNA, complete cds
 1.0:205:61
 Hs.2864:L40157
 30

F-NT2RP1000325
 Phosphate carrier, mitochondrial
 7.7e-84:444:93
 Hs.78713:X60036
 35

F-NT2RP1000448
 ESTs
 9.5e-73:405:93
 Hs.24054:N46499
 40

F-NT2RP1000465
 ESTs
 8.5e-10:81:87
 Hs.18619:AI202769
 45

F-NT2RP1000468
 Homo sapiens clone 24781 mRNA sequence
 2.1e-20:133:92
 Hs.108112:AF070640
 50

F-NT2RP1000551
 Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds
 2.4e-140:742:93
 Hs.75402:U09585
 55

F-NT2RP1000579
 SUCCINATE DEHYDROGENASE

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1.1e-141:798:91
Hs.469:L21936

5 F-NT2RP1000613
Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds
5.5e-11:468:58
Hs.5338:AF037335

10 F-NT2RP1000679
ESTs
0.79:127:65
Hs.146093:AA100242

15 F-NT2RP1000740
Homo sapiens Trio isoform mRNA, complete cds
0.24:160:66
Hs.150625:AF091395

20 F-NT2RP1000903
F-NT2RP1000981

25 F-NT2RP1001004
Human mRNA for Doc2 beta, complete cds
0.00072:520:57
Hs.54402:D70830

30 F-NT2RP1001020
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
2.1e-73:392:94
Hs.4789:AI418298

35 F-NT2RP1001031
Miller-Dieker syndrome chromosome region
4.5e-07:383:61
Hs.77318:L13385

40 F-NT2RP1001563
Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds
0.086:398:59
Hs.57783:U78525

45 F-NT2RP2000092
Zinc finger protein 136 (clone pHZ-20)
5.5e-56:652:70
Hs.69740:U09367

50 F-NT2RP2000178
Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence
0.14:231:62
Hs.159402:AC005609

55 F-NT2RP2000240
Homo sapiens KIAA0415 mRNA, complete cds
3.0e-61:554:76
Hs.7289:AB007875

F-NT2RP2000394

ESTs

0.0063:210:63

Hs.134272:AI220363

- 5 F-NT2RP2000447
Human (clone SY11) golgin-95 mRNA, complete cds
3.8e-22:498:65
Hs.24049:L06147
- 10 F-NT2RP2000479
ESTs
1.3e-46:298:90
Hs.15641:W63676
- 15 F-NT2RP2000514
Homo sapiens roundabout 1 (robo1) mRNA, complete cds
1.2e-37:543:67
Hs.36702:AF040990
- 20 F-NT2RP2000533
ESTs, Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION [Saccha-
romyces cerevisiae]
5.4e-132:647:96
Hs.18120:AA913148
- 25 F-NT2RP2000610
Homo sapiens antigen NY-CO-16 mRNA, complete cds
0.00027:182:66
Hs.132206:AF039694
- 30 F-NT2RP2000616
ESTs
0.44:235:60
Hs.31714:AA514389
- 35 F-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
6.2e-167:802:97
Hs.25846:AB016068
- 40 F-NT2RP2000663
Homo sapiens mRNA for KIAA0512 protein, complete cds
4.8e-15:305:64
Hs.48924:AB011084
- 45 F-NT2RP2000694
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.0e-113:558:96
Hs.82128:AJ012159
- 50 F-NT2RP2000712
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
1.5e-83:442:93
Hs.154226:AA468767
- 55 F-NT2RP2000739
Human mRNA for KIAA0326 gene, partial cds
2.1e-25:574:62

- Hs.6833:AB002324
- F-NT2RP2000818
- 5 F-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
3.5e-112:539:97
Hs.82128:AJ012159
- 10 F-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds
1.1e-111:540:96
Hs.115763:AB014576
- 15 F-NT2RP2001223
ESTs
5.9e-91:461:95
Hs.103733:AA436929
- 20 F-NT2RP2001276
Homo sapiens mRNA for KIAA0634 protein, partial cds
2.4e-11:382:62
Hs.30898:AB014534
- 25 F-NT2RP2001388
- F-NT2RP2001469
ESTs
7.3e-39:213:95
- 30 Hs.151001:AA564706
- F-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
2.9e-141:686:96
- 35 Hs.82165:L38969
- F-NT2RP2001495
Human transporter protein (g17) mRNA, complete cds
6.0e-37:581:64
- 40 Hs.76460:U49082
- F-NT2RP2001514
- F-NT2RP2001529
Homo sapiens mRNA for ZIP-kinase, complete cds
1.5e-153:757:96
Hs.25619:AB007144
- 45 F-NT2RP2001538
ESTs, Highly similar to co-repressor protein [M.musculus]
4.4e-63:329:94
Hs.22583:AA188168
- 50 F-NT2RP2001562
Homo sapiens GLE1 (GLE1) mRNA, complete cds
7.5e-119:572:97
Hs.81449:AF058922
- 55

5
F-NT2RP2001662
H.sapiens mRNA for TGIF protein
2.6e-29:448:67
Hs.90077:X89750

10
F-NT2RP2001755
ESTs, Highly similar to F-SPONDIN PRECURSOR [Rattus norvegicus]
1.0e-47:275:92
Hs.153657:H37929

15
F-NT2RP2001769
Human protein kinase C-L (PRKCL) mRNA, complete cds
1.9e-09:399:59
Hs.89616:M55284

20
F-NT2RP2001817
EST
0.97:133:63
Hs.145274:AI249468

25
F-NT2RP2001878
Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
3.6e-05:491:60
Hs.159234:U89995

30
F-NT2RP2001903
Human mRNA for apolipoprotein E receptor 2, complete cds
0.0023:270:60
Hs.54481:D86407

35
F-NT2RP2001915
Homo sapiens Pig3 (PIG3) mRNA complete cds
3.2e-05:493:60
Hs.50649:AF010309

40
F-NT2RP2001921
F-NT2RP2001948
ESTs
0.55:213:61
Hs.147805:AI221717

45
F-NT2RP2001956
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
8.1e-45:510:70
Hs.13144:T67556

50
F-NT2RP2002015
ESTs
4.3e-20:127:92
Hs.12610:W56112

55
F-NT2RP2002063
ESTs
1.0e-08:73:91
Hs.19814:T81721

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F-NT2RP2002188

F-NT2RP2002232

EST

5 0.82:99:67

Hs.148596:AI202232

F-NT2RP2002304

Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds

10 0.031:107:71

Hs.82210:U47742

F-NT2RP2002409

Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds

15 0.00063:302:65

Hs.105927:AF020044

F-NT2RP2002510

ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)

20 4.4e-09:298:64

Hs.144023:U15197

F-NT2RP2002527

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene

25 5.2e-65:327:96

Hs.132898:AC004770

F-NT2RP2002533

Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds

30 2.1e-142:726:95

Hs.127436:AF040709

F-NT2RP2002564

Homo sapiens mRNA for repressor protein, partial cds

35 3.5e-55:594:74

Hs.58167:D30612

F-NT2RP2002674

Epoxide hydrolase 2, cytoplasmic

40 2.5e-07:332:62

Hs.113:L05779

F-NT2RP2002721

F-NT2RP2002824

ESTs, Weakly similar to ZK858.6 [C.elegans]

50 5.2e-28:190:90

Hs.120416:AA057428

F-NT2RP2002942

Homo sapiens mRNA for KIAA0806 protein, complete cds

55 2.0e-146:758:94

Hs.24279:AB018349

F-NT2RP2002974

ESTs

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4.9e-51:475:77
Hs.137840:AI123378

5 F-NT2RP2002976
ESTs, Weakly similar to No definition line found [C.elegans]
7.8e-50:315:89
Hs.159604:AI380827

10 F-NT2RP2003042
Lecithin-cholesterol acyltransferase
2.4e-25:454:65
Hs.112125:M12625

15 F-NT2RP2003138
H.sapiens mRNA for TGIF protein
2.0e-05:121:75
Hs.90077:X89750

20 F-NT2RP2003179
Homo sapiens mRNA for KIAA0537 protein, complete cds
1.0e-43:587:70
Hs.12836:AB011109

25 F-NT2RP2003210
F-NT2RP2003302
Zinc finger protein 136 (clone pHZ-20)
1.8e-64:691:69
Hs.69740:U09367

30 F-NT2RP2003369
Homo sapiens chromosome 7q22 sequence
5.1e-109:539:96
Hs.125742:AF053356

35 F-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
1.6e-159:801:95
Hs.7414:AB007927

40 F-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
2.2e-116:554:98
Hs.31575:AF100141

45 F-NT2RP2003469
ESTs
0.26:127:69
Hs.62649:AA115328

50 F-NT2RP2003545
ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]
4.2e-111:550:96
Hs.85768:W16504

55 F-NT2RP2003593
EST
8.7e-43:213:99

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Hs.130657:AI005473

F-NT2RP2003599

ESTs

5 7.8e-14:84:98

Hs.107171:H53973

F-NT2RP2003655

10 F-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein

5.4e-134:630:98

Hs.23581:Y12670

15 F-NT2RP2003931

Human mRNA for KIAA0365 gene, partial cds

4.3e-14:101:92

Hs.84123:AB002363

20 F-NT2RP2003940

Zinc finger protein 43 (HTF6)

4.6e-99:693:82

Hs.74107:X59244

25 F-NT2RP2003950

Cell division cycle 25A

0.00041:419:59

Hs.1634:M81933

30 F-NT2RP2004069

ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]

1.3e-75:390:94

Hs.13322:AA151730

35 F-NT2RP2004108

Zinc finger protein 136 (clone pHZ-20)

4.9e-69:548:78

Hs.69740:U09367

40 F-NT2RP2004141

TRICHOHYALIN

4.8e-11:435:63

Hs.82276:L09190

45 F-NT2RP2004179

ESTs

0.0054:180:66

Hs.134917:AI092952

50 F-NT2RP2004205

Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds

0.27:474:56

Hs.112049:U93181

55 F-NT2RP2004447

Homo sapiens LDL receptor member LR3 mRNA, complete cds

0.016:456:57

Hs.6347:AF077820

5
F-NT2RP2004495
Human transporter protein (g17) mRNA, complete cds
1.2e-26:497:61
Hs.76460:U49082

10
F-NT2RP2004524
Human bone morphogenetic protein-3b
0.0016:259:64
Hs.2171:D49493

15
F-NT2RP2004556
ESTs
1.1e-34:181:97
Hs.27160:AA421991

20
F-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
5.7e-107:587:92
Hs.148726:X03124

25
F-NT2RP2004648
TUBULIN ALPHA-4 CHAIN
0.59:186:61
Hs.75318:X06956

30
F-NT2RP2004670
Human mRNA for KIAA0369 gene, complete cds
0.097:309:61
Hs.21355:AB002367

35
F-NT2RP2004794
ESTs
1.3e-60:310:96
Hs.84926:N50073

40
F-NT2RP2004837

45
F-NT2RP2004847
Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)
1.4e-05:396:60
Hs.78247:M58297

50
F-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
7.2e-147:713:96
Hs.7594:M20681

55
F-NT2RP2005069
Human mRNA for KIAA0355 gene, complete cds
0.14:303:61
Hs.153014:AB002353

F-NT2RP2005163
ESTs, Weakly similar to No definition line found [C.elegans]
1.4e-23:334:70
Hs.159604:AI380827

F-NT2RP2005181

- Ecotropic retroviral receptor
8.3e-45:501:70
Hs.2928:X57303
- 5 F-NT2RP2005247
Oxysterol binding protein
4.2e-08:356:62
Hs.143065:M86917
- 10 F-NT2RP2005378
ESTs
1.7e-100:485:97
Hs.151572:AA588083
- 15 F-NT2RP2005391
EST
1.0:264:62
Hs.148259:AA905706
- 20 F-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds
3.3e-118:566:97
Hs.58103:AB018346
- 25 F-NT2RP2005463
- F-NT2RP2005514
ESTs
3.6e-18:193:77
- 30 Hs.153344:R26293
- F-NT2RP2005535
Homo sapiens DNA-binding protein mRNA, complete cds
7.5e-127:726:90
- 35 Hs.137582:AF038951
- F-NT2RP2005541
Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)
1.2e-06:225:64
- 40 Hs.2703:Z12173
- F-NT2RP2005597
- F-NT2RP2005632
ESTs
5.6e-67:344:96
Hs.112011:AA987961
- 45
- F-NT2RP2005666
ESTs
5.8e-71:453:87
Hs.122698:AI042484
- 50
- F-NT2RP2005774
Zinc finger protein 136 (clone pHZ-20)
1.3e-45:451:74
Hs.69740:U09367
- 55

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F-NT2RP2005878
 ESTs, Highly similar to ESTRADIOL 17 BETA-DEHYDROGENASE 3 [Homo sapiens]
 5.9e-10:67:100
 Hs.104523:AA584520
 5 F-NT2RP2005883
 F-NT2RP2005887
 10 F-NT2RP2005941
 Human novel homeobox mRNA for a DNA binding protein
 6.2e-11:464:61
 Hs.37035:U07664
 15 F-NT2RP2005994
 F-NT2RP2006004
 Homo sapiens KIAA0405 mRNA, complete cds
 1.2e-13:273:63
 20 Hs.48998:AB007865
 F-NT2RP2006042
 Human mRNA for KIAA0144 gene, complete cds
 5.6e-12:220:69
 25 Hs.8127:D63478
 F-NT2RP2006092
 Human FE65-like protein (hFE65L) mRNA, partial cds
 2.6e-23:353:65
 30 Hs.24957:U62325
 F-NT2RP2006099
 EST
 2.5e-28:180:90
 35 Hs.160878:A1361890
 F-NT2RP2006134
 Neogenin (chicken) homolog 1
 0.035:219:60
 40 Hs.90408:U61262
 F-NT2RP2006269
 Homo sapiens mRNA for matrilin-3
 1.0:147:65
 45 Hs.119534:AJ224741
 F-NT2RP2006512
 ESTs
 1.6e-09:70:95
 50 Hs.118981:AA282396
 F-NT2RP3000011
 F-NT2RP3000022
 55 EST
 0.016:293:60
 Hs.127706:AA961478

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F-NT2RP3000059

Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds

0.0041:608:59

Hs.89449:L32976

5

F-NT2RP3000063

Excision repair protein ERCC6

1.0:264:59

Hs.99924:L04791

10

F-NT2RP3000125

Human mRNA for KIAA0314 gene, partial cds

6.9e-08:379:59

Hs.155045:AB002312

15

F-NT2RP3000148

Human Chromosome 16 BAC clone CIT987SK-A-635H12

4.5e-40:349:73

Hs.108604:AC002310

20

F-NT2RP3000169

Homo sapiens MRS1 mRNA, complete cds

1.1e-107:501:99

Hs.30985:AF093239

25

F-NT2RP3000171

Homo sapiens methionine synthase reductase (MTRR) mRNA, complete cds

1.0:279:64

Hs.153792:AF025794

30

F-NT2RP3000172

Homo sapiens mRNA for ZIP-kinase, complete cds

7.4e-09:463:59

Hs.25619:AB007144

35

F-NT2RP3000201

Homo sapiens mRNA for KIAA0687 protein, partial cds

3.0e-171:792:98

Hs.3628:AB014587

40

F-NT2RP3000232

ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]

8.6e-24:304:70

Hs.112094:AA447558

45

F-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds

1.1e-172:797:98

Hs.23672:AF074264

50

F-NT2RP3000378

Homo sapiens mRNA for KIAA0700 protein, partial cds

4.3e-45:585:66

Hs.13999:AB014600

55

F-NT2RP3000427

Protein kinase, cAMP-dependent, catalytic, beta

1.2e-15:97:98

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Hs.87773:M34181

F-NT2RP3000436

Human protein disulfide isomerase-related protein P5 mRNA, partial cds

5 4.1e-06:353:59

Hs.85200:D49489

F-NT2RP3000444

Homo sapiens mRNA for KIAA0445 protein, complete cds

10 1.2e-08:542:60

Hs.154139:AB007914

F-NT2RP3000460

ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

15 1.3e-17:181:75

Hs.131840:AI016073

F-NT2RP3000481

Homo sapiens RanBP7/importin 7 mRNA, complete cds

20 5.4e-164:770:98

Hs.5151:AF098799

F-NT2RP3000616

Homo sapiens KIAA0405 mRNA, complete cds

25 1.5e-32:579:62

Hs.48998:AB007865

F-NT2RP3000645

Human KH type splicing regulatory protein KSRP mRNA, complete cds

30 4.6e-06:245:64

Hs.91142:U94832

F-NT2RP3000652

Homo sapiens DNA from chromosome 19, BAC 33152

35 2.6e-135:853:84

Hs.55452:AC003973

F-NT2RP3000676

Homo sapiens mRNA for KIAA0446 protein, complete cds

40 8.8e-88:420:98

Hs.158286:AB007915

F-NT2RP3000677

ESTs

45 3.9e-09:67:97

Hs.98819:AA778727

F-NT2RP3000721

ESTs, Weakly similar to No definition line found [C.elegans]

50 1.2e-57:395:86

Hs.159604:AI380827

F-NT2RP3000789

Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete cds

55 4.8e-75:833:69

Hs.79440:U97188

F-NT2RP3000818

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Homo sapiens chromosome 19, fosmid 39554
5.9e-08:313:63
Hs.129906:AC004410

- 5 F-NT2RP3000820
ESTs, Moderately similar to WSB-1 [M.musculus]
8.8e-127:613:97
Hs.24630:AI365246
- 10 F-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
8.3e-79:682:79
Hs.77864:AB014538
- 15 F-NT2RP3000871
Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds
1.9e-08:350:60
Hs.29287:U72066
- 20 F-NT2RP3000907
Human Ini1 mRNA, complete cds
0.91:345:59
Hs.155626:U04847
- 25 F-NT2RP3000921
Homo sapiens mRNA for KIAA0806 protein, complete cds
2.0e-65:798:68
Hs.24279:AB018349
- 30 F-NT2RP3001012
Homo sapiens mRNA for KIAA0667 protein, partial cds
1.3e-21:383:64
Hs.154740:AB014567
- 35 F-NT2RP3001044

F-NT2RP3001061
KERATIN, TYPE II CYTOSKELETAL 7
3.4e-05:256:62
- 40 Hs.23881:M99063

F-NT2RP3001159
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
1.8e-81:527:70
- 45 Hs.132874:AC004770

F-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
7.3e-183:859:98
- 50 Hs.3657:AB018327

F-NT2RP3001 195
ESTs
3.5e-08:282:62
- 55 Hs.135168:AI394026

F-NT2RP3001240
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

2.8e-64:344:95
Hs.14038:R06800

5 F-NT2RP3001271
Centromere protein B (80kD)
7.6e-08:288:64
Hs.85004:X05299

10 F-NT2RP3001322
ESTs, Weakly similar to W09D10.2 [C.elegans]
1.2e-86:422:98
Hs.26107:R60661

15 F-NT2RP3001388
F-NT2RP3001542

F-NT2RP3001560
20 Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
0.016:190:63
Hs.57764:S87759

F-NT2RP3001592
25 Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398

F-NT2RP3001650
30 Homo sapiens KIAA0415 mRNA, complete cds
1.6e-17:394:66
Hs.7289:AB007875

F-NT2RP3001685
35 F-NT2RP3001738
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
1.9e-54:776:65
Hs.132898:AC004770

40 F-NT2RP3001754
Homo sapiens mRNA for B120, complete cds
2.4e-18:106:100
Hs.123090:AB001895

45 F-NT2RP3001858
Homo sapiens mRNA for KIAA0584 protein, partial cds
1.9e-40:770:63
Hs.106794:AB011156

50 F-NT2RP3001976
Zinc finger protein 140 (clone pHZ-39)
7.3e-33:493:68
Hs.154205:U09368

55 F-NT2RP3002015
Homo sapiens OPA-containing protein mRNA, complete cds
0.018:329:62
Hs.85313:AF071309

F-NT2RP3002160
 Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds
 0.53:182:64
 Hs.113259:AF023456
 5

F-NT2RP3002281
 Homo sapiens mRNA for KIAA0765 protein, partial cds
 5.2e-151:713:98
 Hs.62318:AB018308
 10

F-NT2RP3002286
 ESTs
 0.034:48:95
 Hs.124692:AA777421
 15

F-NT2RP3002311
 Beta-galactosidase (GEB1)
 2.3e-28:633:61
 Hs.79222:M34423
 20

F-NT2RP3002324
 ESTs
 2.5e-28:296:75
 Hs.22822:H06408
 25

F-NT2RP3002342
 Human transporter protein (g17) mRNA, complete cds
 3.2e-37:565:65
 Hs.76460:U49082
 30

F-NT2RP3002353
 Homo sapiens mRNA for KIAA0790 protein, partial cds
 0.0055:271:60
 Hs.12002:AB018333
 35

F-NT2RP3002409
 Homo sapiens mRNA for KIAA0719 protein, complete cds
 6.4e-191:897:98
 Hs.21198:AB018262
 40

F-NT2RP3002411
 Hydroxysteroid (17-beta) dehydrogenase 3
 2.9e-28:604:62
 Hs.477:U05659
 45

F-NT2RP3002448
 Human mRNA for KIAA0233 gene, complete cds
 1.6e-08:721:57
 Hs.79077:D87071
 50

F-NT2RP3002571
 Homo sapiens mRNA for KIAA0603 protein, complete cds
 9.7e-67:707:71
 Hs.16909:AB011175
 55

F-NT2RP3002664
 Homo sapiens Trio isoform mRNA, complete cds
 0.26:160:66

Hs.150625:AF091395

F-NT2RP3002721

Homo sapiens citrate synthase mRNA, complete cds

2.4e-180:873:96

Hs.132991:AF047042

F-NT2RP3002737

Homo sapiens mRNA for voltage gated potassium channel

7.1e-43:409:75

Hs.4975:Y15065

F-NT2RP3002738

Human BMK1 alpha kinase mRNA, complete cds

0.0070:722:57

Hs.3080:U29725

F-NT2RP3002790

Cyclin-dependent kinase inhibitor 1C (p57, Kip2)

7.2e-17:626:62

Hs.106070:U22398

F-NT2RP3002836

Homo sapiens mRNA for KIAA0463 protein, partial cds

2.2e-153:717:99

Hs.77738:AB007932

F-NT2RP3002887

Human plectin (PLEC1) mRNA, complete cds

2.5e-06:605:59

Hs.79706:U53204

F-NT2RP3002900

H.sapiens mRNA for transmembrane protein rnp24

3.1e-09:346:64

Hs.75914:X92098

F-NT2RP3002958

ESTs

8.3e-117:765:86

Hs.107119:AI198794

F-NT2RP3002983

ESTs

1.4e-07:270:67

Hs.160271:AI149075

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds

2.5e-89:555:88

Hs.122359:AF051946

F-NT2RP3003076

Homo sapiens mRNA for APC 2 protein, complete cds

0.00016:522:60

Hs.20912:AB012162

F-NT2RP3003354

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Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds
4.0e-36:625:64
Hs.10761:AF005038

- 5 F-NT2RP3003448
Arginine vasopressin receptor 1B
0.77:149:69
Hs.1372:L37112
- 10 F-NT2RP3003469
ESTs
1.4e-42:239:93
Hs.12610:W56112
- 15 F-NT2RP3003473
ESTs, Highly similar to transcription factor ARF6 chain B [M.musculus]
8.7e-46:281:89
Hs.136172:W28257
- 20 F-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
4.6e-162:769:98
Hs.130988:Y17999
- 25 F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR
1.5e-146:682:98
Hs.79015:M17229
- 30 F-NT2RP3003535
EST
6.7e-10:330:60
Hs.133239:AI052508
- 35 F-NT2RP3003559
Breakpoint cluster region protein BCR
1.0:143:66
Hs.2557:Y00661
- 40 F-NT2RP3003614
ESTs
3.7e-50:327:88
Hs.148873:T33582
- 45 F-NT2RP3003729
ESTs, Weakly similar to unknown [S.cerevisiae]
1.9e-96:449:99
Hs.100843:W28953
- 50 F-NT2RP3003849
ESTs, Weakly similar to rhophilin [M.musculus]
1.7e-32:197:92
Hs.118457:AA019161
- 55 F-NT2RP3003874
Homo sapiens incomplete cDNA for a myosin class I, myh-1c
8.5e-84:494:90
Hs.109805:AJ001381

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F-NT2RP3003939

Peroxisomal biogenesis factor 6

1.5e-05:236:62

Hs.30729:D83703

5

F-NT2RP3003963

F-NT2RP3004000

Homo sapiens mRNA for APC 2 protein, complete cds

10

4.8e-06:669:59

Hs.20912:AB012162

F-NT2RP3004025

ESTs

15

0.0015:68:86

Hs.154835:AI289188

F-NT2RP3004067

ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cerevisiae]

20

2.1e-76:416:94

Hs.9252:R53360

F-NT2RP3004075

ESTs

25

1.1e-54:298:94

Hs.124051:T15786

F-NT2RP3004083

30

F-NT2RP3004090

Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds

2.4e-06:486:62

Hs.135639:U77629

35

F-NT2RP3004119

Human mRNA for KIAA0215 gene, complete cds

4.1e-74:640:75

Hs.82292:D86969

40

F-NT2RP3004130

F-NT2RP3004133

ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]

45

4.6e-52:259:98

Hs.132096:AA314601

F-NT2RP3004202

ALPHA-2C-1 ADRENERGIC RECEPTOR

50

1.0:229:62

Hs.123022:J03853

F-NT2RP3004294

Homo sapiens mRNA for KIAA0741 protein, complete cds

55

2.4e-05:404:59

Hs.3615:AB018284

F-NT2RP3004309

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Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
3.4e-71:756:71
Hs.132874:AC004770

- 5 F-NT2RP3004321
Homo sapiens (clone MG2-5-12) mucin (MG2) mRNA, complete polyA site
0.015:263:60
Hs.103944:L13283
- 10 F-NT2RP3004345
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398
- 15 F-NT2RP3004355
EST
0.25:130:59
Hs.149436:AI274484
- 20 F-NT2RP3004374
ESTs
1.4e-95:480:96
Hs.12610:W56112
- 25 F-NT2RP3004406
Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds
3.4e-45:505:70
Hs.79136:U41060
- 30 F-NT2RP3004481
Homo sapiens mRNA for KIAA0476 protein, complete cds
0.00065:594:58
Hs.6684:AB007945
- 35 F-NT2RP3004552
Biglycan
0.92:347:57
Hs.821:J04599
- 40 F-NT2RP3004557
Human Ki nuclear autoantigen mRNA, complete cds
2.6e-121:626:94
Hs.152978:U11292
- 45 F-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
3.1e-152:710:98
Hs.26285:AF082516
- 50 F-NT2RP3004640
ESTs, Moderately similar to unknown [H.sapiens]
0.76:195:64
Hs.6487:T65302
- 55 F-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
6.6e-111:524:98
Hs.158286:AB007915

F-NT2RP4000108
NEUROFILAMENT TRIPLET L PROTEIN
5.3e-159:862:93
Hs.159540:X05608

5

F-NT2RP4000634
Human MEK kinase 3 mRNA, complete cds
2.3e-54:370:71
Hs.86201:U78876

10

F-NT2RP4000962
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [*Saccharomyces cerevisiae*]
2.3e-95:479:96
Hs.4789:AI418298

15

F-NT2RP4001001
EST
0.98:93:64
Hs.147598:AI217868

20

F-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds
3.1e-176:828:98
Hs.25846:AB016068

25

F-NT2RP4001467
5' nucleotidase (CD73)
1.1e-160:742:98
Hs.153952:X55740

30

F-NT2RP4001877
ESTs, Weakly similar to siah binding protein 1 [*H.sapiens*]
3.3e-103:495:98
Hs.65648:AA600816

35

F-NT2RP4001879
EST
0.78:171:61
Hs.112790:AA609949

40

F-NT2RP4002187
Hydroxysteroid (17-beta) dehydrogenase 3
9.9e-27:534:63
Hs.477:U05659

45

F-NT2RP4002451
ESTs
1.5e-11:106:86
Hs.163724:AA017689

50

F-NT2RP4002715
EST
4.2e-07:64:93
Hs.160901:AI366910

55

F-NT2RP4002750
Ecotropic retroviral receptor
6.6e-51:581:68

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Hs.2928:X57303

F-OVARC1000003

Solute carrier family 17 (sodium phosphate), member 2

6.9e-65:587:73

Hs.936:L13258

F-OVARC1000090

ESTs

4.8e-07:214:65

Hs.87456:AA434484

F-OVARC1000105

Human novel homeobox mRNA for a DNA binding protein

0.00095:204:64

Hs.37035:U07664

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds

4.0e-35:184:98

Hs.31531:U95735

F-OVARC1000208

Human calcium-dependent group X phospholipase A2 mRNA, complete cds

1.5e-61:365:90

Hs.136004:U95301

F-OVARC1000255

Spleen tyrosine kinase

2.2e-88:615:84

Hs.74101:L28824

F-OVARC1000275

ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]

4.7e-85:424:97

Hs.55165:AA573499

F-OVARC1000298

Homo sapiens GABA-B receptor mRNA, complete cds

0.00021:285:61

Hs.12307:AF056085

F-OVARC1000307

ESTs

0.00016:226:63

Hs.162935:AI393970

F-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds

5.5e-121:585:97

Hs.154023:AB011145

F-OVARC1000331

Glucose-6-phosphate dehydrogenase

5.3e-18:213:71

Hs.1435:M24470

F-OVARC1000410

Homo sapiens mRNA for angiopoietin-like factor
1.5e-27:538:62
Hs.146559:Y16132

5 F-OVARC1000439

F-OVARC1000467
ESTs
2.5e-26:173:90
10 Hs.105040:AA292817

F-OVARC1000529
Homo sapiens mRNA for C8FW phosphoprotein
1.1e-12:391:59
15 Hs.143513:AJ000480

F-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894
9.0e-111:425:99
20 Hs.157732:AC005594

F-OVARC1000775
Human chromosome 3p21.1 gene sequence
2.2e-70:380:95
25 Hs.82837:L13435

F-OVARC1000811
HEPATOCTE GROWTH FACTOR ACTIVATOR PRECURSOR
1.2e-06:446:61
30 Hs.104:D14012

F-OVARC1000853
ESTs
7.9e-09:268:63
35 Hs.92700:W37903

F-OVARC1000873
Homo sapiens mRNA for MIFR-1, complete cds
0.038:343:60
40 Hs.58269:AB010962

F-OVARC1000916
H.sapiens PISSLRE mRNA
1.3e-56:435:82
45 Hs.77313:X78342

F-OVARC1000956
Human TBP-associated factor (hTAFII130) mRNA, partial cds
7.7e-05:511:59
50 Hs.24644:U75308

F-OVARC1000995
ESTs
2.4e-39:205:98
55 Hs.163662:AA514348

F-OVARC1001030
EST

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1.1e-44:232:96
Hs.135504:AI091717

5 F-OVARC1001049
ESTs
6.1e-78:373:98
Hs.135022:AI417283

10 F-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
6.0e-166:761:99
Hs.155478:AF048731

15 F-OVARC1001132
ESTs, Weakly similar to GC-RICH SEQUENCE DNA-BINDING FACTOR [Homo sapiens]
7.9e-121:610:96
Hs.26461:AI341685

20 F-OVARC1001163
ESTs
5.9e-39:215:94
Hs.126067:AI344351

25 F-OVARC1001222
ESTs
2.7e-93:467:95
Hs.10267:W27845

30 F-OVARC1001260
Pregnancy-zone protein
1.0:251:58
Hs.74094:X54380

35 F-OVARC1001336
Solute carrier family 17 (sodium phosphate), member 2
1.2e-31:304:74
Hs.936:L13258

40 F-OVARC1001338
Homo sapiens cam kinase I mRNA, complete cds
3.7e-17:570:60
Hs.118414:L41816

45 F-OVARC1001569
Human novel homeobox mRNA for a DNA binding protein
0.038:178:63
Hs.37035:U07664

50 F-OVARC1001570
ESTs
4.5e-10:75:93
Hs.120928:AA703165

55 F-OVARC1001596
Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)
0.0092:287:63
Hs.111301:M55593

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F-OVARC1001607
 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
 5.5e-41:323:80
 Hs.154844:U15128
 5
 F-OVARC 1001725
 F-OVARC1001727
 EST
 10 3.2e-05:237:61
 Hs.119508:AA485732
 F-OVARC1001807
 Hormone receptor (growth factor-inducible nuclear protein N10)
 15 3.4e-91:564:88
 Hs.1119:D49728
 F-OVARC1001833
 ESTs
 20 1.2e-94:444:97
 Hs.155256:AA707750
 F-OVARC1001952
 Myristoylated alanine-rich C-kinase substrate
 25 2.9e-10:364:64
 Hs.75607:D10522
 F-OVARC1001991
 Human mRNA for KIAA0176 gene, partial cds
 30 0.0019:224:62
 Hs.4935:D79998
 F-OVARC1002058
 Human mRNA for KIAA0149 gene, complete cds
 35 5.0e-48:674:67
 Hs.57735:D86864
 F-OVARC1002178
 Homo sapiens zinc-finger protein of the cerebellum 3 (ZIC3) mRNA, complete cds
 40 0.010:310:61
 Hs.111227:AF028706
 F-PLACE1000033
 45 F-PLACE1000231
 Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
 0.00021:235:63
 Hs.1686:M69013
 50 F-PLACE1000258
 KRAB zinc finger protein {alternative products}
 1.2e-14:241:70
 Hs.22556:U37251
 55 F-PLACE1000442
 Zinc finger protein 136 (clone pHZ-20)
 7.3e-89:774:76
 Hs.69740:U09367

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F-PLACE1000560
ESTs
1.5e-36:200:96
Hs.86541:AA214554

5

F-PLACE1000740
Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA, complete cds
6.5e-05:283:62
Hs.113285:AF017988

10

F-PLACE1000907
ESTs, Moderately similar to zinc finger protein [H.sapiens]
8.1e-38:237:89
Hs.139115:AA325104

15

F-PLACE1000912
ESTs
4.6e-61:331:95
Hs.17558:AA155762

20

F-PLACE1000914
Homo sapiens PB39 mRNA, complete cds
3.1e-45:500:69
Hs.18910:AF045584

25

F-PLACE1000927
ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
1.4e-123:655:94
Hs.8661:AI189791

30

F-PLACE1000986
ESTs
1.2e-105:494:99
Hs.19207:AA039595

35

F-PLACE1001016
Calcium channel, voltage-dependent, L type, alpha 1S subunit
0.011:432:59
Hs.1294:L33798

40

F-PLACE1001100
Human clone 23839 mRNA sequence
0.38:342:60
Hs.78362:U79249

45

F-PLACE1001114
Human mRNA for KIAA0303 gene, partial cds
0.085:339:59
Hs.54985:AB002301

50

F-PLACE1041123
ESTs
5.0e-14:505:61
Hs.99272:AI147740

55

F-PLACE1001183
ESTs, Weakly similar to gene pp21 protein [H.sapiens]
0.66:361:58

Hs.15984:A,1085974

F-PLACE1001229

ESTs, Weakly similar to D9481.15 gene product [S.cerevisiae]

9.3e-110:561:96

Hs.125155:W52093

F-PLACE1001231

ESTs, Weakly similar to sodium iodide symporter [H.sapiens]

1.0e-17:120:91

Hs.5167:AA053914

F-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds

4.1e-132:636:97

Hs.21198:AB018262

F-PLACE1001401

ESTs, Weakly similar to IgE receptor beta subunit [H.sapiens]

3.1e-100:516:95

Hs.43900:AA418443

F-PLACE 1001407

H.sapiens mRNA for B-HLH DNA binding protein

0.00015:244:66

Hs.66744:X99268

F-PLACE1001464

5' nucleotidase (CD73)

1.6e-152:742:96

Hs.153952:X55740

F-PLACE1001500

Bloom syndrome

5.7e-05:450:58

Hs.36820:U39817

F-PLACE1001516

Homo sapiens Rigui (RIGUI) mRNA, complete cds

2.3e-07:663:58

Hs.8114:AF022991

F-PLACE1001536

ESTs

4.6e-60:318:97

Hs.13026:H04491

F-PLACE1001564

H.sapiens mRNA for HE6 Tm7 receptor

8.8e-41:499:70

Hs.155681:X81892

F-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K⁺ channel alpha subunit (KCNS3) mRNA, complete cds

4.3e-125:585:98

Hs.47584:AF043472

F-PLACE1001788

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Homo sapiens mRNA for HYA22, complete cds
3.2e-22:234:75
Hs.147189:D88153

5 F-PLACE1001795

F-PLACE1001836
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
1.1e-18:162:80

10 Hs.157223:AA309318

F-PLACE1001918
Human p76 mRNA, complete cds
1.3e-22:693:60
Hs.28757:U81006

15

F-PLACE1001949
ESTs
0.97:243:63
Hs.151143:AA576926

20

F-PLACE1002080
Homo sapiens mRNA for KIAA0600 protein, partial cds
2.4e-130:622:98
Hs.9028:AF039691

25

F-PLACE1002095

F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds
2.7e-162:764:98
Hs.90415:AF095791

30

F-PLACE1002329
ESTs
1.5e-107:556:95
Hs.28907:AI343292

35

F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds
9.0e-19:190:77
Hs.137574:AF055917

40

F-PLACE1002374
Cathepsin L
2.0e-163:716:94
Hs.78056:X12451

45

F-PLACE1002518
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds
7.0e-19:396:64
Hs.28285:AF064801

50

F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds
8.3e-173:819:98
Hs.21198:AB018262

55

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F-PLACE1002726

Human mRNA for KIAA0362 gene, partial cds

1.0:310:59

Hs.25515:AB002360

5

F-PLACE1002905

ESTs

2.4e-74:415:92

Hs.110298:AA621807

10

F-PLACE1002911

ESTs, Weakly similar to Y53C12A.3 [C.elegans]

0.030:279:58

Hs.107747:AI357868

15

F-PLACE1002967

ESTs

3.3e-120:574:98

Hs.11090:W37646

20

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds

1.5e-50:450:75

Hs.72292:AF024636

25

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds

1.5e-153:722:98

Hs.15250:AF069301

30

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds

2.0e-142:682:97

Hs.30213:AF068227

35

F-PLACE1003428

Biotinidase

8.2e-06:265:62

Hs.78885:AF018631

40

F-PLACE1003438

ESTs

0.018:470:60

Hs.119482:AI361002

45

F-PLACE1003460

ESTs

0.019:211:60

Hs.92700:W37903

50

F-PLACE1003529

130 KD LEUCINE-RICH PROTEIN

0.53:208:63

Hs.87157:M92439

55

F-PLACE1003573

F-PLACE1003598

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Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
0.00064:302:64
Hs.96253:U79666

5 F-PLACE1003644
ESTs
1.3e-06:265:63
Hs.163564:R43678

10 F-PLACE1003737

F-PLACE1003772
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds
7.0e-09:448:61
15 Hs.155302:U57317

F-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
7.7e-109:521:97
20 Hs.154050:AC004131

F-PLACE1003845
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.2e-92:432:100
25 Hs.153778:AI246000

F-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.4e-172:814:98
30 Hs.22039:AB018301

F-PLACE1004028

F-PLACE1004078
35 GELSOLIN PRECURSOR, PLASMA
3.1e-49:616:67
Hs.80562:X04412

F-PLACE1004166
40 ESTs
7.6e-79:415:94
Hs.163741:AA551077

45 F-PLACE1004168

F-PLACE1004199
EST
6.8e-15:147:80
50 Hs.128205:AA972308

F-PLACE1004279
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
3.9e-20:456:62
55 Hs.23965:AF057039

F-PLACE1004282

F-PLACE1004305

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Homo sapiens mRNA for KIAA0740 protein, complete cds
8.7e-123:612:96
Hs.15099:AB018283

5 F-PLACE1004441
Human G protein-coupled receptor (GPR1) gene, complete cds
8.6e-99:501:96
Hs.159248:U13666

10 F-PLACE1004450
AMINOPEPTIDASE N
1.1e-09:587:57
Hs.1239:M22324

15 F-PLACE1004482

F-PLACE1004492
ESTs
2.1e-25:134:100
20 Hs.154475:AI199037

F-PLACE1004519
ESTs
1.0e-110:518:99
25 Hs.128505:AA306435

F-PLACE1004520
Pregnancy-specific beta 1-glycoprotein 7
1.3e-110:606:92
30 Hs.119662:M34715

F-PLACE1004630
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds
2.0e-139:749:92
35 Hs.82582:AB008375

F-PLACE1004637

40 F-PLACE1004648

F-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds
1.2e-99:590:90
45 Hs.9225:D88587

F-PLACE1004887
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
5.1e-06:486:62
50 Hs.135639:U77629

F-PLACE1005003
Human SNC19 mRNA sequence
1.5e-21:472:63
55 Hs.56937:U20428

F-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
4.7e-42:245:93

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Hs.151614:AF032456

F-PLACE1005031

ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]

2.9e-43:538:70

Hs.118991:AA675919

F-PLACE1005239

ESTs

2.4e-42:209:100

Hs.154475:AI199037

F-PLACE1005250

F-PLACE1005383

Homo sapiens UP50 mRNA, complete cds

8.5e-128:633:96

Hs.11494:AF093118

F-PLACE1005410

ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

1.3e-17:181:75

Hs.131840:AI016073

F-PLACE1005426

Pregnancy-specific beta-1 glycoprotein 4

2.3e-109:596:93

Hs.108936:X17097

F-PLACE1005519

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds

3.3e-55:521:74

Hs.72292:AF024636

F-PLACE1005539

HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U

5.8e-05:277:63

Hs.103804:AF068846

F-PLACE1005544

F-PLACE1005569

EST

0.38:60:75

Hs.137086:AA912486

F-PLACE1005601

Homo Sapiens angiotensin II receptor gene, complete cds

0.016:72:84

Hs.20954:AI054441

F-PLACE1005660

F-PLACE1005669

Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds

3.5e-08:461:60

Hs.113286:U77783

F-PLACE1005682

F-PLACE1005725

Huntingtin (Huntington disease)

5 1.1e-06:401:61

Hs.79391:L12392

F-PLACE1005736

ESTs

10 3.6e-63:343:94

Hs.17757:AA875839

F-PLACE1005745

ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]

15 6.9e-66:351:94

Hs.7870:AI078137

F-PLACE1005768

ESTs

20 7.9e-60:318:95

Hs.143856:AI186351

F-PLACE1005815

Mutated in colorectal cancers

25 0.0029:199:62

Hs.1345:M62397

F-PLACE1005878

ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]

30 5.0e-38:464:70

Hs.118991:AA675919

F-PLACE1005927

INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR

35 0.010:511:59

Hs.839:M86826

F-PLACE1006071

EST

40 0.68:224:59

Hs.161788:AA371859

F-PLACE1006073

Homo sapiens mRNA for glucuronyltransferase I, complete cds

45 5.5e-96:464:98

Hs.26492:AB009598

F-PLACE1006079

Homo sapiens BAC clone RG300E22 from 7q21-q31.1

50 1.5e-18:402:65

Hs.99348:AC004774

F-PLACE1006093

Homo sapiens mRNA for protein phosphatase 1 (PPP1R6)

55 0.0022:306:59

Hs.106471:Y18206

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F-PLACE1006208

HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1

0.022:425:57

Hs.74095:L20433

5

F-PLACE1006219

ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]

1.7e-61:294:100

Hs.153778:AI246000

10

F-PLACE1006277

EST

0.42:60:75

Hs.137086:AA912486

15

F-PLACE1006290

ESTs, Weakly similar to similar to M. musculus MERS and other AHPC/TSA proteins [C.elegans]

1.3e-51:260:98

Hs.132096:AA314601

20

F-PLACE1006443

Homo sapiens PB39 mRNA, complete cds

1.2e-53:553:70

Hs.18910:AF045584

25

F-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds

1.3e-141:655:99

Hs.14687:AB011148

30

F-PLACE1006716

EST

7.2e-12:148:75

Hs.162969:AA677315

35

F-PLACE1006786

ESTs

0.0050:125:72

Hs.109156:AA193501

40

F-PLACE1006809

ESTs

4.5e-99:477:98

Hs.135208:AI093908

45

F-PLACE1006959

ESTs

7.4e-72:381:93

Hs.4963:W29030

50

F-PLACE1007028

Homo sapiens p17-Beckwith-Wiedemann region 1 C (BWR1C) mRNA, complete cds

1.8e-18:364:65

Hs.154036:AF035444

55

F-PLACE1007040

H.sapiens NF-H gene, exon 1 (and joined CDS)

1.4e-09:501:61

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Hs.75735:X15306

F-PLACE1007077

ESTs, Moderately similar to testis-specific TCP20 [H.sapiens]

0.88:192:62

Hs.85818:AI216525

F-PLACE1007081

Human plectin (PLEC1) mRNA, complete cds

0.079:403:60

Hs.79706:U53204

F-PLACE1007096

YY1 transcription factor

0.64:173:64

Hs.97496:M77698

F-PLACE1007296

ER LUMEN PROTEIN RETAINING RECEPTOR 1

4.2e-73:542:83

Hs.78040:X55885

F-PLACE1007591

EST

0.026:136:64

Hs.130897:AI014389

F-PLACE1007626

Homo sapiens unknown mRNA, complete cds

2.6e-105:516:97

Hs.11441:AF047439

F-PLACE1007702

Homo sapiens mRNA for UTF1, complete cds

0.033:297:62

Hs.158307:AB011076

F-PLACE1007845

ESTs

4.8e-22:158:89

Hs.23445:AA489015

F-PLACE1007881

F-PLACE1007971

ESTs, Weakly similar to K07F5.14 [C.elegans]

1.1e-128:599:99

Hs.157918:AA313781

F-PLACE1008282

ESTs, Highly similar to HEME-EGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryctolagus cuniculus]

2.4e-65:353:94

Hs.130830:W27380

F-PLACE1008297

F-PLACE1008359

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Human arginine-rich protein (ARP) gene, complete cds
0.020:197:64
Hs.75412:M83751

5 F-PLACE1008469
Homo sapiens PB39 mRNA, complete: cds
5.3e-20:620:60
Hs.18910:AF045584

10 F-PLACE1008549
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
1.8e-145:693:98
Hs.159267:AF049703

15 F-PLACE1008657
VILLIN
2.3e-10:356:61
Hs.3046:X12901

20 F-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
1.5e-31:191:92
Hs.154844:U15128

25 F-PLACE1008744

F-PLACE1008984
Pregnancy-associated plasma protein A
0.0085:268:60
30 Hs.158229:U28727

F-PLACE1008985
Signal transducer and activator of transcription 5A
0.0047:249:64
35 Hs.14203:U43185

F-PLACE1009067
Human density enhanced phosphatase-1 mRNA, complete cds
2.0e-06:453:60
40 Hs.1177:U10886

F-PLACE1009196

F-PLACE1009279
45 Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
1.9e-11:327:64
Hs.75111:D87258

F-PLACE1009527
50 Human DNA-binding protein ABP/ZF mRNA, complete cds
6.8e-21:125:96
Hs.86185:U82613

F-PLACE1009546
55 TRANSCRIPTION FACTOR RELB
0.051:248:61
Hs.858:M83221

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F-PLACE1009600
 ESTs
 1.0:124:64
 Hs.52794:W51887
 5

F-PLACE1009735
 ESTs
 0.022:387:61
 Hs.132253:AI027207
 10

F-PLACE1009982
 F-PLACE1010011
 Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
 15
 1.3e-09:330:66
 Hs.143551:AF048693

F-PLACE1010078
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
 20
 8.3e-47:474:72
 Hs.13144:T67556

F-PLACE1010081
 Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
 25
 2.2e-151:733:97
 Hs.103755:AF027706

F-PLACE1010251
 Homo sapiens Na⁺/H⁺ exchanger regulatory factor 2 (NHERF-2) mRNA, complete cds
 30
 0.0037:405:60
 Hs.101813:AB016243

F-PLACE1010445
 ESTs
 35
 1.7e-45:235:97
 Hs.144501:N39767

F-PLACE1010713
 Hydroxysteroid (17-beta) dehydrogenase 3
 40
 2.8e-20:447:62
 Hs.477:U05659

F-PLACE1010784
 Human protease-activated receptor 3 (PAR3) mRNA, complete cds
 45
 0.56:199:59
 Hs.159196:U92971

F-PLACE 1010827
 H.sapiens mRNA for transmembrane protein rnp24
 50
 2.9e-09:346:64
 Hs.75914:X92098

F-PLACE1010968
 ESTs
 55
 0.00062:52:98
 Hs.119408:T87544

- 5 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds
6.0e-129:595:99
Hs.28190:AF094516
- 10 F-PLACE1011116

F-PLACE1011181
ESTs
1.0:301:58
Hs.80285:AI092519
- 15 F-PLACE1011236
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
1.1e-41:776:62
Hs.23965:AF057039
- 20 F-PLACE1011364
ESTs, Weakly similar to HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II [C.elegans]
3.7e-53:276:96
Hs.106499:W28299
- 25 F-PLACE1011407
ESTs, Moderately similar to ZINC FINGER PROTEIN 140 [H.sapiens]
3.2e-15:228:70
Hs.152174:AI199619
- 30 F-PLACE1011516
ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
1.7e-85:444:95
Hs.110978:AA843431
- 35 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
5.9e-145:722:96
Hs.148318:AF034611
- 40 F-PLACE1011824
Human Ste20-like kinase (MST2) mRNA, complete cds
1.6e-101:561:92
Hs.92317:U26424
- 45 F-PLACE1011978
Homo sapiens DNA from chromosome 19, BAC 33152
3.8e-67:733:72
Hs.55452:AC003973
- 50 F-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence)
7.8e-115:568:95
Hs.120856:AL022578
- 55 F-PLACE2000219
EST

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8.7e-11:137:75
Hs.98191:AA417044

5 F-PLACE3000181
Human protocadherin 42 mRNA, complete cds for abbreviated PC42
1.5e-128:745:90
Hs.79769:L11370

10 F-PLACE3000213
EST
1.0:219:63
Hs.98452:AA426058

15 F-PLACE4000354
ESTs
1.4e-13:190:71
Hs.138841:R94879

20 F-PLACE4000455
F-SKNMC1000004
Homo sapiens GABA-B receptor mRNA, complete cds
0.00039:275:62
Hs.12307:AF056085

25 F-SKNMC1000014
ESTs
3.3e-38:196:98
Hs.113307:H16716

30 F-SKNMC1000082
Complement component 4A
0.98:324:63
Hs.76682:K02403

35 F-THYRO1000036
Homo sapiens mRNA for putative ATPase, partial
0.98:199:60
Hs.91471:AJ006268

40 F-THYRO1000061
Human kinase Myt1 (Myt1) mRNA, complete cds
1.0:210:62
Hs.77783:AF014118

45 F-THYRO1000099
ESTs
2.5e-119:605:96
Hs.11782:W07369

50 F-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
1.6e-126:475:98
Hs.115418:AF016272

55 F-THYRO1000400
Human R kappa B mRNA, complete cds
0.64:223:63

Hs.95262:U08191

F-THYRO1000580

ESTs, Weakly similar to ZINC FINGER PROTEIN 7 [H.sapiens]

5.4e-27:248:76

Hs.25465:AA528105

F-THYRO1000584

Alpha mannosidase II isozyme

2.2e-06:528:60

Hs.155961:L28821

F-THYRO1000678

Gap junction protein, beta 2, 26kD (connexin 26)

1.3e-33:266:80

Hs.81795:M86849

F-THYRO1000776

Human involucrin mRNA

0.0025:497:59

Hs.157091:M13903

F-THYRO1000795

MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN

4.1e-19:532:62

Hs.3816:AF070548

F-THYRO1000846

Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds

0.029:387:60

Hs.27910:AF049105

F-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds

1.1e-92:529:89

Hs.12912:AF015913

F-THYRO1000956

Homo sapiens mRNA for G-protein coupled receptor

1.8e-15:474:64

Hs.155235:Y13583

F-THYRO1000964

Human OB binding protein-2 (OB-BP2) mRNA, complete cds

0.22:303:61

Hs.117005:U71383

F-THYRO1000999

EST

2.0e-05:198:63

Hs.146520:AI130948

F-THYRO1001063

Human mRNA for cerebroside sulfotransferase, complete cds

0.51:448:60

Hs.17958:D88667

F-THYRO1001071

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ESTs

2.1e-29:237:83

Hs.155582:AI125241

5 F-THYRO1001102
ESTs, Weakly similar to growth arrest inducible gene product [H.sapiens]
4.7e-32:208:88
Hs.7854:W21970

10 F-THYRO1001113
Homo sapiens dysferlin mRNA, complete cds
3.2e-53:684:68
Hs.143897:AF075575

15 F-THYRO1001128
ESTs
2.1e-120:589:97
Hs.62595:AA306052

20 F-THYRO1001205

F-THYRO1001237
ESTs
0.66:326:60
25 Hs.148352:U80757

F-THYRO1001242
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
0.017:188:63
30 Hs.57764:S87759

F-THYRO1001266
Human sodium iodide symporter mRNA, complete cds
8.6e-43:806:62
35 Hs.103983:U66088

F-THYRO1001327
ESTs
2.8e-50:264:96
40 Hs.154667:AI343524

F-THYRO1001456
EST
0.90:84:72
45 Hs.130049:AA902650

F-THYRO1001457
Protein kinase C, mu
6.0e-53:705:67
50 Hs.2891:X75756

F-THYRO1001471
ESTs
8.0e-52:278:94
55 Hs.7604:W31115

F-THYRO1001478
Human mRNA for KIAA0150 gene, partial cds

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- 0.79:150:66
Hs.98508:D63484
- 5 F-THYRO1001495
Homo sapiens KIAA0415 mRNA, complete cds
9.5e-75:550:82
Hs.7289:AB007875
- 10 F-THYRO1001523
ESTs
7.2e-19:142:86
Hs.140588:H60533
- 15 F-THYRO1001529
ESTs
5.7e-24:141:95
Hs.114172:AA703201
- 20 F-THYRO1001593
H.sapiens mRNA for serine/threonine protein kinase EMK
1.4e-70:643:74
Hs.157199:X97630
- 25 F-THYRO1001608
Human mRNA for KIAA0227 gene, partial cds
2.6e-07:533:59
Hs.79170:D86980
- 30 F-THYRO1001641
ESTs
0.87:269:59
Hs.14599:AA522511
- 35 F-THYRO1001700
Homo sapiens c-Jun N-terminal kinase kinase 2 (JNKK2) mRNA, complete cds
3.3e-05:441:59
Hs.110299:AF013589
- 40 F-THYRO1001702
Human plectin (PLEC1) mRNA, complete cds
0.00017:346:62
Hs.79706:U53204
- 45 F-THYRO1001725
Homo sapiens mRNA for procollagen I-N proteinase
1.3e-06:275:64
Hs.120330:AJ003125
- 50 F-THYRO1001770
Homo sapiens mRNA for HsGAK, complete cds
0.046:265:58
Hs.153227:D88435
- 55 F-THYRO1001803
EST
0.0085:201:63
Hs.158782:AI376601

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5 F-Y79AA1000030
ESTs
0.00051:276:60
Hs.111999:AA465020

10 F-Y79AA1000127
ESTs
1.3e-85:430:96
Hs.49932:W58552

15 F-Y79AA1000207
ESTs
4.5e-81:407:96
Hs.125308:A1376737

20 F-Y79AA1000226
ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis elegans]
0.00081:76:84
Hs.11221:A1192291

25 F-Y79AA1000270
Human mRNA for ORF, Xq terminal portion
9.9e-97:590:88
Hs.6551:D16469

30 F-Y79AA1000426
CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
0.045:507:59
Hs.82914:X68264

35 F-Y79AA1000521
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
0.0029:489:58
Hs.159543:AJ000479

40 F-Y79AA1000750
ESTs
9.9e-12:252:65
Hs.52885:H29851

45 F-Y79AA1000776
ESTs
1.4e-50:340:87
Hs.144198:A1017555

50 F-Y79AA1000777
Homo sapiens mRNA for putative transcription factor, partial
3.9e-10:501:61
Hs.26782:AJ009770

55 F-Y79AA1000876
Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds
1.3e-11:323:66
Hs.30250:AF055376

F-Y79AA1000888
Homo sapiens mRNA for KIAA0469 protein, complete cds

1.5e-05:641:58
Hs.7764:AB007938

F-Y79AA1000959

5 Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
5.3e-54:277:96
Hs.53066:AF093420

F-Y79AA1000967

10 Human mRNA for KIAA0369 gene, complete cds
8.1e-10:517:61
Hs.21355:AB002367

F-Y79AA1001013

15 ESTs
2.4e-44:259:93
Hs.109468:W52074

F-Y79AA1001056

20 ESTs, Moderately similar to maternal transcript Maid [M.musculus]
4.7e-07:90:87
Hs.36794:AI038407

F-Y79AA1001062

25 ESTs, Weakly similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]
1.6e-60:320:96
Hs.13982:W27344

F-Y79AA1001090

30 H.sapiens DAP-kinase mRNA
2.3e-06:465:59
Hs.153924:X76104

F-Y79AA1001212

35 Homo sapiens SL15 protein mRNA, complete cds
1.5e-163:763:98
Hs.6710:AF038961

F-Y79AA1001264

40 Homo sapiens mRNA for MSJ-1, complete cds
5.3e-15:367:64
Hs.3845:AB014888

F-Y79AA1001272

45 Human plectin (PLEC1) mRNA, complete cds
6.3e-05:325:63
Hs.79706:U53204

F-Y79AA1001328

50 Homo sapiens Delta mRNA, complete cds
1.8e-07:271:61
Hs.144631:AF003522

F-Y79AA1001426

55 Aldehyde dehydrogenase 7
0.94:485:56
Hs.83155:U10868

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F-Y79AA1001427
 NADH-CYTOCHROME B5 REDUCTASE
 1.7e-56:649:69
 Hs.75666:M28713
 5

F-Y79AA1001430
 Homo sapiens mRNA for KIAA0469 protein, complete cds
 2.8e-124:577:99
 Hs.7764:AB007938
 10

F-Y79AA1001523
 Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds
 1.1e-92:496:93
 Hs.128763:AF009353
 15

F-Y79AA1001530
 Human beta-tubulin gene (5-beta) with ten Alu family members
 1.0e-131:669:95
 Hs.108014:X00734
 20

F-Y79AA1001592
 ESTs
 1.2e-88:212:97
 Hs.131180:AA594251
 25

F-Y79AA1001727
 F-Y79AA1001787
 Human mRNA for KIAA0315 gene, partial cds
 0.48:248:63
 Hs.3989:AB002313
 30

F-Y79AA1001793
 ESTs
 1.4e-67:192:98
 Hs.118559:AA887084
 35

F-Y79AA1001795
 Homo sapiens mRNA for GalT4 protein
 5.3e-89:431:98
 Hs.21495:AL031228
 40

F-Y79AA1001799
 NUCLEAR FACTOR RIP140
 0.54:182:62
 Hs.155017:X84373
 45

F-Y79AA1001803
 ESTs, Highly similar to MELANOMA-ASSOCIATED ANTIGEN XP [Homo sapiens]
 0.72:169:63
 Hs.94011:AA627644
 50

F-Y79AA1001863
 EST
 1.0:114:63
 Hs.152260:AA489703
 55

F-Y79AA1002022

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B94 PROTEIN
5.7e-13:469:65
Hs.75522:M92357

5 F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence
1.7e-154:740:98
Hs.21970:AF052149

10 F-Y79AA1002121
EST
0.14:104:66
Hs.100070:M91493

15 F-Y79AA1002129
ESTs
5.1e-90:431:98
Hs.40719:AI183452

20 F-Y79AA1002213

F-Y79AA1002334
ESTs
5.0e-20:187:80
25 Hs.111900:AA397579

F-Y79AA1002373
ESTs
4.5e-37:192:98
30 Hs.118559:AA887084

F-Y79AA1002376
Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
1.2e-36:657:64
35 Hs.65248:AF063228

F-Y79AA1002378
Homo sapiens KIAA0426 mRNA, complete cds
4.9e-38:424:72
40 Hs.97476:AB007886

F-Y79AA1002381
CELL DIVISION PROTEIN KINASE 3
8.4e-17:580:61
45 Hs.100009:X66357

Homology search result 9

50 **[0302]** The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the
clone sequences of the 3'-ends.

Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
55 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0303] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

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[0304] Data were not shown for the clones in which the P-value was higher than 1.

5	R-HEMBA1000006 ESTs 1.0:85:71 Hs.130699:AA621478
10	R-HEMBA1000121 ESTs 1.3e-111:545:97 Hs.153432:AA098922
15	R-HEMBA1000128 ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae] 3.0e-98:532:93 Hs.7745:H92988
20	R-HEMBA1000275 ESTs 6.5e-11:81:81 Hs.163492:AI334460
25	R-HEMBA1000300 Homo sapiens mRNA for putative lipoic acid synthetase, partial 1.2e-39:309:81 Hs.53531:AJ224162
30	R-nnnnnnnnnnnnn ESTs 4.9e-95:455:98 Hs.154009:AI284184
35	R-HEMBA1000462 Homo sapiens clone 243 unknown mRNA, complete sequence 3.6e-91:313:94 Hs.20423:AF091094
40	R-HEMBA1000477 ESTs 4.7e-111:541:97 Hs.84526:AI341541
45	R-HEMBA1000590 Homo sapiens mRNA for matrilin-4, partial 2.6e-102:547:93 Hs.129361:AJ007581
50	R-HEMBA1000634 ESTs 0.85:189:62 Hs.131268:AA909162
55	R-HEMBA1000671 ESTs 6.5e-84:432:96 Hs.31991:T78668

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R-HEMBA1000713
 Homo sapiens 10kD protein (BC10) mRNA, complete cds
 4.0e-119:575:97
 Hs.5300:AF053470
 5

R-HEMBA1000732
 EST
 3.9e-81:435:92
 Hs.146718:AI146722
 10

R-nnnnnnnnnnnnn
 R-HEMBA1000875
 EST
 0.023:207:62
 Hs.148275:AA907849
 15

R-HEMBA1000940
 Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
 7.4e-31:211:81
 Hs.97203:U83171
 20

R-HEMBA1000962
 ESTs
 1.1e-104:515:97
 Hs.8978:W63573
 25

R-HEMBA1001 184
 EST
 7.1e-07:382:62
 Hs.124559:AA847550
 30

R-HEMBA1001221
 ESTs, Weakly similar to transmembrane protein [H.sapiens]
 1.2e-95:487:95
 Hs.22791:AI056665
 35

R-HEMBA1001228
 Human germline oligomeric matrix protein (COMP) mRNA, complete cds
 4.0e-42:170:92
 Hs.1584:AC003107
 40

R-HEMBA1001272
 ESTs
 5.7e-71:514:84
 Hs.26966:N74056
 45

R-HEMBA1001296
 EST
 1.7e-93:494:95
 Hs.102465:N27272
 50

R-HEMBA1001297
 Homo sapiens putative transcription factor CA150 mRNA, complete cds
 1.5e-93:466:96
 Hs.13063:AF017789
 55

R-HEMBA1001390

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ESTs

1.6e-42:181:89
Hs.139190:N55515

- 5 R-HEMBA1001563
Homo sapiens DEC-205 mRNA, complete cds
8.4e-42:311:83
Hs.153563:AF011333
- 10 R-HEMBA1001621
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
4.2e-56:386:86
Hs.9305:W84893
- 15 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
1.1e-80:433:93
Hs.10290:AF090988
- 20 R-HEMBA1001886
Zinc finger protein 141 (clone pHZ-44)
5.9e-61:530:80
Hs.159596:L15309
- 25 R-HEMBA1002048
ESTs
0.95:127:63
Hs.98690:AA431162
- 30 R-HEMBA1002131

R-HEMBA1002163
ESTs, Weakly similar to K09E9.2 [C.elegans]
5.9e-36:225:90
35 Hs.26813:AI339473

R-HEMBA1002167
ESTs
1.5e-35:325:80
40 Hs.124171:N98933

R-HEMBA1002178
MICROSOMAL DIPEPTIDASE PRECURSOR
0.99:243:61
45 Hs.109:J05257

R-HEMBA1002195
Deoxyhypusine synthase
1.9e-19:109:100
50 Hs.79064:U79262

R-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
2.0e-116:567:97
55 Hs.75607:D10522

R-HEMBA1002316
Homo sapiens mRNA for putative GTP-binding protein

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8.2e-20:160:85
Hs.101033:Y14391

5 R-HEMBA1002420
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.7e-78:402:97
Hs.108354:W19984

10 R-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
1.9e-91:443:97
Hs.1501:J04621

15 R-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
1.0e-111:551:96
Hs.41548:U63336

20 R-HEMBA1002551
ESTs
3.4e-107:553:96
Hs.92071:W80592

25 R-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
5.5e-108:568:95
Hs.19154:AF038660

30 R-HEMBA1002985
ESTs
4.4e-39:211:96
Hs.126894:AA932538

35 R-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.6e-115:571:96
Hs.148318:AF034611

40 R-HEMBA1003072
EST
0.044:220:61
Hs.136349:AA490873

45 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.2e-117:575:97
Hs.26350:AF049891

50 R-HEMBA1003120
Zinc finger protein 10 (KOX 1)
5.8e-41:412:73
Hs.2479:X78933

55 R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
4.2e-44:258:93
Hs.11494:AF093118

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R-HEMBA1003294
ESTs
4.3e-84:410:98
Hs.113517:AA418756

5

R-HEMBA1003315
ESTs, Weakly similar to TIP49 [R.norvegicus]
7.3e-73:476:87
Hs.6455:AA515838

10

R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
8.3e-117:557:98
Hs.23672:AF074264

15

R-HEMBA1003399
ESTs, Highly similar to MVP1 PROTEIN [Saccharomyces cerevisiae]
8.0e-94:526:92
Hs.12169:N38744

20

R-HEMBA1003487
ESTs
4.5e-84:417:96
Hs.21835:AA458524

25

R-HEMBA1003497
ESTs
1.4e-72:346:99
Hs.129837:AA778570

30

R-HEMBA1003530
ESTs
8.5e-82:459:91
Hs.22140:R41751

35

R-HEMBA1003602
ESTs
1.0e-101:592:90
Hs.124342:AA829829

40

R-HEMBA1003732
ESTs
2.1e-111:530:99
Hs.101660:AA481200

45

R-HEMBA1003945
Calcineurin B
2.9e-83:410:97
Hs.1335:M30773

50

R-HEMBA1004007
Homo sapiens PYRIN (MEFV) mRNA, complete cds
3.8e-57:382:77
Hs.113283:AF018080

55

R-HEMBA1004085
ESTs
3.0e-59:396:87

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Hs.102480:AA520980

R-nnnnnnnnnnnnn

Homo sapiens intersectin short form mRNA, complete cds

5 2.0e-116:569:97
Hs.66392:AF064244

R-HEMBA1004250

ESTs

10 1.6e-97:469:97
Hs.125529:AA883986

R-HEMBA1004391

EST

15 0.085:113:63
Hs.157582:AI356856

R-HEMBA1004444

ESTs

20 2.3e-88:430:98
Hs.141680:N98441

R-HEMBA1004454

ESTs

25 1.7e-71:338:100
Hs.103913:AA740543

R-HEMBA1004505

ESTs

30 2.2e-63:329:95
Hs.4814:AA631254

R-HEMBA1004785

EST

35 1.0:77:67
Hs.144066:AA905236

R-HEMBA1004797

ESTs

40 4.1e-11:71:100
Hs.27206:AA626782

R-HEMBA1004952

ESTs

45 6.0e-93:435:99
Hs.115120:AA935633

R-HEMBA1004971

ESTs

50 0.98:152:58
Hs.112621:AA608964

R-HEMBA1004982

ESTs

55 2.3e-109:516:98
Hs.14877:AA749081

R-HEMBA1005070

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Human mRNA for KIAA0310 gene, complete cds
4.0e-96:381:91
Hs.5716:AB002308

5 R-HEMBA1005084
ESTs
1.0:75:80
Hs.62119:AA043299

10 R-HEMBA1005145
Homo sapiens LIM protein mRNA, complete cds
1.6e-58:278:84
Hs.154103:AF061258

15 R-HEMBA1005230
ESTs
3.7e-65:336:95
Hs.124946:AI026708

20 R-HEMBA1005246

R-HEMBA1005267
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds
7.8e-75:536:81
25 Hs.44566:U28831

R-HEMBA1005337
EST
8.7e-58:291:97
30 Hs.48956:N64339

R-HEMBA1005430
ESTs
7.6e-83:388:100
35 Hs.28968:AA524690

R-HEMBA1005449
ESTs
5.0e-47:317:86
40 Hs.23650:H21144

R-HEMBA1005489
ESTs
1.8e-96:504:94
45 Hs.8028:AA053817

R-HEMBA1005522
EST
1.0:98:64
50 Hs.157385:AI364194

R-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
6.3e-117:579:96
55 Hs.7138:U29589

R-HEMBA1005698
ESTs

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- 1.6e-113:562:96
Hs.12942:AI042353
- 5 R-HEMBA1005913
ESTs
2.8e-109:564:94
Hs.28827:AI125541
- 10 R-HEMBA1005929
Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
9.6e-63:497:77
Hs.97203:U83171
- 15 R-HEMBA1005945
ESTs
1.1e-74:412:92
Hs.32246:AA464020
- 20 R-HEMBA1006016
ESTs
1.4e-18:162:82
Hs.149448:AI082465
- 25 R-HEMBA1006171
EST
0.049:94:69
Hs.159919:AA961766
- 30 R-HEMBA1006276
ESTs
6.3e-22:257:75
Hs.138847:N64493
- 35 R-HEMBA1006299
ESTs, Weakly similar to R06B9.b [C.elegans]
3.9e-107:596:91
Hs.30432:W28988
- 40 R-HEMBA1006311
Homo sapiens SALL1 gene, partial
0.99:273:60
Hs.123094:X98833
- 45 R-HEMBA1006335
ESTs
2.5e-72:447:89
Hs.23579:W38893
- 50 R-HEMBA1006357
ESTs
6.3e-15:187:74
Hs.161714:AA229078
- 55 R-HEMBA1006430
Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds
2.9e-47:303:88
Hs.129708:AF064090

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R-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds

5.5e-107:537:96

Hs.14511:AF026852

5

R-HEMBA1006517

ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]

2.7e-43:173:86

Hs.141505:N30650

10

R-HEMBA1006544

Homo sapiens mRNA for small GTP-binding protein, complete cds

5.8e-60:329:80

Hs.115325:D84488

15

R-HEMBA1006572

ESTs

7.2e-94:450:99

Hs.123933:AA758566

20

R-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds

2.3e-112:570:94

Hs.3628:AB014587

25

R-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial

1.7e-79:389:97

Hs.129361:AJ007581

30

R-HEMBA1006724

R-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial

1.0e-89:472:94

Hs.129361:AJ007581

35

R-HEMBA1006770

ESTs, Moderately similar to CAGH4 [H.sapiens]

2.0e-112:554:96

Hs.41641:AA428519

40

R-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial

3.0e-113:540:98

Hs.129361:AJ007581

45

R-HEMBA1006912

H.sapiens mRNA for phosphoinositide 3-kinase

5.9e-45:297:86

Hs.101238:Y11312

50

R-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds

5.8e-116:346:99

Hs.83070:L76687

55

R-HEMBA1006960

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ESTs
1.7e-110:519:99
Hs.22015:AI359551

5 R-HEMBA1007013
ESTs
0.53:280:59
Hs.143532:AI087321

10 R-HEMBA1007057

R-HEMBA1007063
EST
3.2e-41:310:83
15 Hs.163333:AA879053

R-HEMBA1007241
ESTs
1.8e-103:492:98
20 Hs.127478:AI188768

R-HEMBA1007291
Human mRNA for KIAA0266 gene, complete cds
8.7e-46:283:89
25 Hs.78878:D87455

R-HEMBA1007332
ESTs, Weakly similar to hTAFII100 [H.sapiens]
2.8e-17:161:80
30 Hs.3727:AA205887

R-HEMBA1000106
ESTs
1.3e-100:491:97
35 Hs.27774:AA576731

R-HEMBA1000276

R-HEMBA1000309
EST
1.0:150:64
40 Hs.125409:AA879096

R-HEMBA1000407
ESTs, Weakly similar to C47D12.2 [C.elegans]
4.1e-110:535:97
45 Hs.14328:AA503393

R-HEMBA1000447
Homo sapiens JWA protein mRNA, complete cds
5.6e-109:533:97
50 Hs.92384:AF070523

R-HEMBA1000542
ESTs, Weakly similar to C01H6.7 [C.elegans]
1.6e-88:497:91
55 Hs.18171:AA524327

R-HEMBB1000567

Insulin-like growth factor 2 (somatomedin A)

8.9e-61:369:88

Hs.155487:J03242

5

R-HEMBB1000642

ESTs

2.2e-44:308:84

Hs.141318:N71080

10

R-HEMBB1000668

ESTs, Weakly similar to hTAFII100 [H.sapiens]

2.5e-102:520:95

Hs.3830:AA167691

15

R-HEMBB1000679

ESTs

6.7e-36:188:97

Hs.154218:AA169554

20

R-HEMBB1000881

ESTs

8.4e-105:519:96

Hs.110967:AA570505

25

R-HEMBB1000905

ESTs

1.1e-94:454:98

Hs.52515:AA464314

30

R-HEMBB1001026

ESTs

0.22:93:69

Hs.119510:AA630235

35

R-HEMBB1001048

EST

0.42:127:66

Hs.147466:AI215091

40

R-HEMBB1001200

ESTs

3.7e-07:330:62

Hs.10109:AI148628

45

R-HEMBB1001407

MHC class II transactivator

3.8e-35:414:71

Hs.3076:U18259

50

R-HEMBB1001530

ESTs

2.4e-95:455:98

Hs.8956:AI146421

55

R-HEMBB1001547

ESTs

1.0e-111:533:98

Hs.33979:AI074147

R-HEM BB1001573

ESTs, Moderately similar to LL5 protein [R.norvegicus]

1.7e-06:64:95

Hs.131327:AI148746

R-HEM BB1001847

ESTs

1.4e-54:280:96

Hs.109755:AA180809

R-HEM BB1001959

Homo sapiens clone 24781 mRNA sequence

1.5e-104:504:97

Hs.108112:AF070640

R-HEM BB1001978

Homo sapiens mRNA for TRAF5, complete cds

7.0e-28:220:84

Hs.29736:AB000509

R-HEM BB1002039

ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]

1.5e-34:423:72

Hs.154912:N63897

R-HEM BB1002041

ESTs, Weakly similar to transmembrane protein [H.sapiens]

7.0e-122:575:98

Hs.22791:AI056665

R-HEM BB1002051

ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]

4.2e-43:298:84

Hs.141429:AA631915

R-HEM BB1002120

ESTs

1.4e-91:438:99

Hs.145014:AI218562

R-HEM BB1002162

ESTs

1.0e-34:238:86

Hs.164036:AA845659

R-HEM BB1002228

Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds

1.7e-59:583:77

Hs.129735:AF010144

R-HEM BB1002245

ESTs

9.1e-66:383:91

Hs.8989:R71365

5 R-HEMBB1002302
ESTs
3.6e-54:329:89
Hs.37706:AA005120

10 R-HEMBB1002427
ESTs
4.2e-83:400:98
Hs.130783:AI263114

15 R-HEMBB1002465
EST
9.9e-38:231:90
Hs.133443:AI061405

20 R-HEMBB1002661
ESTs
2.5e-101:472:99
Hs.26878:AI421289

25 R-HEMBB1002663
Small inducible cytokine A5 (RANTES)
7.1e-43:268:88
Hs.155464:AF088219

30 R-HEMBB1002693
ESTs
4.6e-84:435:96
Hs.155522:AA829725

35 R-MAMMA1000046
EST
3.9e-06:196:65
Hs.136664:AA707467

40 R-MAMMA1000102
Human G protein-coupled receptor (STRL22) mRNA, complete cds
1.1e-31:237:83
Hs.46468:U45984

45 R-MAMMA1000106
ESTs
1.3e-65:333:95
Hs.130749:AI284219

50 R-MAMMA1000118
ESTs
7.3e-95:465:97
Hs.119286:AA126730

55 R-MAMMA1000141
ESTs
4.2e-94:515:93
Hs.8116:H23508

R-MAMMA1000204
Homo sapiens dysferlin mRNA, complete cds
2.3e-108:542:96

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Hs.143897:AF075575

R-MAMMA1000226

ESTs

5 2.1e-112:535:98

Hs.105761:AA903862

R-MAMMA1000403

ESTs

10 1.5e-36:162:83

Hs.152413:AA780515

R-MAMMA1000449

EST

15 1.5e-40:347:78

Hs.163333:AA879053

R-MAMMA1000457

Homo sapiens clone 638 unknown mRNA, complete sequence

20 2.6e-117:570:97

Hs.5825:AF091084

R-MAMMA1000473

ESTs

25 1.3e-62:308:99

Hs.53565:W02102

R-MAMMA1000496

Phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1)

30 0.051:125:68

Hs.189:AC005759

R-MAMMA1000528

ESTs

35 2.4e-12:216:71

Hs.134105:AI078038

R-MAMMA1000591

ESTs

40 5.0e-104:509:98

Hs.151678:AA032243

R-MAMMA1000614

Homo sapiens mRNA for KIAA0665 protein, complete cds

45 0.57:251:62

Hs.119004:AB014565

R-MAMMA1000652

ESTs

50 0.93:49:87

Hs.13248:R54144

R-MAMMA1000681

ESTs

55 1.3e-87:434:97

Hs.46668:N47089

R-MAMMA1000706

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Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds
3.7e-48:232:100
Hs.18953:AF067223

5 R-MAMMA1000788
ESTs
3.7e-108:559:94
Hs.38969:AA130220

10 R-MAMMA1000810
ESTs
1.2e-45:347:80
Hs.146811:AA410788

15 R-MAMMA1000814
ESTs
1.1e-18:288:70
Hs.140608:N53448

20 R-MAMMA1000881
ESTs
1.9e-107:557:96
Hs.141602:N63562

25 R-MAMMA1000986
ESTs
3.8e-46:342:83
Hs.132722:AA618531

30 R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds
1.2e-109:552:96
Hs.102171:AB003184

35 R-MAMMA1001043
ESTs
2.3e-88:445:96
Hs.20450:AI094818

40 R-MAMMA1001066
Homo sapiens KIAA0414 mRNA, partial cds
1.5e-43:282:81
Hs.127649:AB007874

45 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
3.0e-116:566:97
Hs.20423:AF091094

50 R-MAMMA1001141
ESTs
1.2e-104:496:98
Hs.29669:AI285856

55 R-MAMMA1001150
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
1.9e-59:284:100
Hs.9915:AI300083

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R-MAMMA1001237
 ESTs
 0.45:206:62
 Hs.121366:AA758653
 5

R-MAMMA1001284
 ESTs
 6.3e-40:279:85
 Hs.109765:AI096738
 10

R-MAMMA1001310
 ESTs, Moderately similar to !!!! ALU SUBFAMTLY J WARNING ENTRY !!!! [H.sapiens]
 5.1e-98:498:96
 Hs.27264:AA159597
 15

R-MAMMA1001418
 Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds
 1.2e-41:302:85
 Hs.86188:D87845
 20

R-MAMMA1001532
 ESTs
 3.9e-22:331:71
 Hs.141840:AA028117
 25

R-MAMMA1001609
 Small inducible cytokine A5 (RANTES)
 1.5e-31:277:78
 Hs.155464:AF088219
 30

R-MAMMA1001615
 ESTs
 1.1e-72:376:95
 Hs.135569:AA923461
 35

R-MAMMA1001623
 ESTs
 7.9e-106:505:98
 Hs.22908:AI224910
 40

R-MAMMA1001634
 Homo sapiens PYRIN (MEFV) mRNA, complete cds
 1.9e-44:428:76
 Hs.113283:AF018080
 45

R-MAMMA1001893
 ESTs
 8.0e-67:367:92
 Hs.19210:W26097
 50

R-MAMMA1001901
 Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492
 4.7e-35:342:69
 Hs.127338:AB007961
 55

R-MAMMA1001957
 Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
 5.5e-47:383:79

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	Hs.1361:M55053
	R-MAMMA1001978
	ESTs
5	6.6e-108:560:95
	Hs.8859:AA191552
	R-MAMMA1002070
10	R-MAMMA1002080
	ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]
	9.8e-105:542:94
	Hs.10092:AI189282
15	R-MAMMA1002087
	ESTs
	4.0e-19:153:84
	Hs.136678:AA730474
20	R-MAMMA1002095
	ESTs
	6.8e-34:196:93
	Hs.48119:AA454227
25	R-MAMMA1002128
	ESTs, Highly similar to ABC1 PROTEIN PRECURSOR [Saccharomyces cerevisiae]
	9.0e-96:503:94
	Hs.39088:AA194773
30	R-MAMMA1002142
	ESTs
	5.6e-21:145:90
	Hs.62119:AA043299
35	R-MAMMA1002165
	ESTs
	1.6e-35:351:76
	Hs.140413:N47721
40	R-MAMMA1002205
	Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds
	6.4e-42:217:79
	Hs.133089:AF064019
45	R-MAMMA1002224
	ESTs
	0.50:170:64
	Hs.144140:H04293
50	R-MAMMA1002234
	R-MAMMA1002586
	ESTs
	5.0e-105:529:96
55	Hs.4814:AA631254
	R-MAMMA1002633
	ESTs

7.3e-97:470:98
Hs.38039:AI360128

5 R-MAMMA1003126
ESTs
6.1e-114:567:97
Hs.20733:AI417917

10 R-NT2RM4000100
ESTs
3.6e-71:343:99
Hs.92186:AI080282

15 R-NT2RM4000115
ESTs
1.5e-86:405:100
Hs.129151:AA988192

20 R-NT2RM4000198
ESTs
8.4e-83:462:93
Hs.96772:AI369496

25 R-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds
5.4e-95:440:100
Hs.110804:U12255

30 R-NT2RM4000295
ESTs
1.1e-112:544:97
Hs.21452:AA581881

35 R-NT2RM4000326
EST
4.0e-59:301:96
Hs.86264:AA206496

40 R-NT2RM4000417
ESTs
2.0e-88:489:93
Hs.29098:AA521439

45 R-NT2RM4000444
ESTs
6.4e-90:497:92
Hs.6129:U66676

50 R-NT2RM4000587
ESTs
1.0e-97:473:98
Hs.24947:AA039350

55 R-NT2RM4000593
ESTs
9.8e-109:554:95
Hs.7579:AA775865

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R-NT2RM4000648
 ESTs, Moderately similar to GLYPICAN-1 PRECURSOR [Homo sapiens]
 7.6e-39:262:85
 Hs.118407:AA001322
 5

R-NT2RM4000761
 ESTs
 6.4e-86:433:95
 Hs.153428:AI246519
 10

R-NT2RM4000965
 ESTs
 2.8e-102:523:96
 Hs.61790:AA421156
 15

R-NT2RM4000997
 R-NT2RM4001321
 ESTs
 2.4e-66:315:100
 Hs.75425:AA149434
 20

R-NT2RM4001325
 ESTs
 0.99:104:62
 Hs.116257:AA628680
 25

R-NT2RM4001377
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 9.3e-113:553:96
 Hs.77864:AB014538
 30

R-NT2RM4001735
 Homo sapiens clone 23904 mRNA sequence
 1.5e-107:553:94
 Hs.67364:AF052129
 35

R-NT2RM4001768
 EST
 1.6e-14:82:85
 Hs.140922:R51520
 40

R-NT2RM4001843
 ESTs
 2.1e-123:579:98
 Hs.3741:AI057614
 45

R-NT2RM4002352
 Homo sapiens hLRp105 mRNA for LIJL receptor related protein 105, complete cds
 1.8e-109:557:95
 Hs.143641:AB009462
 50

R-NT2RP2000092
 ESTs
 3.3e-08:286:65
 Hs.79881:AA401302
 55

R-NT2RP2000178

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ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
2.3e-95:462:98
Hs.47305:AA195153

5 R-NT2RP2000240
ESTs
1.3e-55:272:98
Hs.125522:AI299693

10 R-NT2RP2000394
ESTs
2.4e-107:528:96
Hs.28555:W55892

15 R-NT2RP2000447
ESTs, Moderately similar to dynamin, internal form 2, short C-terminal form [H.sapiens]
1.6e-67:357:94
Hs.128788:AA424076

20 R-NT2RP2000479
ESTs
2.6e-48:312:86
Hs.146811:AA410788

25 R-NT2RP2000514
EST
3.2e-63:348:93
Hs.44542:N33966

30 R-NT2RP2000533
ESTs
0.017:307:57
Hs.97873:AA402799

35 R-NT2RP2000616
ESTs
1.0e-91:475:95
Hs.50344:AI300539

40 R-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
1.4e-66:322:98
Hs.25846:AB016068

45 R-NT2RP2000663
ESTs
8.2e-59:311:96
Hs.9728:T98746

50 R-NT2RP2000712
EST
1.7e-27:239:76
Hs.161561:W60681

55 R-NT2RP2000739
ESTs, Weakly similar to zinc finger protein [H.sapiens]
6.3e-86:462:93
Hs.13323:AA897542

R-NT2RP2000818
ESTs
7.3e-99:485:97
Hs.100525:AI310204

5

R-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.2e-100:505:96
Hs.82128:AJ012159

10

R-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds
6.6e-59:306:95
Hs.115763:AB014576

15

R-NT2RP2001223
ESTs
1.2e-94:475:95
Hs.27556:AA115361

20

R-NT2RP2001276
ESTs, Moderately similar to regulatory protein [M.musculus]
4.7e-65:354:92
Hs.105547:AI361036

25

R-NT2RP2001388
ESTs
5.5e-83:459:93
Hs.15713:AA485755

30

R-NT2RP2001469
ESTs, Weakly similar to teg292 protein [M.musculus]
2.0e-30:233:83
Hs.68791:AA527270

35

R-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
2.1e-84:426:95
Hs.82165:L38969

40

R-NT2RP2001495
ESTs, Weakly similar to transporter protein [H.sapiens]
1.7e-14:130:84
Hs.18272:N78499

45

R-NT2RP2001514
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
3.3e-45:242:95
Hs.9275:AA973284

50

R-NT2RP2001538
EST
1.4e-05:111:73
Hs.137268:T39311

55

R-NT2RP2001562
EST
0.50:35:91

Hs.140505:AA804211

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence

1.0e-95:485:95

Hs.94785:AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds

4.2e-105:576:92

Hs.5378:AB018305

R-NT2RP2001769

ESTs

4.2e-102:548:93

Hs.14014:AA745592

R-NT2RP2001817

ESTs

6.0e-97:472:97

Hs.31176:AI037953

R-NT2RP2001878

ESTs

3.3e-94:475:95

Hs.144655:AI279798

R-NT2RP2001903

ESTs

1.7e-88:461:95

Hs.112218:AI038601

R-NT2RP2001915

ESTs

7.8e-96:480:96

Hs.100890:AA779892

R-NT2RP2001921

ESTs

2.5e-88:466:94

Hs.104859:AA779101

R-NT2RP2001948

ESTs

1.9e-81:439:91

Hs.105463:AA583017

R-NT2RP2001956

ESTs

8.7e-85:477:91

Hs.12101:AA677423

R-NT2RP2002015

ESTs

3.5e-85:431:95

Hs.75425:AA149434

R-NT2RP2002063

EST
0.0083:199:62
Hs.48699:N63049

5 R-NT2RP2002188
ESTs
1.5e-108:559:94
Hs.47320:AA057440

10 R-NT2RP2002232
ESTs
2.5e-113:576:95
Hs.7099:AI089774

15 R-ntntntntntntntntntntnt
Human mRNA for KIAA0383 gene, partial cds
8.0e-102:511:96
Hs.27590:AB002381

20 R-NT2RP2002409
ESTs
3.2e-84:432:95
Hs.128443:AI281991

25 R-NT2RP2002510
ESTs
1.3e-42:303:82
Hs.146811:AA410788

30 R-NT2RP2002527
Thromboxane A2 receptor
2.9e-23:164:88
Hs.89887:D38081

35 R-NT2RP2002533
Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds
4.0e-117:580:96
Hs.127436:AF040709

40 R-NT2RP2002564
Human zinc-finger protein C2H2-150 mRNA, complete cds
4.0e-111:569:94
Hs.108139:U38864

45 R-NT2RP2002674
ESTs, Weakly similar to putative p150 [H.sapiens]
0.010:293:60
Hs.140964:AI214400

50 R-NT2RP2002721
ESTs
5.6e-10:165:69
Hs.108745:H95644

55 R-NT2RP2002824
EST
0.0055:209:58

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Hs.136259:AA347883

5 R-NT2RP2002942
ESTs
9.2e-82:422:96
Hs.140952:R59211

10 R-NT2RP2002974
ESTs
5.6e-99:507:96
Hs.43314:AA160543

15 R-NT2RP2002976
ESTs
2.9e-78:397:91
Hs.83575:N28730

20 R-NT2RP2003042
ESTs
2.7e-107:526:97
Hs.6770:AA972732

25 R-NT2RP2003179
ESTs
2.9e-59:335:92
Hs.87019:AA760977

30 R-NT2RP2003210
ESTs
2.1e-80:419:94
Hs.25354:N28667

35 R-NT2RP2003302
ESTs, Moderately similar to ZINC FINGER PROTEIN 7 [Homo sapiens]
2.1e-92:443:98
Hs.112508:AA599140

40 R-NT2RP2003369
ESTs
9.7e-84:462:92
Hs.155116:C16874

45 R-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
1.3e-112:549:97
Hs.7414:AB007927

50 R-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
4.9e-56:286:96
Hs.31575:AF100141

55 R-NT2RP2003469
Human mRNA for KIAA0355 gene, complete cds
6.6e-40:302:83
Hs.153014:AB002353

R-NT2RP2003545

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- ESTs
8.0e-121:572:98
Hs.23643:AI299952
- 5 R-NT2RP2003593
EST
1.0:124:62
Hs.59890:AA001879
- 10 R-NT2RP2003599
EST
5.2e-06:319:60
Hs.147887:AI223203
- 15 R-NT2RP2003655
ESTs
9.3e-107:519:97
Hs.5831:AA176450
- 20 R-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein
5.3e-112:549:96
Hs.23581:Y12670
- 25 R-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds
1.7e-113:571:96
Hs.84123:AB002363
- 30 R-NT2RP2003940
EST
3.0e-71:385:93
Hs.162657:AA603590
- 35 R-NT2RP2003950
Homo sapiens clone 24778 unknown mRNA
5.0e-98:494:95
Hs.25306:AF070572
- 40 R-NT2RP2004069
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end
6.3e-54:556:74
Hs.103948:K00627
- 45 R-NT2RP2004108
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
6.9e-92:442:98
Hs.14831:AI261191
- 50 R-NT2RP2004141
ESTs
8.3e-29:171:93
Hs.25700:AI338437
- 55 R-NT2RP2004179
ESTs
3.1e-71:461:88
Hs.6748:R68509

5 R-NT2RP2004205
 ESTs
 2.6e-44:397:78
 Hs.95115:AA206594

10 R-NT2RP2004447
 ESTs
 4.0e-101:494:97
 Hs.51655:AA523276

15 R-NT2RP2004495
 ESTs, Weakly similar to transporter protein [H.sapiens]
 6.1e-71:417:92
 Hs.18272:N78499

20 R-NT2RP2004524
 ESTs
 1.8e-93:482:95
 Hs.119285:AI225008

25 R-NT2RP2004556
 Homo sapiens mRNA for KIAA0459 protein, partial cds
 8.8e-48:353:82
 Hs.28169:AB007928

30 R-NT2RP2004606
 Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
 3.5e-116:576:96
 Hs.148726:X03124

35 R-NT2RP2004648
 ESTs
 5.9e-114:600:93
 Hs.3741:AI057614

40 R-NT2RP2004670
 ESTs
 1.7e-92:488:94
 Hs.6262:T89093

45 R-NT2RP2004794
 EST
 0.44:205:57
 Hs.147759:AI220726

50 R-NT2RP2004837
 ESTs
 6.9e-111:576:94
 Hs.12305:AA166889

55 R-NT2RP2004847
 ESTs
 8.3e-94:445:99
 Hs.53996:AI268861

R-NT2RP2005027
 GLUCOSE TRANSPORTER TYPE 3, BRAIN
 2.5e-104:508:97

Hs.7594:M20681

R-NT2RP2005069

ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]

5 4.7e-111:541:97

Hs.26510:AA700425

R-NT2RP2005163

ESTs

10 6.8e-64:327:89

Hs.83575:N28730

R-NT2RP2005181

ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]

15 1.6e-106:527:97

Hs.86362:AA205485

R-NT2RP2005247

MHC class II transactivator

20 7.9e-35:465:69

Hs.3076:U18259

R-NT2RP2005378

ESTs

25 3.4e-110:566:94

Hs.23060:N64748

R-NT2RP2005391

ESTs

30 5.5e-82:463:92

Hs.118793:AA192438

R-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds

35 2.6e-101:526:94

Hs.58103:AB018346

R-NT2RP2005463

ESTs, Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C.elegans]

40 7.6e-111:554:97

Hs.16492:N95400

R-NT2RP2005514

ESTs

45 1.8e-97:490:95

Hs.109677:AA447864

R-NT2RP2005535

EST

50 5.1e-40:399:73

Hs.127142:AA937570

R-NT2RP2005541

ESTs

55 5.2e-114:573:96

Hs.70823:AI378619

R-NT2RP2005597

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ESTs, Weakly similar to rotated abdomen protein [D.melanogaster]
3.7e-109:543:96
Hs.99654:AA670164

5 R-nnnnnnnnnnnnn
ESTs
1.1 e-100:501:97
Hs.112011:AA987961

10 R-NT2RP2005666
ESTs
2.7e-106:560:94
Hs.42814:AA205754

15 R-NT2RP2005774
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence
7.0e-96:440:96
Hs.139345:AF035364

20 R-NT2RP2005878
ESTs
2.8e-89:479:93
Hs.142305:R42591

25 R-NT2RP2005883
ESTs
1.0e-85:431:96
Hs.6909:AA928115

30 R-NT2RP2005887
ESTs
5.5e-109:566:94
Hs.12305:AA166889

35 R-nnnnnnnnnnnnn
Paired box homeotic gene 6 (aniridia, keratitis)
1.6e-116:578:96
Hs.89506:M93650

40 R-NT2RP2005994
EST
0.0061:129:68
Hs.160756:AI310589

45 R-NT2RP2006004
ESTs, Weakly similar to KIAA0405 [H.sapiens]
4.7e-45:303:86
Hs.14146:W92235

50 R-NT2RP2006042
EST
0.64:84:71
Hs.133275:AI053487

55 R-NT2RP2006092
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
1.1e-75:384:95
Hs.32822:AI194045

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BNSDOCID: <EP___1130094A2_I_>

EP 1 130 094 A2

Hs.147759:AI220726

R-NT2RP3000172

ESTs

5 2.0e-89:494:93

Hs.6262:T89093

R-NT2RP3000201

Human mRNA for KIAA0355 gene, complete cds

10 1.1e-40:305:83

Hs.153014:AB002353

R-NT2RP3000232

ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]

15 5.7e-65:386:90

Hs.4841:AI279875

R-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds

20 1.1e-109:541:97

Hs.23672:AF074264

R-NT2RP3000378

EST

25 2.0e-05:112:74

Hs.137268:T39311

R-NT2RP3000436

EST

30 1.2e-08:347:62

Hs.158830:AI377454

R-NT2RP3000444

ESTs

35 3.3e-70:314:99

Hs.57973:AI263207

R-NT2RP3000460

EST

40 1.9e-50:294:92

Hs.7260:T23737

R-NT2RP3000481

PROBABLE G PROTEIN-COUPLED RECEPTOR GPR6

45 1.0:183:59

Hs.46332:U18549

R-NT2RP3000616

ESTs

50 3.0e-71:309:93

Hs.41296:N71923

R-NT2RP3000645

ESTs

55 1.5e-101:550:92

Hs.21910:AA020743

R-NT2RP3000652

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ESTs

6.6e-88:411:100

Hs.43134:AA766138

- 5 R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds
1.0e-104:542:94
Hs.158286:AB007915
- 10 R-NT2RP3000677
ESTs
0.33:307:59
Hs.133022:AI374739
- 15 R-NT2RP3000721
ESTs
1.6e-75:390:90
Hs.83575:N28730
- 20 R-NT2RP3000789
ESTs
1.5e-71:340:99
Hs.37776:H93038
- 25 R-NT2RP3000818
ESTs
1.9e-52:330:88
Hs.111052:H80504
- 30 R-NT2RP3000820
EST
9.1e-05:82:74
Hs.124352:AA830406
- 35 R-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
1.5e-100:522:94
Hs.77864:AB014538
- 40 R-NT2RP3000871
ESTs
3.9e-76:424:91
Hs.121642:AA772262
- 45 R-NT2RP3000907
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
4.5e-95:493:94
Hs.9275:AA973284
- 50 R-NT2RP3000921
ESTs
4.1e-52:283:94
Hs.49714:AA442453
- 55 R-NT2RP3001012
Homo sapiens mRNA for CMP-sialic acid transporter, complete cds
0.60:250:61
Hs.82921:D87969

5
R-NT2RP3001044
ESTs
3.5e-106:547:95
Hs.12305:AA166889

10
R-NT2RP3001061
ESTs
1.3e-96:453:99
Hs.4916:AI149707

15
R-NT2RP3001159
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.8e-47:302:90
Hs.6281:AA523081

20
R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
2.8e-118:561:98
Hs.3657:AB018327

25
R-NT2RP3001195
ESTs
1.5e-40:461:72
Hs.152438:AI334078

30
R-NT2RP3001240
EST
1.9e-50:294:92
Hs.7260:T23737

35
R-NT2RP3001271
ESTs
1.1e-77:432:92
Hs.12211:AA908631

40
R-NT2RP3001322
ESTs
0.25:331:60
Hs.44330:N32264

45
R-NT2RP3001542
EST
0.0032:432:58
Hs.148107:AA693476

50
R-NT2RP3001560
EST
3.5e-50:281:93
Hs.101727:H16171

55
R-NT2RP3001592
ESTs
3.2e-65:344:93
Hs.28964:AA715101

R-NT2RP3001685
EST
3.0e-37:165:81

Hs.160895:AI365871

R-NT2RP3001738

ESTs, Weakly similar to T13F2.1 [C.elegans]

5 3.8e-47:302:90

Hs.6281 :AA523081

R-NT2RP3001754

EST

10 0.00043:104:69

Hs.148331:AA911426

R-NT2RP3001858

ESTs

15 7.6e-93:502:93

Hs.153524:AA533582

R-NT2RP3001976

ESTs

20 5.0e-104:516:96

Hs.35461:AA777644

R-NT2RP3002015

25 R-NT2RP3002160

ESTs

1.4e-34:178:99

Hs.130783:AI263114

30 R-NT2RP3002281

Homo sapiens mRNA for KIAA0765 protein, partial cds

3.5e-83:446:93

Hs.62318:AB018308

35 R-NT2RP3002286

ESTs

2.1e-103:513:97

Hs.58570:AA521423

40 R-NT2RP3002311

ESTs

1.4e-108:538:96

Hs.3741:AI057614

45 R-NT2RP3002324

ESTs

3.7e-102:483:99

Hs.99668:AA829521

50 R-NT2RP3002342

ESTs, Weakly similar to transporter protein [H.sapiens]

2.0e-60:339:95

Hs.18272:N78499

55 R-NT2RP3002353

ESTs

6.8e-98:484:97

Hs.9732:AA527784

NNNNNNNNNNNNNNNN

Homo sapiens mRNA for KIAA0788 protein, partial cds

2.7e-29:214:85

Hs.2397:Z70200

5

NNNNNNNNNNNNNNNN

ESTs

3.0e-72:389:94

Hs.32246:AA464020

10

R-NT2RP3002448

ESTs, Weakly similar to Y48E1B.t [C.elegans]

1.0e-19:131:75

Hs.8715:H58021

15

R-NT2RP3002571

ESTs

1.1e-78:407:95

Hs.27356:AA740928

20

R-NT2RP3002664

ESTs

1.2e-56:341:90

Hs.23308:AA115020

25

R-NT2RP3002721

EST

2.8e-41:302:82

Hs.124936:AA825548

30

R-NT2RP3002737

EST

1.7e-51:267:97

Hs.161348:AI422470

35

R-NT2RP3002738

ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]

1.7e-106:530:96

Hs.4894:AI191323

40

R-NT2RP3002790

R-NT2RP3002836

ESTs

4.6e-49:282:92

Hs.107979:AA146994

45

R-NT2RP3002887

ESTs

6.3e-98:516:94

Hs.11900:AA535065

50

R-NT2RP3002900

ESTs

2.0e-29:155:99

Hs.153329:AA112325

55

R-NT2RP3002958

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Homo sapiens clone 23851 mRNA sequence

6.6e-119:575:98

Hs.10065:AF035313

5 R-NT2RP3002983
ESTs
1.1e-61:374:90
Hs.17834:AA128246

10 R-NT2RP3003000
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds
4.1e-65:358:94
Hs.122359:AF051946

15 R-NT2RP3003076
ESTs
2.6e-95:507:93
Hs.21910:AA020743

20 R-NT2RP3003354
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
2.1e-78:385:96
Hs.92177:AI207792

25 R-NT2RP3003448
ESTs
6.7e-105:521:96
Hs.106833:AA470128

30 R-NT2RP3003469
ESTs
1.1e-91:461:96
Hs.75425:AA149434

35 R-NT2RP3003473

R-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
1.6e-92:445:97

40 Hs.130988:Y17999

R-NT2RP3003532
ESTs
0.022:193:63

45 Hs.122593:Z99400

R-nnnnnnnnnnnnnnn
EST
0.036:279:59

50 Hs.158745:AI375513

R-NT2RP3003559
ESTs

55 9.8e-106:513:97
Hs.44970:AI061464

R-NT2RP3003614
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510

0.00016:113:69
Hs.92660:AB007979

5 R-NT2RP3003729
ESTs
1.2e-43:289:86
Hs.106401:R50967

10 R-NT2RP3003849
ESTs
5.4e-91:435:98
Hs.144840:AI221746

15 R-NT2RP3003874
ESTs
0.21:323:59
Hs.42919:AA805764

20 R-NT2RP3003963
ESTs
1.7e-90:438:97
Hs.105894:AA564110

25 R-NT2RP3004000
ESTs
2.9e-101:559:91
Hs.21910:AA020743

30 R-NT2RP3004025
ESTs
2.3e-108:517:98
Hs.15356:AA911109

35 R-NT2RP3004075
ESTs
7.4e-84:453:93
Hs.22412:AA523036

40 R-NT2RP3004083
ESTs, Weakly similar to R06B9.b [C.elegans]
4.2e-84:474:91
Hs.30432:W28988

45 R-NT2RP3004090
ESTs
1.0:207:61
Hs.92832:AA631027

50 R-NT2RP3004119
EST
1.8e-50:248:99
Hs.162023:AA506128

55 R-NT2RP3004130
ESTs
1.1e-103:520:96
Hs.10491:W28968

5 R-NT2RP3004133
ESTs
4.7e-104:545:93
Hs.15727:H98190

10 R-NT2RP3004202
ESTs
1.1e-98:471:98
Hs.61884:AI335985

15 R-NT2RP3004294
ESTs, Weakly similar to R06B9.b [C.elegans]
2.4e-96:500:94
Hs.30432:W28988

20 R-NT2RP3004309
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.5e-48:308:90
Hs.6281:AA523081

25 R-NT2RP3004321
ESTs
2.6e-99:494:97
Hs.19306:N53491

30 R-NT2RP3004345
ESTs
5.4e-95:444:99
Hs.107149:AI379497

35 R-NT2RP3004355
ESTs
3.9e-99:490:97
Hs.43410:N23651

40 R-NT2RP3004374
ESTs
1.2e-90:462:95
Hs.75425:AA149434

45 R-NT2RP3004406
ESTs
1.9e-100:502:96
Hs.24936:AA479402

50 R-NT2RP3004481
ESTs
1.6e-53:370:87
Hs.11953:AA194120

55 R-NT2RP3004552
ESTs, Weakly similar to gene SEZ-6 [M.musculus]
7.8e-92:488:93
Hs.6314:AA522619

R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
2.6e-50:352:84

EP 1 130 094 A2

Hs.26285:AF082516

R-NT2RP3004640

ESTs

5 1.1e-105:551:94

Hs.83348:AA527170

R-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds

10 4.9e-111:555:96

Hs.158286:AB007915

R-NT2RP4000108

ESTs

15 2.9e-94:479:96

Hs.6625:AA115182

R-NT2RP4000634

ESTs

20 3.0e-120:572:98

Hs.28827:AI125541

R-NT2RP4000962

ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [*Saccharomyces cerevisiae*]

25 6.0e-17:98:98

Hs.4789:AI418298

R-NT2RP4001001

ESTs

30 3.1e-117:567:97

Hs.4931:AA523860

R-NT2RP4001009

Homo sapiens mRNA for Hs Ste24p, complete cds

35 1.6e-83:404:98

Hs.25846:AB016068

R-NT2RP4001467

5' nucleotidase (CD73)

40 5.9e-113:545:97

Hs.153952:X55740

R-NT2RP4001877

ESTs, Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [*Rattus norvegicus*]

45 2.2e-67:375:93

Hs.16389:AA206356

R-NT2RP4001879

50 R-NT2RP4002187

EST

0.010:117:70

Hs.160416:AI394161

55 R-NT2RP4002451

EST

1.3e-62:386:87

Hs.57082:H25761

EP 1 130 094 A2

R-NT2RP4002715
ESTs
6.9e-111:552:96
Hs.12305:AA166889

5

R-NT2RP4002750
ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
7.0e-109:532:97
Hs.86362:AA205485

10

R-OVARC1000003
ESTs
1.3e-74:391:95
Hs.105039:AA477819

15

R-OVARC1000090
Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
9.9e-44:471:75
Hs.129735:AF010144

20

R-OVARC1000105
60S RIBOSOMAL PROTEIN L38
8.8e-14:83:100
Hs.2017:Z26876

25

R-OVARC1000137
ESTs
3.0e-84:387:95
Hs.22028:AA167715

30

R-OVARC1000208
Human mRNA for KIAA0392 gene, partial cds
2.8e-51:313:89
Hs.40100:AB002390

35

R-OVARC1000255
Spleen tyrosine kinase
2.8e-106:510:98
Hs.74101:L28824

40

R-OVARC1000275
ESTs, Highly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB [Saccharomyces cerevisiae]
6.9e-105:556:94
Hs.5748:AA608559

45

R-OVARC1000298
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.4e-56:338:90
Hs.108354:W19984

50

R-OVARC1000307
ESTs
2.4e-101:563:93
Hs.24479:N25972

55

R-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds

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5.0e-98:534:93
Hs.154023:AB011145

5 R-OVARC1000331
Homo sapiens chromosome 9, P1 clone 11659
1.0e-55:281:97
Hs.3439:AC004472

10 R-OVARC1000410
Homo sapiens clone 23767 and 23782 mRNA sequences
3.3e-90:462:94
Hs.8025:AF007150

15 R-OVARC1000439
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
[Caenorhabditis elegans]
1.6e-99:510:95
Hs.7471:AI143226

20 R-OVARC1000467

R-OVARC1000529
ESTs
5.7e-93:461:96
25 Hs.21396:AA114834

R-OVARC1000553
ESTs
4.3e-51:351:87
30 Hs.42979:W31096

R-OVARC1000775

35 R-OVARC1000811
ESTs
1.3e-82:441:95
Hs.73452:AA581386

40 R-OVARC1000853
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3.1e-95:492:95
Hs.6853:AA401703

45 R-OVARC1000873
ESTs
2.4e-46:281:91
Hs.43857:R91358

50 R-OVARC1000916
H.sapiens PISSLRE mRNA
1.9e-112:588:94
Hs.77313:X78342

55 R-OVARC1000956
Homo sapiens mRNA for MDC3, complete cds
0.18:259:62
Hs.7164:AB009672

R-OVARC1000995
EST
6.6e-43:343:81
Hs.149580:AI281881

5

R-OVARC1001030
ESTs, Weakly similar to neuroendocrine-specific protein C [H.sapiens]
1.5e-21:116:100
Hs.65450:AA055913

10

R-OVARC1001049
ESTs
1.2e-70:369:95
Hs.42949:N21131

15

R-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
1.3e-106:569:94
Hs.155478:AF048731

20

R-OVARC1001132
INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR
0.16:170:64
Hs.149894:L34600

25

R-OVARC1001163
ESTs
1.9e-39:219:94
Hs.126067:AI344351

30

R-OVARC1001222
ESTs
0.62:177:63
Hs.141162:H66213

35

R-OVARC1001260
ESTs
2.1e-79:425:94
Hs.105039:AA477819

40

R-OVARC1001336
ESTs
9.2e-75:439:91
Hs.105039:AA477819

45

R-OVARC1001338
ESTs
2.3e-19:139:92
Hs.7978:W05059

50

R-OVARC1001569
ESTs
2.4e-83:412:97
Hs.21396:AA114834

55

R-OVARC1001570
ESTs
2.6e-49:280:94

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Hs.3854:R12478

R-OVARC1001596
EST
5 8.2e-15:93:97
Hs.136918:AA811543

R-OVARC1001607
ESTs
10 0.019:413:56
Hs.24684:AA587245

R-OVARC1001725
ESTs
15 1.4e-96:504:95
Hs.23754:N29716

R-OVARC1001727

20 R-OVARC1001807
Hormone receptor (growth factor-inducible nuclear protein N10)
8.5e-78:425:94
Hs.1119:D49728

25 R-OVARC1001833
ESTs
1.0e-63:325:96
Hs.126912:AA469087

30 R-OVARC1001991
ESTs
1.3e-92:467:95
Hs.26506:AI348000

35 R-OVARC1002058
ESTs
2.5e-89:512:91
Hs.58093:W63576

40 R-OVARC1002178
ESTs
3.3e-99:487:96
Hs.136527:AI419398

45 R-PLACE1000033
ESTs
0.012:202:59
Hs.157400:AI370528

50 R-PLACE1000231
ESTs
2.9e-56:285:96
Hs.36688:AA603479

55 R-PLACE1000258
EST
3.4e-50:353:83
Hs.146794:AI149478

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R-PLACE1000442
 ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
 5.5e-91:437:98
 Hs.14831:AI261191
 5
 R-PLACE1000560
 ESTs
 3.7e-60:317:94
 Hs.65713:AI269328
 10
 R-PLACE1000740
 ESTs
 4.2e-67:362:94
 Hs.163434:T79849
 15
 R-PLACE1000912
 ESTs
 3.4e-57:329:92
 Hs.121907:R66773
 20
 R-PLACE1000914
 ESTs
 2.6e-71:419:89
 Hs.90809:AA010979
 25
 R-PLACE1000927
 ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
 7.8e-111:545:97
 Hs.8661:AI189791
 30
 R-PLACE1000986
 ESTs
 1.5e-91:431:99
 Hs.42458:AA452296
 35
 R-PLACE1001016
 ESTs
 3.4e-45:231:97
 Hs.121013:AA324765
 40
 R-PLACE1001100
 Homo sapiens nephrin (NPHS1) mRNA, complete cds
 3.5e-43:321:83
 Hs.128834:AF035835
 45
 R-PLACE1001114
 Human clone 23732 mRNA, partial cds
 1.6e-42:305:83
 Hs.81281:U79258
 50
 R-PLACE1001123
 ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD [Saccharomyces cerevisiae]
 1.2e-51:310:90
 55
 Hs.7773:AA127629
 R-PLACE1001183
 Human mRNA for KIAA0308 gene, partial cds

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0.88:182:65
Hs.10351:AB002306

5 R-PLACE1001229
ESTs
5.2e-90:471:95
Hs.18271:N92774

10 R-PLACE1001231

R-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.6e-53:265:98
Hs.21198:AB018262

15 R-PLACE1001401
ESTs
1.9e-72:362:96
Hs.20161:AA056410

20 R-PLACE1001407
ESTs
2.1e-36:249:85
Hs.23579:W38893

25 R-PLACE1001464
5' nucleotidase (CD73)
1.0e-91:457:96
Hs.153952:X55740

30 R-PLACE1001500
ESTs, Weakly similar to DNA helicase Q1 [H.sapiens]
2.0e-19:150:87
Hs.154199:AA155882

35 R-PLACE1001516
EST
1.9e-11:109:82
Hs.137486:AA425225

40 R-PLACE1001536
Human BRCA2 region, mRNA sequence CG016
0.28:146:63
Hs.112434:U50529

45 R-PLACE1001564
ESTs
6.3e-14:109:88
Hs.26519:AA442703

50 R-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K⁺ channel alpha subunit (KCNS3) mRNA, complete cds
1.2e-118:578:97
Hs.47584:AF043472

55 R-PLACE1001788
ESTs
8.4e-38:205:95

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Hs.23800:AA524095

R-PLACE1001795

ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae]

2.5e-77:392:96

Hs.7745:H92988

R-PLACE1001836

ESTs

1.5e-49:296:90

Hs.17691:H60366

R-PLACE1001918

ESTs, Weakly similar to multispanning membrane protein [H.sapiens]

2.0e-42:304:85

Hs.110439:N93209

R-PLACE1001949

R-PLACE1002080

Small inducible cytokine A5 (RANTES)

8.5e-41:296:82

Hs. 155464:AF088219

R-PLACE1002095

ESTs

8.5e-25:227:81

Hs.110488:AA034235

R-PLACE1002153

Homo sapiens TACC2 protein (TACC2) mRNA, partial cds

1.5e-101:514:95

Hs.90415:AF095791

R-PLACE1002329

ESTs

8.7e-48:257:94

Hs.126062:AA411593

R-PLACE1002355

ESTs

7.7e-71:362:95

Hs.120866:AI076780

R-PLACE1002374

Cathepsin L

8.4e-103:501:97

Hs.78056:X12451

R-PLACE1002518

ESTs

6.9e-97:471:97

Hs.104893:AA576941

R-PLACE1002547

Homo sapiens mRNA for KIAA0719 protein, complete cds

6.5e-55:276:97

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Hs.21198:AB018262

R-PLACE1002726

Human DNA-binding protein ABP/ZF mRNA, complete cds

3.8e-39:212:94

Hs.86185:U82613

R-PLACE1002905

Homo sapiens mRNA for KIAA0563 protein, complete cds

2.9e-41:330:81

Hs.15731:AB011135

R-PLACE1002911

R-PLACE1002967

ESTs

1.0e-43:384:77

Hs.132722:AA618531

R-PLACE1003135

ESTs

8.2e-94:462:97

Hs.23643:AI299952

R-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds

3.5e-110:541:96

Hs.15250:AF069301

R-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds

5.5e-49:287:91

Hs.30213:AF068227

R-PLACE1003428

ESTs, Moderately similar to BIOTINIDASE PRECURSOR [Homo sapiens]

6.8e-83:406:97

Hs.17586:AA461448

R-PLACE1003438

ESTs

2.9e-83:463:92

Hs.11067:H30385

R-PLACE1003460

ESTs

7.0e-27:187:87

Hs.18763:H56292

R-nnnnnnnnnnnnnnn

ESTs

1.7e-52:265:97

Hs.114049:AI091839

R-PLACE1003573

Human mRNA for KIAA0160 gene, partial cds

0.13:102:69

Hs.79880:D63881

5
R-PLACE1003598
ESTs
8.0e-39:210:95
Hs.26286:AA040823

10
R-PLACE1003644
EST
0.47:84:73
Hs.105856:AA551478

15
R-PLACE1003737
ESTs
1.1e-77:366:100
Hs.62699:AA707766

20
R-PLACE1003772
Human mRNA for KIAA0355 gene, complete cds
6.1e-27:551:65
Hs.153014:AB002353

25
R-PLACE1003839
ESTs
0.019:244:59
Hs.137825:AA778400

30
R-PLACE1003845
EST
5.3e-79:416:93
Hs.150153:AI300555

35
R-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.2e-87:439:96
Hs.22039:AB018301

40
R-PLACE1004028
Sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase)
0.73:128:71
Hs.60617:L13972

45
R-PLACE1004078
ESTs
1.7e-69:353:96
Hs.142075:AA654529

50
R-PLACE1004166
ESTs
1.7e-64:362:92
Hs.10177:AA191619

55
R-PLACE1004199
ESTs
1.3e-55:279:97

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Hs.147585:AI217699

R-PLACE1004279

ESTs

5 3.7e-68:373:93

Hs.145531:H87181

R-PLACE1004282

10 R-PLACE1004305

Homo sapiens mRNA for KIAA0740 protein, complete cds

6.4e-79:377:99

Hs.15099:AB018283

15 R-PLACE1004441

ESTs

1.8e-46:244:95

Hs.107082:R63714

20 R-PLACE1004450

R-PLACE1004482

ESTs

1.2e-92:491:93

25 Hs.17840:AI269915

R-PLACE1004492

ESTs

6.1e-54:278:95

30 Hs.55862:A1341676

R-PLACE1004519

ESTs

3.1e-25:133:100

35 Hs.47378:AI193598

R-PLACE1004520

Pregnancy-specific beta-1 glycoprotein 4

2.8e-66:390:89

40 Hs.108936:X17097

R-PLACE1004630

ESTs

7.3e-58:338:92

45 Hs.155506:AI281549

R-PLACE1004637

ESTs

1.1e-37:309:82

50 Hs.20102:AA150165

R-PLACE1004648

ESTs

2.3e-67:340:96

55 Hs.69321:AA633240

R-PLACE1004816

Homo sapiens mRNA for Hakata antigen, complete cds

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1.8e-104:586:90
Hs.9225:D88587

5 R-PLACE1004887
ESTs, Weakly similar to GOLIATH PROTEIN [D.melanogaster]
2.6e-30:222:86
Hs.18557:AA203416

10 R-PLACE1005003
ESTs
0.99:123:68
Hs.146244:AI276718

15 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
6.8e-58:299:95
Hs.151614:AF032456

20 R-PLACE1005031
ESTs
4.7e-57:325:92
Hs.31196:H13265

25 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-17
1.4e-86:450:93
Hs.26484:AJ223351

30 R-PLACE1005250
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
1.7e-106:521:97
Hs.36794:AI038407

35 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds
6.3e-79:471:88
Hs.11494:AF093118

40 R-PLACE1005410
EST
2.3e-49:296:90
Hs.7260:T23737

45 R-PLACE1005426
Pregnancy-specific beta-1 glycoprotein 4
8.0e-109:576:93
Hs.108936:X17097

50 R-PLACE1005519
ESTs
5.4e-108:569:93
Hs.23643:AI299952

55 R-PLACE1005539
ESTs, Weakly similar to p20 protein [R.norvegicus]
4.5e-05:107:77
Hs.56874:W61026

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5	R-PLACE1005544 ESTs 4.2e-57:280:98 Hs.155391:AA451633
10	R-PLACE1005569 ESTs 2.7e-90:470:94 Hs.8904:AI129815
15	R-PLACE1005601 R-PLACE1005660 ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III [Caenorhabditis elegans] 1.4e-91:483:93 Hs.7471:AI143226
20	R-PLACE1005669 ESTs 1.7e-84:438:95 Hs.18271:N92774
25	R-PLACE1005682 ESTs 6.3e-80:482:88 Hs.128679:AI160081
30	R-PLACE1005725 ESTs 1.5e-98:519:93 Hs.11360:AI147467
35	R-PLACE1005736 ESTs 3.1e-110:561:95 Hs.24111:AI346026
40	R-PLACE1005745 ESTs 2.4e-96:473:97 Hs.126935:AA603217
45	R-PLACE1005768 Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2 4.0e-46:387:77 Hs.1361:M55053
50	R-PLACE1005815 Homo sapiens PYRIN (MEFV) mRNA, complete cds 7.1e-56:324:79 Hs.113283:AF018080
55	R-PLACE1005878 ESTs 3.1e-75:388:94 Hs.153483:AA569128

5 R-PLACE1005927
ESTs
4.3e-64:403:87
Hs.126899:N50907

10 R-PLACE1006071
ESTs
5.3e-96:510:93
Hs.24398:AI262946

15 R-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds
3.0e-97:504:93
Hs.26492:AB009598

20 R-PLACE1006079
ESTs
3.1e-79:453:90
Hs.134194:AI142137

25 R-PLACE1006093
ESTs
1.3e-78:378:98
Hs.129327:AI201040

R-nnnnnnnnnnnnn

30 R-PLACE1006219
EST
1.6e-75:412:92
Hs.150153:AI300555

35 R-PLACE1006277
ESTs
2.8e-92:493:93
Hs.8904:AI129815

40 R-PLACE1006290
ESTs
2.8e-92:433:99
Hs.23445:AA489015

45 R-PLACE1006443
ESTs
2.5e-73:419:91
Hs.90809:AA010979

50 R-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds
6.9e-78:413:94
Hs.14687:AB011148

55 R-PLACE1006716
ESTs
4.8e-44:262:88
Hs.8503:AI393886

R-PLACE1006786

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	ESTs 6.3e-89:431:98 Hs.42458:AA452296
5	R-PLACE1006809 ESTs 1.6e-68:377:92 Hs.8956:AI146421
10	R-PLACE1006959 EST 0.00065:211:63 Hs.136605:AA665784
15	R-PLACE1007028 ESTs 7.4e-92:475:94 Hs.110222:AA532444
20	R-PLACE1007040 ESTs 5.1e-103:509:97 Hs.71190:AA524036
25	R-PLACE1007077 ESTs 1.0e-98:529:93 Hs.24398:AI262946
30	R-PLACE1007081 Human growth factor independence-1 (Gfi-1) mRNA, complete cds 0.57:238:61 Hs.73172:U67369
35	R-PLACE1007096 ESTs 1.2e-88:466:94 Hs.8268:N70144
40	R-PLACE1007296 EST 4.3e-53:338:86 Hs.147274:AI206582
45	R-PLACE1007591 EST 4.6e-76:384:97 Hs.94445:N90719
50	R-PLACE1007626 Homo sapiens unknown mRNA, complete cds 5.0e-30:179:91 Hs.11441:AF047439
55	R-PLACE1007702 ESTs 1.0e-52:341:87 Hs.103382:AA026923

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5 R-PLACE1007845
 ESTs
 2.2e-102:541:93
 Hs.15727:H98190

10 R-PLACE1007881
 ESTs
 4.1e-75:398:93
 Hs.55560:AI142804

15 R-PLACE1007971
 ESTs
 2.8e-43:304:85
 Hs.82933:AA058963

20 R-PLACE1008282
 ESTs, Highly similar to HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryc-
 tolagus cuniculus]
 2.2e-74:393:94
 Hs.77613:AI367385

25 R-PLACE1008297
 ESTs
 6.5e-101:506:96
 Hs.44274:AA523749

30 R-PLACE1008359
 ESTs
 1.8e-94:469:96
 Hs.160551:AI281417

35 R-PLACE1008469
 ESTs
 7.0e-74:421:90
 Hs.90809:AA010979

40 R-PLACE1008549
 ESTs
 2.0e-81:474:90
 Hs.11713:T65960

45 R-PLACE1008657
 ESTs
 9.5e-89:512:89
 Hs.142075:AA654529

50 R-PLACE1008716
 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
 5.6e-100:504:95
 Hs.154844:U15128

55 R-PLACE1008744
 ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
 2.3e-107:528:96
 Hs.8963:AI379350

R-PLACE1008984
 ESTs

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2.0e-76:464:89
Hs.40094:D12041

5 R-PLACE1008985
EST, Highly similar to SYNAPTOTAGMIN B [Discopyge ommata]
2.2e-59:343:90
Hs.161031:H72014

10 R-PLACE1009067
ESTs
7.7e-90:503:92
Hs.55067:AA037664

15 R-PLACE1009196
EST
0.011:243:60
Hs.149839:AI287601

20 R-PLACE1009279
Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
5.4e-27:553:62
Hs.75111:D87258

25 R-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds
2.7e-92:497:91
Hs.86185:U82613

30 R-PLACE1009546
ESTs
5.9e-80:461:90
Hs.134292:AA603031

35 R-PLACE1009600
ESTs
5.5e-98:509:93
Hs.21015:AA428288

40 R-PLACE1009735
ESTs
1.1e-85:462:93
Hs.48563:AA526595

45 R-nnnnnnnnnnnnn
ESTs
6.8e-82:499:87
Hs.43498:AA570507

50 R-PLACE1010011
ESTs, Moderately similar to synaptonemal complex protein [M.musculus]
2.7e-15:171:78
Hs.31655:AI075991

55 R-PLACE1010078
ESTs
1.2e-48:267:92
Hs.12101:AA677423

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R-PLACE1010081
 Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
 3.0e-106:560:93
 Hs.103755:AF027706
 5

R-PLACE1010251
 ESTs
 0.00049:248:60
 Hs.154164:AI246893
 10

R-PLACE1010445
 ESTs
 1.5e-90:496:92
 Hs.163999:AA778110
 15

R-PLACE1010713
 Interleukin 1 receptor antagonist
 4.1e-07:307:59
 Hs.81134:U65590
 20

R-PLACE1010784
 ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]
 1.5e-21:206:78
 Hs.29202:R71586
 25

R-PLACE1010827
 R-PLACE 1010968
 ESTs
 2.6e-75:385:95
 Hs.109884:AA766018
 30

R-PLACE1011045
 Homo sapiens E1-like protein mRNA, complete cds
 5.3e-92:453:96
 Hs.28190:AF094516
 35

R-PLACE1011116
 Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds
 1.5e-73:385:94
 Hs.44053:AF006621
 40

R-PLACE1011236
 R-PLACE1011364
 ESTs
 2.3e-47:289:89
 Hs.6163:W26652
 45

R-PLACE1011407
 ESTs
 1.1e-09:191:64
 Hs.118620:T60326
 50

R-PLACE1011516
 ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
 6.3e-75:441:88
 55

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Hs.110978:AA843431

R-PLACE1011708

Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds

7.7e-93:521:91

Hs.148318:AF034611

R-PLACE1011824

ESTs

0.013:199:62

Hs.44343:AA532514

R-PLACE1011978

EST

4.0e-97:462:98

Hs.116391:AA644085

R-PLACE2000118

ESTs

1.2e-83:468:92

Hs.110578:AA115763

R-PLACE2000219

Homo sapiens KIAA0414 mRNA, partial cds

2.0e-44:344:81

Hs.127649:AB007874

R-PLACE3000181

Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8

1.3e-82:441:94

Hs.115642:L11369

R-PLACE3000213

ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]

2.3e-114:557:97

Hs.8963:AI379350

R-PLACE4000354

ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]

3.4e-105:518:97

Hs.8963:AI379350

R-PLACE4000455

ESTs

9.0e-57:289:96

Hs.42458:AA452296

R-THYRO1000036

Collagen, type IX, alpha 3

1.3e-100:527:93

Hs.53563:L41162

R-THYRO1000061

ESTs

1.8e-87:460:94

Hs.124869:H98977

R-THYRO1000099

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ESTs

1.2e-34:193:94
Hs.149488:AI243816

- 5 R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
3.7e-106:530:96
Hs.115418:AF016272
- 10 R-THYRO1000400
Human HU-K4 mRNA, complete cds
0.99:227:60
Hs.74573:U60644
- 15 R-THYRO1000580
Homo sapiens mRNA for KIAA0628 protein, complete cds
0.21:126:67
Hs.43133:AB014528
- 20 R-THYRO1000584
ESTs, Weakly similar to golgi alpha-mannosidasell [H.sapiens]
3.0e-106:529:96
Hs.12183:AA888145
- 25 R-THYRO1000678
EST
2.9e-62:304:99
Hs.48956:N64339
- 30 R-THYRO1000776
ESTs
1.3e-102:533:94
Hs.4866:AA582196
- 35 R-THYRO1000795
ESTs
3.3e-98:529:92
Hs.55263:AI344338
- 40 R-THYRO1000846
ESTs
1.6e-105:522:96
Hs.135106:AI335251
- 45 R-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds
1.3e-43:251:92
Hs.12912:AF015913
- 50 R-THYRO1000956
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
5.2e-106:548:94
Hs.9305:W84893
- 55 R-THYRO1000964

R-THYRO1000999
ESTs

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1.9e-18:150:84
Hs.111583:AA463590

5 R-THYRO1001063
ESTs
1.5e-95:464:97
Hs.142684:AA902402

10 R-THYRO1001071
ESTs
2.5e-104:496:98
Hs.6071:AA868544

15 R-THYRO1001102

R-THYRO1001113
ESTs, Weakly similar to FER-1 [C.elegans]
7.1e-90:446:97
Hs.8076:AA115644

20 R-THYRO1001128
ESTs
1.9e-16:270:68
Hs.140194:N35720

25 R-THYRO1001205
Small inducible cytokine A5 (RANTES)
1.9e-58:400:84
Hs.155464:AF088219

30 R-THYRO1001237
ESTs
1.5e-104:532:96
Hs.6603:AA772122

35 R-THYRO1001242
EST
1.7e-50:281:93
Hs.101727:H16171

40 R-THYRO1001266
Homo sapiens mRNA for KIAA0650 protein, partial cds
0.00037:403:60
Hs.8118:AB014550

45 R-THYRO1001327
ESTs
1.2e-96:530:93
Hs.28786:AA034412

50 R-THYRO1001456
ESTs, Weakly similar to Similar to phytoene desaturase [C.elegans]
3.3e-43:257:92
Hs.97031:AA773647

55 R-THYRO1001457
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
4.8e-59:284:99

Hs.9915:AI300083

R-THYRO1001471

ESTs

5 1.1e-67:378:93
Hs.52113:R40587

R-THYRO1001478

10 R-THYRO1001495

H.sapiens mRNA for Zinc-finger protein (ZNFpT17)

1.6e-63:434:84

Hs.32954:X65233

15 R-THYRO1001523

ESTs

5.8e-75:388:96

Hs.6527:R21517

20 R-THYRO1001529

ESTs

1.1e-25:184:87

Hs.18441:AA005104

25 R-THYRO1001593

ESTs

4.7e-34:182:98

Hs.8312:AA813022

30 R-THYRO1001608

ESTs

2.8e-107:547:95

Hs.23765:AA524283

35 R-THYRO1001641

Homo sapiens clone 24448 unknown mRNA, partial cds

1.1e-111:562:96

Hs.4973:AF070638

40 R-THYRO1001700

ESTs

1.3e-78:407:95

Hs.86987:N99896

45 R-THYRO1001702

ESTs

4.3e-98:566:92

Hs.119447:AA524436

50 R-THYRO1001725

ESTs

1.3e-84:424:96

Hs.38039:AI360128

55 R-THYRO1001770

ESTs

1.0e-62:325:97

Hs.20137:R08273

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5 R-THYRO1001803
ESTs
6.8e-90:456:96
Hs.134438:R42585

10 R-Y79AA1000030
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
2.4e-98:515:94
Hs.32822:AI194045

15 R-Y79AA1000127
ESTs, Weakly similar to ! ! ! ! ALU SUBFAMILY J WARNING ENTRY ! ! ! ! [H.sapiens]
1.1e-57:307:95
Hs.83513:W05849

20 R-Y79AA1000207
EST
1.0e-97:411:96
Hs.141431:N21286

25 R-Y79AA1000226
ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis
elegans]
7.2e-102:545:94
Hs.11221:AI192291

30 R-Y79AA1000270
Human mRNA for ORF, Xq terminal portion
3.3e-107:564:93
Hs.6551:D16469

35 R-Y79AA1000426
H.sapiens mRNA for activin beta-C chain
2.5e-10:217:66
Hs.83267:X82540

40 R-Y79AA1000521
Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
0.73:257:59
Hs.113286:U77783

45 R-Y79AA1000750
ESTs
4.3e-75:391:95
Hs.157192:W84862

50 R-Y79AA1000776
ESTs
3.5e-56:303:95
Hs.118559:AA887084

55 R-Y79AA1000777
ESTs, Weakly similar to LIS-1 protein [H.sapiens]
9.5e-98:515:95
Hs.59461:W93217

R-Y79AA1000876
EST

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2.7e-23:173:84
Hs.135872:AI037885

5 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
3.4e-80:453:92
Hs.53066:AF093420

10 R-Y79AA1000967
ESTs
7.3e-86:461:93
Hs.6262:T89093

15 R-Y79AA1001013
ESTs
1.4e-115:566:97
Hs.108408:N31922

20 R-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
8.7e-111:557:95
Hs.36794:AI038407

25 R-Y79AA1001062
ESTs
0.0021:365:59
Hs.106129:AA292171

30 R-Y79AA1001090
ESTs
5.0e-52:255:99
Hs.106214:AI123831

35 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.8e-83:407:97
Hs.6710:AF038961

40 R-Y79AA1001264
ESTs, Highly similar to DNAJ PROTEIN HOMOLOG 2 [Homo sapiens]
2.8e-111:552:96
Hs.62489:AI057091

45 R-Y79AA1001272
Zinc finger protein, X-linked
0.019:317:59
Hs.2074:X59739

50 R-Y79AA1001328
ESTs
3.6e-67:385:92
Hs.127792:AI421472

55 R-Y79AA1001426
ESTs
2.0e-13:92:93
Hs.105607:AA478379

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R-Y79AA1001430
 Homo sapiens mRNA for KIAA0469 protein, complete cds
 2.0e-112:555:96
 Hs.7764:AB007938
 5

R-Y79AA1001523
 EST
 1.7e-07:120:73
 Hs.130984:AI015430
 10

R-Y79AA1001530
 Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds
 0.030:169:63
 Hs.155489:AF037448
 15

R-Y79AA1001592
 ESTs
 5.0e-60:340:91
 Hs.87019:AA760977
 20

R-Y79AA1001727
 ESTs
 6.1e-101:547:93
 Hs.7404:W29012
 25

R-Y79AA1001787
 ESTs
 8.8e-84:449:95
 Hs.128866:AA977749
 30

R-Y79AA1001795
 Homo sapiens mRNA for GalT4 protein
 9.9e-110:541:97
 Hs.21495:AL031228
 35

R-Y79AA1001799
 ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]
 1.6e-94:567:90
 Hs.34401:AA447775
 40

R-Y79AA1001803
 ESTs, Highly similar to SECRETORANIN III PRECURSOR [Mus musculus]
 1.2e-86:509:90
 Hs.22215:AI371482
 45

R-Y79AA1001863
 ESTs
 1.4e-23:268:73
 Hs.131613:AI190576
 50

R-Y79AA1002022
 ESTs
 8.9e-97:462:98
 Hs.6140:D52151
 55

R-nnnnnnnnnnnnn
 R-nnnnnnnnnnnnn

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Homo sapiens DNA recombination and repair protein (MRE11B) mRNA, complete cds
0.00075:456:59
Hs.153855:AF022778

- 5 R-Y79AA1002213
Human mRNA for KIAA0392 gene, partial cds
6.2e-45:304:85
Hs.40100:AB002390
- 10 R-Y79AA1002334
ESTs
7.7e-91:495:92
Hs.90804:W28091
- 15 R-Y79AA1002373
Human kpnI repeat mma (cdna clone pcd-kpni-8), 3' end
5.2e-98:545:91
Hs.103948:K00627
- 20 R-Y79AA1002376
ESTs
2.0e-91:455:97
Hs.153375:AI287812
- 25 R-Y79AA1002378
ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-35 [Mus musculus]
9.4e-15:131:83
Hs.20082:W89121
- 30 R-Y79AA1002381
ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1/thailand)]
1.5e-104:531:95
Hs.26322:AA156858
- 35

Homology search result 10

[0305] Data obtained by the homology search for full length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

- 45 C-HEMBA1000006//Homo sapiens mRNA; cDNA DKFZp564G1762 (from clone DKFZp564G1762)//0//1230bp//92%//AB026894
C-nnnnnnnnnnnnn//GAMETOGENESIS EXPRESSED PROTEIN GEG-154//2.30E-71//344aa//50%//P50636
C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III//4.80E-05//83aa//27%//P34679
- 50 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1)//3.20E-07//89aa//34%//P33154
C-HEMBA1000275
C-HEMBA1000300
C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1//5.30E-65//352aa//39%//P41233
C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds//4.70E-129//686bp//91%//AF151854
- 55 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial//2.00E-273//1254bp//99%//AJ007581
C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds//0//994bp//99%//AF116272
C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds//0//1254bp//99%//AF053470

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%//P02454
 C-HEMBA1000907
 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%//
 P41987
 5 C-HEMBA1000962
 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%//P31696
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//
 1105bp//94%//L32137
 C-HEMBA1001297
 10 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//
 464bp//82%//AF036249
 C-HEMBA1001563
 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%//P35414
 C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-85//293aa//50%//
 15 P51523
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%//
 AF090988
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//
 30%//P24802
 20 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//
 309aa//30%//Q04651
 C-HEMBA1002164
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%//U22952
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC
 25 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%//P24802
 C-nnnnnnnnnnnn//Human glycyl-tRNA synthetase mRNA, complete cds.//0//2380bp//99%//U09587
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%//Q00808
 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%//D10522
 C-HEMBA1002239
 30 C-HEMBA1002316
 C-HEMBA1002420
 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%//J04621
 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%//
 U63336
 35 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//
 37%//P49695
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//
 0//1497bp//99%//AF038660
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%//P48510
 40 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//
 99%//AF034611
 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//
 73%//U68380
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%//
 45 AF049891
 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%//AJ133490
 C-HEMBA1003294
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%//AB013912
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//
 50 100%//AF074264
 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959
 C-HEMBA1003487
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027
 C-HEMBA1003602//Homo sapiens CGI-67 protein mRNA, complete cds.//3.50E-70//732bp//66%//AF151825
 55 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166
 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//
 AF077030
 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243

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C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//
 277aa//35%//P33450
 C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//P70211
 C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869
 5 C-HEMBA1004454
 C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC
 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624
 C-HEMBA1004797
 10 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//
 Q07282
 C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//
 29%//P17437
 C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//1.20E-07//102aa//37%//P18160
 15 C-HEMBA1005145
 C-HEMBA1005430
 C-HEMBA1005449//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.40E-10//224aa//24%//P13983
 C-HEMBA1005489
 20 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139
 C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//2121aa//100%//U29589
 C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//
 753bp//99%//AF039568
 C-HEMBA1005913
 25 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630
 C-HEMBA1005945//Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete Gds.//
 1.90E-44//666bp//65%//AF004161
 C-HEMBA1006016
 C-HEMBA1006171
 30 C-HEMBA1006299
 C-HEMBA1006311
 C-HEMBA1006335
 C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//
 1108bp//65%//L38961
 35 C-HEMBA1006482//Homo sapiens h-scol (SCOI) mRNA, nuclear gene encoding mitochondrial protein, complete
 cds.//0//1101bp//98%//AF026852
 C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803
 C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581
 C-HEMBA1006724
 40 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581
 C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687
 C-HEMBA1006960
 C-HEMBA1007013
 C-HEMBA1007057
 45 C-HEMBA1007241
 C-HEMBA1007291
 C-HEMBA1007332
 C-HEMBA1007376
 C-HEMBA1007426
 C-HEMBA1007476
 C-HEMBA1007526
 C-HEMBA1007576
 C-HEMBA1007626
 C-HEMBA1007676
 C-HEMBA1007726
 C-HEMBA1007776
 C-HEMBA1007826
 C-HEMBA1007876
 C-HEMBA1007926
 C-HEMBA1007976
 C-HEMBA1008026
 C-HEMBA1008076
 C-HEMBA1008126
 C-HEMBA1008176
 C-HEMBA1008226
 C-HEMBA1008276
 C-HEMBA1008326
 C-HEMBA1008376
 C-HEMBA1008426
 C-HEMBA1008476
 C-HEMBA1008526
 C-HEMBA1008576
 C-HEMBA1008626
 C-HEMBA1008676
 C-HEMBA1008726
 C-HEMBA1008776
 C-HEMBA1008826
 C-HEMBA1008876
 C-HEMBA1008926
 C-HEMBA1008976
 C-HEMBA1009026
 C-HEMBA1009076
 C-HEMBA1009126
 C-HEMBA1009176
 C-HEMBA1009226
 C-HEMBA1009276
 C-HEMBA1009326
 C-HEMBA1009376
 C-HEMBA1009426
 C-HEMBA1009476
 C-HEMBA1009526
 C-HEMBA1009576
 C-HEMBA1009626
 C-HEMBA1009676
 C-HEMBA1009726
 C-HEMBA1009776
 C-HEMBA1009826
 C-HEMBA1009876
 C-HEMBA1009926
 C-HEMBA1009976
 C-HEMBA1010026
 C-HEMBA1010076
 C-HEMBA1010126
 C-HEMBA1010176
 C-HEMBA1010226
 C-HEMBA1010276
 C-HEMBA1010326
 C-HEMBA1010376
 C-HEMBA1010426
 C-HEMBA1010476
 C-HEMBA1010526
 C-HEMBA1010576
 C-HEMBA1010626
 C-HEMBA1010676
 C-HEMBA1010726
 C-HEMBA1010776
 C-HEMBA1010826
 C-HEMBA1010876
 C-HEMBA1010926
 C-HEMBA1010976
 C-HEMBA1011026
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C-HEMBB1001200
 C-HEMBB1001407
 C-HEMBB1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158
 C-HEMBB1001573
 5 C-nnnnnnnnnnn//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//1.50E-251//
 1146bp//99%//AF118670
 C-HEMBB1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645
 C-HEMBB1001978
 C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AP062354
 10 C-HEMBB1002228
 C-HEMBB1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR
 (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786
 C-HEMBB 1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC
 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-AL-
 15 PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-
 FERASE) (NAGAT).//1.80E-70//221aa//50%//P16442
 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857
 C-HEMBB1002663
 C-HEMBB1002693
 20 C-MAMMA1000046
 C-MAMMA1000118
 C-nnnnnnnnnnn//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.50E-312//1594bp//93%//
 AF067420
 C-MAMMA1000449
 25 C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462
 C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-
 AMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537
 C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530
 30 C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN)(BLAST-1)
 (CD48).//2.90E-12//239aa//28%//P10252
 C-MAMMA1001893
 C-NT2RM2000241
 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%//P91917
 35 C-NT2RM2000410
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%//
 P48982
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%//P22516
 C-NT2RM2000514//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2381bp//99%//AB020682
 40 C-NT2RM2000622
 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%//AJ0001319
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312
 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482
 45 C-NT2RM4000198
 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//
 P51523
 50 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//
 189aa//30%//P25234
 55 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001735

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C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//2184bp//99%//AB009462
C-NT2RP1000002
C-NT2RP1000050
5 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//AF126799
C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082
C-NT2RP1000325//H.sapiens gene for phosphate carner.//0//439bp//98%//X77337
10 C-NT2RP1000448
C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//99%//U09585
C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//1951bp//94%//L21936
15 C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//3.40E-52//304aa//40%//P08060
C-NT2RP1000903
C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795
C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446
20 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036
C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//AF029071
25 C-NT2RP2000479
C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991
C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654
C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068
30 C-NT2RP2000663
C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159
C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159
C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969
C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082
35 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//41%//P39986
C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144
C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//O13310
40 C-NT2RP2001878
C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
C-NT2RP2001915
C-NT2RP2001956//ORM1 PROTEIN.//3.90E-19//137aa//37%//P53224
45 C-NT2RP2002063//GNS1 PROTEIN.//3.60E-18//231aa//33%//P25358
C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663
C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//1.90E-93//420aa//43%//Q09782
C-NT2RP2002304//Human mRNA for KIAA0383 gene, partial cds.//0//1640bp//99%//AB002381
50 C-NT2RP2002409
C-NT2RP2002510
C-NT2RP2002527//CYTOCHROME B5.//1.30E-11//92aa//38%//P40312
C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//2365bp//99%//AF042792
55 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864
C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH).//5.50E-38//201aa//39%//P34913
C-NT2RP2002721//REGULATORY PROTEIN UHPC.//1.60E-23//153aa//30%//P27669

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C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT)//3.50E-63//404aa//33%/P32802

C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349

C-NT2RP2002974//HOMEOBOX PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT)//8.20E-241//555aa//84%//P70178

C-NT2RP2002976

C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)
(FRAGMENT).//2.10E-109//385aa//52%/P53760

C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//2.60E-67//256aa//49%//Q05512

C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899

C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//5.90E-20//204aa//34%//Q15404

C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927

C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//1.10E-45//324aa//29%//P37021

C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%/AF024636

C-NT2RP2003593

C-NT2RP2003599

C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%/P38869

C-NT2RP2003931

C-NT2RP2004141

C-NT2RP2004179

C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT).//1.60E-21//276aa//32%//Q62556

C-NT2RP2004447

C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//U49082

C-NT2RP2004524

C-NT2RP2004556

C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670

C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734

U01250bp//86%//L22557

C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//203aa//26%/P40857

C-NT2RP2004837

C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742

-nnnnnnnnnnnn//Homo sapiens SCG10-like-protein (SCLIP) mRNA, complete cds.//2.90E-170//813bp//98%//AF069709

C-NT2RP2005027

C-NT2RP2005163

U70859:126bp//81%//U70859

C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN)//5.00E-53//296aa//37%//Q62158

-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693

-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857

5-NT2RP2005514

NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%/P15586

C-NT2RP2005632

-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-)//3.60E-55//238aa//50%/57314

NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-

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C-NT2RP3002448
C-NT2RP3002321 //Bacine citrate synthase mRNA, complete cds //0.105.381//1454bp//93% //M21197

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C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//65%//L43821
C-NT2RP3002790
5 C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//8.00E-08//197aa//26%//P19814
C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//96%//AF051946
10 C-NT2RP3003076
C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//O35609
C-NT2RP3003469
C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999
15 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
C-NT2RP3003559
C-NT2RP3003614
C-NT2RP3003729
20 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130
C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381
C-NT2RP3003963
25 C-NT2RP3004000
C-NT2RP3004075
C-NT2RP3004083
C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467
30 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
C-NT2RP3004202
C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118
C-NT2RP3004321
35 C-NT2RP3004355
C-NT2RP3004374
C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544
C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//8.50E-24//263aa//33%//P17927
40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292
C-NT2RP3004625//Homo sapiens mRNA for KIAA0975 protein, partial cds.//0//1339bp//99%//AB023192
C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228
C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829
45 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//AF176680
C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834
C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
50 C-OVARC1000090
C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//4.20E-47//171aa//56%//P33296
C-OVARC1000137
C-OVARC1000208
55 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630
C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT).//9.90E-16//352aa//23%//P15924
C-OVARC1000298
C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253
C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-

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33//143aa//53%//P34280
C-OVARC1000467
C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.40E-23//
165aa//39%//P34244
5 C-OVARC1000775
C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 157 //1.00E-35//130aa//46%//P51786
C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%//Q01177
C-OVARC1000853
C-OVARC1000916//H.sapiens PISSLRE mRNA //7.30E-280//1117bp//95%//X78342
10 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.20E-09//250aa//
28%//P17437
C-OVARC1001030//Homo Sapiens mRNA for KIAA0886 protein, complete cds //0//907bp//99%//AB020693
C-OVARC1001049//TRANSCRIPTION FACTOR HES- (C-HAIRY1) //7.50E-14//96aa//36%//O57337
C-OVARC1001086//Homo Sapiens cyclin T2a mRNA, complete cds //0//1593bp//98%//AF048731
15 C-OVARC10011321//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)
(TCF-9) //2.30E-44//268aa//36%//P16383
C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I //2.30E-20//152aa//
30%//Q09906
C-OVARC1001222
20 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-)//8.80E-30//
125aa//40%//P53104
C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.50E-22//
164aa//39%//P34244
C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds //0//1766bp//99%//
25 AF126062
C-OVARC1001725
C-OVARC1001727
C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds //1.10E-243//1145bp//98%//L13740
C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) //8.30E-06//114aa//
30 35%//Q01956
C-OVARC1002058//Human 18S rRNA gene, complete //1.50E-164//921bp//91%//M10098
C-OVARC1002178
C-PLACE100033//VON WILLEBRAND FACTOR PRECURSOR //3.80E-17//190aa//28%//Q28295
C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds //
35 2.70E-101//947bp//74%//AF037272
C-PLACE1000258//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //1.70E-55//431aa//
35%//Q05481
C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT) //1.00E-88//213aa//67%//P16415
C-PLACE1000560
40 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds //5.60E-122//893bp//81%//M93661
C-PLACE1000912
C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds //7.50E-88//500bp//69%//AF045584
C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X //6.30E-21//123aa//
37%//Q11079
45 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC
PROTEIN) //6.80E-12//133aa//28%//P35500
C-nnnnnnnnnnnn//Homo sapiens T245 protein (T245) mRNA, complete cds //0//1801bp//99%//AF043906
C-PLACE1001100
C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN //9.20E-06//389aa//31%//P03181
50 C-PLACE1001123
C-PLACE1001183
C-PLACE1001229
C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
cds //2.20E-137//918bp//80%//AF026554
55 C-nnnnnnnnnnnn//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds //
7.60E-293//1631bp//90%//U18469
C-PLACE1001340//Homo sapiens mRNA for KIAA0719 protein, complete cds //0//2868bp//99%//AB018262
C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE

FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%/P13386

C-PLACE1001407

C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%/X55740

C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%/AB006533

C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%/Q28181

C-PLACE1001536

C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%/X81892

C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.//0//1708bp//99%/AF043472

C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds.//0//1776bp//99%/AF013759

C-PLACE1001788

C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.//3.40E-20//159aa//40%/P47032

C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P2OE].//5.00E-27//134aa//47%/P10269

C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-OMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//2.30E-53//339aa//33%/P32802

C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%/Q12697

C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691

C-PLACE1002095

C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791

C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//213aa//45%/Q08509

C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//40%/P01029

C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%/X12451

C-PLACE1002518

C-PLACE1002547//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2985bp//99%/AB018262

C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//82%/AJ133128

C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%/P07106

C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%/P32507

C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%/Q01362

C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%/P08458

C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/AF069301

C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099

C-PLACE1003438

C-PLACE1003460

C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//1.30E-09//281aa//22%/P11414

C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).//3.70E-16//226aa//26%/P20937

C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%/P90917

C-PLACE1003644

C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%/P08953

C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//2.40E-12//124aa//38%/P 13983

C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//

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771bp//58%//AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
 GALACTOSE 4-EPIMERASE).//3.40E-37//302aa//30%//Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%//AB018301
 5 C-PLACE1004028
 C-PLACE1004166//CREB-BINDING PROTEIN.//1.80E-12//147aa//35%//P45481
 C-PLACE1004168//Homo sapiens mRNA for KIAA1007 protein, partial cds.//0//2637bp//99%//AB023224
 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.//1.40E-08//166aa//
 10 30%//P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//2.10E-11//
 189aa//30%//P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%//P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//AC007383
 15 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 TIGEN CD13).//1.30E-91//562aa//35%//P15541
 C-PLACE 1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%//AF097723
 C-PLACE1004519
 20 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%//M20881
 C-PLACE1004630
 C-PLACE1004637
 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 25 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.40E-18//395aa//25%//P08640
 C-nnnnnnnnnnnnn//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1825bp//99%//
 AF049891
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTEIN).//4.80E-33//179aa//47%//Q06003
 30 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-).//2.20E-52//269aa//41%//Q16651
 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%//AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%//P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).//1.80E-235//1010bp//84%//
 35 AJ223351
 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%//AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629
 40 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 0//1629bp//95%//U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//
 AF024636
 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 45 1237bp//76%//U89915
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-
 33//143aa//53%//P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).//4.90E-09//183aa//33%//
 50 P20749
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 27%//Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311
 C-PLACE1005768
 55 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AP047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-

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GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 5 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADI-
 POCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 C-PLACE1006959
 10 C-PLACE1007028
 C-PLACE1007040
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GETA.//2.70E-17//174aa//27%//O34368
 C-nnnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1373bp//99%//AJ224875
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 15 C-PLACE1007591
 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//
 20 42%//Q19425
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//
 P90648
 C-nnnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1616bp//99%//AJ224875
 C-PLACE1008469
 25 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//
 AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 1888bp//99%//U15128
 30 C-PLACE1008984
 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//
 35 6.60E-86//1414bp//64%//E12965
 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//
 AJ133128
 C-PLACE1009546
 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//
 40 88%//D88315
 C-PLACE1009735
 C-PLACE1009982//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224
 C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//
 45 AF027706
 C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555
 C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//
 1146bp//99%//AF008670
 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-
 50 19//163aa//34%//P49020
 C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN- TY-
 ROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
 C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516
 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE)
 55 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
 C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451
 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
 C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//

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139aa//34%/P53073
 C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%/AF034611
 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%/U26424
 5 C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%/Q05481
 C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%/P70315
 C-PLACE2000219
 10 C-SKNMC1000004
 C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%/L41162
 C-THYRO1000061
 C-THYRO1000099
 15 C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%/AF016272
 C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%/AL109665
 C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%/Q99676
 C-THYRO1000584//Homo sapiens mRNA for KIAA0935 protein, partial cds.//0//1338bp//99%/AB023152
 20 C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%/AJ005585
 C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%/X76114
 C-THYRO1000846
 C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%/P78963
 C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%/U03642
 25 C-THYRO1000999
 C-THYRO1001063
 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%/P22892
 C-THYRO1001102
 30 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%/AL096713
 C-THYRO1001128
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%/P21334
 35 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%/U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%/Q10555
 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%/X75756
 40 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%/P04839
 45 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%/AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%/Q09925
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%/Q60855
 50 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%/AJ001616
 C-THYRO1001725
 C-THYRO1001803
 55 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//

- 83%/U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%/U96386
 C-Y79AA1000521
 C-Y79AA1000776
- 5 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%/Q00808
 C-nnnnnnnnnnnn//Homo sapiens intersectin long form mRNA, complete cds.//0//1519bp//99%/AF064244
 C-Y79AA1000876//PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%/P13667
- 10 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%/AF093420
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.00E-77//359aa//44%/Q14012
 C-Y79AA1001013
 C-Y79AA1001056
- 15 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%/Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31 %/Q63369
- 20 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%/Q10005
 C-Y79AA1001272
 C-Y79AA1001328//Mus musculus mRNA for DII3 protein, complete cds.//1.90E-263//1988bp//79%/ABO13440
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%/AB007938
- 25 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PECURSOR.//2.20E-06//140aa//26%/P32507
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%/P03891
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%/Q02280
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%/U71267
- 30 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%/P40085
 C-HEMBA1000671//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%/Q99676
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%/Y13622
- 35 C-HEMBA1000835
 C-HEMBA1000875
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822
- 40 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997
 C-HEMBA1001296
 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803
 C-HEMBA1002985
- 45 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676
 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%/Q60821
 C-HEMBA1004007
 C-HEMBA1004085
- 50 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%/P30658
 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%/P52738
 C-HEMBA1005246
- 55 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//187aa//33%/Q01484
 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//57%/Q61967
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%/

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O15127
C-HEMBA1006517
C-HEMBA1006544
C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581
5 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425
C-HEMBA1006912
C-HEMBA1007063
C-HEMBA1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
C-HEMBA1000407
10 C-HEMBA1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//1452bp//85%//AF084259
C-HEMBA1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937
C-HEMBA1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
15 C-HEMBA1002039
C-HEMBA1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//99%//AF179274
C-HEMBA1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//AF115403
20 C-HEMBA1002120//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558
C-HEMBA1002302
C-HEMBA1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//2174bp//99%//AF179274
25 C-HEMBA1000106
C-HEMBA1000141
C-HEMBA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575
C-HEMBA1000226
C-HEMBA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//1165bp//99%//AF117959
30 C-HEMBA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//299aa//34%//P47088
C-HEMBA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258
C-HEMBA1000528
35 C-HEMBA1000614//Homo sapiens pseudouridine synthase 1 (PUS1) mRNA, partial cds.//2.10E-302//1370bp//99%//AF116238
C-HEMBA1000652
C-HEMBA1000706
C-HEMBA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349
40 C-HEMBA1000810
C-HEMBA1000814
C-HEMBA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035
C-HEMBA1000986
45 C-HEMBA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA, complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536
C-HEMBA1001141
C-HEMBA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139
C-HEMBA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988
C-HEMBA1001284
50 C-HEMBA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225
C-HEMBA1001344
C-HEMBA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%//P44742
C-HEMBA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%//P51523
55 C-HEMBA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%//Q13562
C-HEMBA1001623//Homo sapiens mRNA; cDNA DKFZp434J1027 (from clone DKFZp434J1027); partial cds.//1.30E-269//1222bp//99%//AL133084

C-MAMMA1001634
 C-MAMMA1001957
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%//AF085499
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%//Q01177
 5 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%//P51153
 C-MAMMA1002087
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-22//867aa//52%//O43108
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%//Q92338
 10 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.80E-17//146aa//35%//P18160
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%//AF100780
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%//AL050119
 15 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%//Q00004
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%//AF148509
 C-MAMMA1002633
 C-MAMMA1003126//Human Hpast (HPAST) mRNA, complete cds.//3.70E-162//1355bp//75%//AF001434
 20 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%//S70011
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//9.40E-94//394aa//43%//Q09782
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%//AB028976
 25 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%//U55042
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%//Q03468
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%//AB017335
 30 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%//AF093408
 C-NT2RM2001626//FLIGHTLESS-1 PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750
 35 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-11//488aa//26%//P23253
 C-NT2RM4000100//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2678bp//99%//AB023206
 40 C-NT2RM4000115//HYPOTHETICAL 68.8 KD PROTEIN B0464.6 IN CHROMOSOME III.//1.20E-16//204aa//30%//Q03564
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//24%//Q10297
 45 C-NT2RM4000761//H.sapiens mitochondrial genome (consensus sequence).//0//1931bp//99%//X62996
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//520aa//29%//O60100
 C-NT2RM4001377//Homo sapiens mRNA for KIAA0638 protein, partial cds.//0//1346bp//99%//AB014538
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840
 50 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//P48982
 C-NT2RP1000239
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 55 C-NT2RP1000679
 C-NT2RP1000740//Homo sapiens mRNA; cDNA DKFZp586F1918 (from clone DKFZp586F1918).//4.60E-97//456bp//99%//AL050091

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C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%/P48378
C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%/AF117106
C-NT2RP3000818
5 C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%/Q07283
C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%/P43146
C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%/AL050118
10 C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.60E-09//334aa//22%/P52178
C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//4.70E-11//132aa//37%/Q13829
C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%/P77495
15 C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%/P51523
C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%/AF151829
C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%/AB018308
C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE 1 mRNA, complete cds.//0//2719bp//99%/AF097645
20 C-NT2RP3002324
C-NT2RP3002353
C-NT2RP3002571//Homo sapiens mRNA for KIAA1108 protein, partial cds.//4.40E-273//1311bp//97%/AB029031
C-NT2RP3002664
25 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//1552bp//99%/AF105202
C-NT2RP3002887
C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%/AF151867
C-NT2RP3002983
30 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%/AF151813
C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%/P41217
C-NT2RP3004025
C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%/AB026894
35 C-NT2RP3004119//PEREGRIN (BE140 PROTEIN).//7.30E-39//227aa//43%/P55201
C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%/AF015454
C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%/P15565
C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%/AF111105
40 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%/AF131856
C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%/AF127761
45 C-NT2RP4001879
C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%/AF078850
C-NT2RP4002451
C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//2084bp//81%/U70859
50 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete cds.//4.30E-220//1158bp//94%/AF111856
C-OVARC1000313//Homo sapiens mRNA for KIAA0573 protein, partial cds.//0//1833bp//99%/AB011145
C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).//9.40E-44//106aa//59%/P36959
55 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).//1.30E-23//169aa//40%/P28843
C-OVARC1000873//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2178bp//99%/AB033073

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C-OVARC1000995
 C-OVARC1001260
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//0//1435bp//99%//AF111856
 5 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//
 100%//AF190725
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 1836bp//96%//U15128
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839
 10 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283
 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//
 99%//AL117450
 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//
 99%//AF068227
 15 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%//D26549
 C-PLACE1004492//VERPROLIN.//3.30E-07//149aa//29%//P37370
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//
 3.10E-08//84aa//34%//Q00649
 C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 20 C-PLACE1005601
 C-PLACE1005745//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%//
 P23508
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//
 25 33%//Q09875
 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%//
 P02469
 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%//
 AB009598
 30 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%//
 AF028233
 C-PLACE1006786
 C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194
 C-PLACE1007971
 35 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-)
 (HRI).//7.10E-274//627aa//82%//P33279
 C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
 C-PLACE1008744//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114.//0//1757bp//99%//
 AL079279
 40 C-PLACE1010445
 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
 AF078850
 C-nnnnnnnnnnnnn//Homo sapiens angiopoietin-2 mRNA, complete cds.//0//2227bp//99%//AF004327
 C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815
 45 C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE)
 (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
 C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//
 L11370
 C-SKNMC1000014
 50 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//30%//P29518
 C-THYRO1000964
 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
 0//2468bp//99%//AF037339
 C-THYRO1001608
 55 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-
 20//1169aa//35%//P53974
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247

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C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
6.20E-66//609aa//31%//P48751
5 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
AF169481
C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
99%//AF119042
C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
C-Y79AA1001592
10 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
Q12697
C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
C-Y79AA1001795//Homo sapiens mRNA for GaIT4 protein.//2.30E-250//1137bp//99%//Y15061
15 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
C-Y79AA1001863
C-Y79AA1002058//Mus musculus Gng31g mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
20 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
41%//Q03567
C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
304//1667bp//90%//U39045
25 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
AF155100
C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013
C-BNGH41000087//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2294bp//99%//AB033073
C-HEMBA1001886
30 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//8.30E-309//623bp//99%//
AB020666
C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//
1242bp//99%//AF192529
C-HEMBA1000309
35 C-HEMBA1000567
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791
C-MAMMA1001066
C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
1394bp//93%//U71267
40 C-MAMMA1001609
C-MAMMA1001901
C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%//AF039916
C-NT2RM1000462
45 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//
43%//P48982
C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%//Y11306
C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%//P23500
C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737
50 C-NT2RP2001538//Homo sapiens mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K2235).//0//2139bp//
99%//AL117513
C-NT2RP2001921
C-NT2RP2003138//5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).//2.10E-08//104aa//46%//
P70284
55 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
cds.//0//2891bp//99%//AB021644
C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572
C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//

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62%//Q03923
 C-NT2RP2005774//Homo sapiens GLOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644
 C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//P51523
 5 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676
 C-NT2RP3000427
 C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//107aa//42%//P98063
 10 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850
 C-NT2RP3003448
 15 C-NT2RP4002715
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%//Q50658
 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//P51522
 C-PLACE1007081
 20 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431
 C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070
 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927
 25 C-PLACE4000455
 C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%//P27448
 C-Y79AA1000750
 30 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973
 C-Y79AA1002129
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%//P03891
 35 C-BNGH41000087//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//1.20E-17//83aa//40%//P50426
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%//Q02280
 C-HEMBA1000006//Homo sapiens mRNA for NESCA, complete cds.//0//1230bp//92%//AB026894
 40 C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//P34679
 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//P33154
 C-HEMBA1000275
 45 C-HEMBA1000300
 C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
 C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%//U71267
 50 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%//P40085
 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
 C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//AF116272
 55 C-HEMBA1000671//ZINC FINGER. PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%//Q99676
 C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%//Y13622

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%/P02454
 C-HEMBA1000835//FIBRILLIN 2 PRECURSOR.//1.30E-42//214aa//45%/P35556
 C-HEMBA1000875
 C-HEMBA1000907
 5 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%/P41987
 C-HEMBA1000962
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822
 10 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%/P31696
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//1105bp//94%/L32137
 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997
 C-HEMBA1001296
 15 C-HEMBA1001297//Homo sapiens putative transcription factor CA150 mRNA, complete cds.//4.60E-276//1081bp//99%/AF017789
 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//464bp//82%/AF036249
 C-HEMBA1001563
 20 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%/P35414
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%/AF090988
 C-HEMBA1001886//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-148//421aa//60%/Q03923
 25 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//30%/P24802
 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//309aa//30%/Q04651
 30 C-HEMBA1002164
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%/U22952
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%/P24802
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%/Q00808
 35 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%/D10522
 C-HEMBA1002239
 C-HEMBA1002316//GTP-BINDING PROTEIN HFLX.//5.80E-12//196aa//29%/P25519
 C-HEMBA1002420
 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%/J04621
 40 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%/U63336
 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//37%/P49695
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//0//1497bp//99%/AF038660
 45 C-HEMBA1002985
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%/P48510
 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//99%/AF034611
 50 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//73%/U68380
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%/AF049891
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676
 55 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%/AJ133490
 C-HEMBA1003294
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%/AB013912
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//

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100%//AF074264
 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959
 C-HEMBA1003487
 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING
 5 PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%//Q60821
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027
 C-HEMBA1003602//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//2.80E-21//200aa//33%//Q50658
 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166
 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//
 10 AF077030
 C-HEMBA1004007
 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//0.00E+00//623bp//99%//
 AB020666
 C-HEMBA1004085
 15 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243
 C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//
 277aa//35%//P33450
 C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//F70211
 C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869
 20 C-HEMBA1004454
 C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC
 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%//P30658
 C-HEMBA1004797
 25 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//
 Q07282
 C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//
 30 29%//P17437
 C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//1.20E-07//102aa//37%//P18160
 C-HEMBA1005145
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%//P52738
 35 C-HEMBA1005246//HEPATOCTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 4 (HFH-4).//2.10E-15//
 230aa//28%//Q92949
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//
 187aa//33%//Q01484
 C-HEMBA1005430
 40 C-HEMBA1005449//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 5.40E-10//224aa//24%//P13983
 C-HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA,
 complete cds.//8.40E-255//924bp//80%//AF127084
 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139
 45 C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//590aa//100%//P20309
 C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//
 753bp//99%//AF039568
 C-HEMBA1005913
 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630
 50 C-HEMBA1005945//BRITTLE-1 PROTEIN PRECURSOR.//1.70E-29//220aa//35%//P29518
 C-HEMBA1006016
 C-HEMBA1006171
 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//
 57%//Q61967
 55 C-HEMBA1006299
 C-HEMBA1006311
 C-HEMBA1006335
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%//

O15127

C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//1108bp//65%//L38961

C-HEMBA1006482//Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//1101bp//98%//AF026852

C-HEMBA1006517

C-HEMBA1006544

C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803

C-HEMBA1006658//Homo sapiens mRNA for NIK, partial cds.//0//1500bp//98%//AB013385

C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581

C-HEMBA1006724

C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581

C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425

C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581

C-HEMBA1006912

C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687

C-HEMBA1006960

C-HEMBA1007013//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//1.10E-14//412bp//63%//AF068749

C-HEMBA1007057

C-HEMBA1007063

C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//1242bp//99%//AF192529

C-HEMBA1007241//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-14//106aa//42%//P40857

C-HEMBA1007291

C-HEMBA1007332//Homo sapiens mRNA for unr-interacting protein.//6.40E-83//266bp//98%//AJ010025

C-HEMBA1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996

C-HEMBA1000276

C-HEMBA1000309

C-HEMBA1000407

C-HEMBA1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%//AF070523

C-HEMBA1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//1452bp//85%//AF084259

C-HEMBA1000567

C-HEMBA1000642

C-HEMBA1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%//AB020700

C-HEMBA1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%//X63678

C-HEMBA1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%//AB006085

C-HEMBA1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%//P78706

C-HEMBA1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//5.30E-11//142aa//30%//P32802

C-HEMBA1001048//SARCALUMENIN PRECURSOR.//6.50E-18//154aa//33%//P13666

C-HEMBA1001200

C-HEMBA1001407

C-HEMBA1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158

C-HEMBA1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937

C-HEMBA1001573

C-HEMBA1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645

C-HEMBA1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210

C-HEMBA1001978

C-HEMBA1002039

C-HEMBA1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//99%//AF179274

C-HEMBA1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//AF115403

- C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558
C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AF062534
C-HEMBB1002228
5 C-HEMBB 1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786
C-HEMBB1002302
C-HEMBB1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).//1.80E-70//221aa//50%//P16442
10 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857
C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//2174bp//99%//AF176422
15 C-HEMBB1002663
C-HEMBB1002693
C-MAMMA1000046
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791
C-MAMMA1000106
20 C-MAMMA1000118
C-MAMMA1000141
C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575
C-MAMMA1000226
C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//1165bp//99%//AF117959
25 C-MAMMA1000449
C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462
C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//299aa//34%//P47088
30 C-MAMMA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258
C-MAMMA1000528
C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537
35 C-MAMMA10006141//Homo sapiens pseudouridine synthase I (PUS1) mRNA, partial cds.//2.10E-302//1370bp//99%//AF116238
C-MAMMA1000652
C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530
C-MAMMA1000706
40 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349
C-MAMMA1000810
C-MAMMA1000814
C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035
C-MAMMA1000986
45 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA, complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536
C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).//2.90E-12//239aa//28%//P10252
C-MAMMA1001066
50 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//1394bp//93%//U71267
C-MAMMA1001141
C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139
C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988
55 C-MAMMA1001284
C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225
C-MAMMA1001344

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C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%/P44742
 C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%/P51523
 C-MAMMA1001609//MYOSIN II HEAVY CHAIN, NON MUSCLE.//1.50E-26//204aa//38%/P05659
 5 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%/Q13562
 C-MAMMA1001623
 C-MAMMA1001634
 C-MAMMA1001893
 C-MAMMA1001901
 10 C-MAMMA1001957
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%/AF085499
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%/Q01177
 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%/P51153
 C-MAMMA1002087
 15 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%/AF039916
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-222//867aa//52%/O43108
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%/Q92338
 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 20 TEIN KINASE 1).//9.80E-17//146aa//35%/P18160
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%/AF100780
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%/AL050119
 25 C-MAMMA1002224
 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%/Q00004
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%/AF148509
 C-MAMMA1002633
 C-MAMMA1003126//SARCALUMENIN PRECURSOR.//1.10E-51//388aa//32%/P13666
 30 C-NT2RM1000462//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//8.60E-14//104aa//40%/P15287
 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//43%/P48982
 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%/P43636
 35 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%/Y11306
 C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%/AF084458
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%/S70011
 C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%/P23500
 C-NT2RM2000241
 40 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%/P91917
 C-NT2RM2000410
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%/P48982
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%/P22516
 45 C-NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//4.40E-304//1374bp//99%/AF174601
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//4.40E-304//394aa//43%/Q09782
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%/AB028976
 50 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%/U55042
 C-NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.//3.00E-203//915bp//91%/AF176524
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%/Q03468
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%/AB017335
 55 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%/AJ001319
 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%/AF093408

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C-NT2RM2001626//FLIGHTLESS-I PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750
 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//
 5 AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-
 11//488aa//26%//P23253
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312
 10 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482
 C-NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//2678bp//99%//
 AF175966
 C-NT2RM4000115
 C-NT2RM4000198//BUTYROPHILIN PRECURSOR (BT).//5.10E-12//162aa//33%//Q13410
 15 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//
 P51523
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097
 20 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//
 24%//Q10297
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655
 25 C-NT2RM4000761//CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).//2.50E-245//306aa//91%//
 P00395
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//
 520aa//29%//O60100
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//
 30 189aa//30%//P25234
 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001377//R.norvegicus LL5 mRNA.//8.50E-236//990bp//87%//X74226
 35 C-NT2RM4001735
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840
 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//
 P48982
 C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//
 40 2184bp//99%//AB009462
 C-NT2RP1000002
 C-NT2RP1000050
 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//
 AF126799
 45 C-NT2RP1000239
 C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-NT2RP1000271//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//4.70E-199//547aa//
 66%//Q03923
 C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082
 50 C-NT2RP1000325//H.sapiens gene for phosphate carrier.//0//439bp//98%//X77337
 C-NT2RP1000448
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 55 C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//
 99%//U09585
 C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//
 1951bp//94%//L21936

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C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI)//
 3.40E-52//304aa//40%//P08060
 C-NT2RP1000679
 C-NT2RP1000740
 5 C-NT2RP1000903
 C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR//3.60E-14//286aa//27%//Q99795
 C-NT2RP1001004//F-SPONDIN PRECURSOR//9.20E-43//322aa//35%//P35446
 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-
 10 VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B)//9.70E-22//227aa//31%//Q61036
 C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//3.40E-42//285aa//35%//Q00808
 C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-
 AL AUTOANTIGEN) (AA1)//9.70E-19//201aa//31%//Q60477
 C-NT2RP2000092//ZINC FINGER PROTEIN 136//1.90E-117//419aa//54%//P52737
 C-NT2RP2000178//MITOCHONDRIAL ION PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//2.40E-192//
 15 778aa//48%//P93647
 C-NT2RP2000240
 C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds//1.60E-90//956bp//70%//
 AF029071
 C-NT2RP2000447//GOLGIN-95//2.80E-33//99aa//66%//Q08379
 20 C-NT2RP2000479
 C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds//3.00E-185//855bp//99%//AF040991
 C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds//1.30E-290//1324bp//99%//AF070654
 C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B)//1.50E-13//97aa//38%//P25210
 25 C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 4.10E-12//323aa//30%//P13983
 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds//0//2847bp//99%//AB016068
 C-NT2RP2000663
 C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene//0//2278bp//99%//AJ012159
 30 C-NT2RP2000712//ZINC FINGER PROTEIN 135//3.70E-87//296aa//53%//P52742
 C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.50E-73//387aa//37%//
 P51522
 C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete
 cds//0//2724bp//99%//AF089744
 35 C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene//0//2276bp//100%//AJ012159
 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds//0//1539bp//100%//AB014576
 C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT)//3.30E-05//76aa//39%//Q13615
 C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR//3.00E-133//331aa//77%//Q64322
 C-NT2RP2001388//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
 40 NUCLEASE)//5.90E-13//157aa//33%//P16658
 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.30E-14//242aa//24%//Q00808
 C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds//0//2547bp//99%//L38969
 C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds//2.20E-65//641bp//65%//U49082
 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38)//1.20E-133//429aa//
 45 41%//P39986
 C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds//0//2079bp//99%//AB007144
 C-NT2RP2001538//Mus musculus mSin3A (sin3A) mRNA, complete cds//7.60E-272//1480bp//84%//U22394
 C-NT2RP2001562//Homo sapiens GLE1 (GLE1) mRNA, complete cds//0//1899bp//98%//AF058922
 C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN)//1.80E-49//
 50 94aa//81%//Q90655
 C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds//0//2974bp//86%//M88469
 C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-)//9.10E-47//185aa//44%//
 O13310
 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds//0//3092bp//99%//AF083106
 55 C-NT2RP2001878
 C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (MU/M-TYPE)//3.80E-58//475aa//34%//P00789
 C-NT2RP2001915

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C-NT2RP2001921
 C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2)//1.40E-08//191aa//27%//P53686
 C-NT2RP2001956//ORM1 PROTEIN//3.90E-19//137aa//37%//P53224
 C-NT2RP2002015
 5 C-NT2RP2002063//GNS1 PROTEIN//3.60E-18//231aa//33%//P25358
 C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663
 C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I//1.90E-93//420aa//43%//Q09782
 10 C-NT2RP2002304//Homo sapiens histone acetyltransferase MORF mRNA, complete cds.//0//2737bp//99%//AF113514
 C-NT2RP2002409
 C-NT2RP2002510
 C-NT2RP2002527//CYTOCHROME B5//1.30E-11//92aa//38%//P40312
 15 C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//2365bp//99%//AF042792
 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864
 C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH)//5.50E-38//201aa//39%//P34913
 C-NT2RP2002721//REGULATORY PROTEIN UHPC//1.60E-23//153aa//30%//P27669
 20 C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT)//3.50E-63//404aa//33%//P32802
 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349
 25 C-NT2RP2002974//HOMEODOMAIN PROTEIN SIXS (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT)//8.20E-241//555aa//84%//P70178
 C-NT2RP2002976//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION//1.30E-20//99aa//47%//P38800
 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT)//2.10E-109//385aa//52%//P53760
 30 C-NT2RP2003138//5'-TG-3' INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF)//2.10E-08//104aa//46%//P70284
 C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//2.60E-67//256aa//49%//Q05512
 35 C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899
 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//0//2891bp//99%//AB021644
 C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//5.90E-20//204aa//34%//Q15404
 40 C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927
 C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%//AJ011779
 C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER)//1.10E-45//324aa//29%//P37021
 45 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//AF024636
 C-NT2RP2003593
 C-NT2RP2003599
 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//P38869
 50 C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%//Y12670
 C-NT2RP2003931
 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//7.00E-111//401aa//43%//P28160
 55 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572
 C-NT2RP2004069
 C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.30E-171//474aa//62%//P16415
 C-NT2RP2004141

- C-NT2RP2004179
 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT)//1.60E-21//276aa//32%//Q62556
 C-NT2RP2004447
 5 C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//L149082
 C-NT2RP2004524
 C-NT2RP2004556
 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670
 10 C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
 C-NT2RP2004670//Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.//0//1250bp//86%//L22557
 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//203aa//26%//P40857
 C-NT2RP2004837
 15 C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
 C-NT2RP2005027//GLUCOSE TRANSPORTER TYPE 3, BRAIN.//6.20E-67//130aa//100%//P11169
 C-NT2RP2005069//Rat vacuolar protein sorting homolog vps33b mRNA, complete cds.//0//1792bp//87%//U35245
 C-NT2RP2005163
 20 C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//2126bp//81%//U70859
 C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158
 C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-28//183aa//47%//P10496
 25 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
 C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
 C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
 C-NT2RP2005514
 30 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//62%//Q03923
 C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586
 C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//97%//AF095136
 35 C-NT2RP2005632
 C-NT2RP2005666
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644
 40 C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//O57314
 C-NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101
 C-NT2RP2005887
 45 C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//M93650
 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//47%//P49191
 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//227aa//36%//Q06828
 50 C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640
 C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247
 C-NT2RP2006099
 55 C-NT2RP2006134
 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109).//2.30E-78//679aa//32%//P31382
 C-NT2RP2006512//GNS1 PROTEIN.//2.00E-21//290aa//29%//P25358

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C-NT2RP2006580//Homo sapiens transitional epithelia response protein (TERE1) mRNA, complete cds.//0//1483bp//99%//AF117064

C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%//Q00808

5 C-NT2RP3000022//Rat heart mRNA serine/threonine protein kinase, complete cds.//4.80E-203//1496bp//78%//D26178

C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.70E-12//133aa//32%//Q01485

C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//5.00E-29//596aa//30%//P19246

10 C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375

C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//P51523

C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239

15 C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//Z97207

C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.30E-80//359aa//44%//Q14012

C-NT2RP3000201//Homo sapiens HPK/GCK-like kinase HGK mRNA, complete cds.//1.30E-270//1231bp//99%//AF096300

20 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676

C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%//AF074264

C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579

C-NT2RP3000427

25 C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660

C-NT2RP3000444

C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%//M96629

C-NT2RP3000481//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//0//2623bp//100%//AF098799

30 C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//227aa//36%//Q06828

C-NT2RP3000645

C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160

C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829

35 C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%//P48378

C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//171aa//36%//P38800

C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%//AF117106

40 C-NT2RP3000818

C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//33%//P49695

C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%//Q07283

C-NT2RP3000871

45 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//42%//P39986

C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%//P43146

C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636

50 C-NT2RP3001044

C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%//AB020660

C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%//AL050118

55 C-NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.//4.80E-240//850bp//88%//AF068198

C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//29%//P37021

C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%//M96629

- C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.60E-09//34aa//22%//P52178
- C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-ATPASE).//1.70E-21//220aa//30%//P39524
- 5 C-NT2RP3001388//SYNAPTOTAGMIN IV.//2.00E-118//430aa//54%//P50232
- C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//4.70E-11//132aa//37%//Q13829
- C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339
- 10 C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//1.30E-18//279aa//27%//P15565
- C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//107aa//42%//P98063
- C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495
- 15 C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%//P00169
- C-NT2RP3001754
- C-NT2RP3001858
- C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//P51523
- 20 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
- C-NT2RP3002160//HISTO-BLOOD GROUP ABO SYSTEM TRANSFERASE (NAGAT) [INCLUDES: GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE); GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE)].//3.50E-72//231aa//49%//P16442
- 25 C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
- C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds.//0//2719bp//99%//AF097645
- 30 C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//43%//P48982
- C-NT2RP3002324
- C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082
- C-NT2RP3002353
- 35 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
- C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850
- C-NT2RP3002448
- C-NT2RP3002571//Bos taurus mRNA for lyncein.//7.30E-169//1115bp//84%//Y17923
- 40 C-NT2RP3002664
- C-NT2RP3002721//CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).//5.80E-249//466aa//98%//O75390
- C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//1552bp//99%//AF105202
- 45 C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//65%//L43821
- C-NT2RP3002790
- C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
- C-NT2RP3002887
- 50 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
- C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//8.00E-08//197aa//26%//P19814
- C-NT2RP3002983
- C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//96%//AF051946
- 55 C-NT2RP3003076
- C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//O35609

C-NT2RP3003448
 C-NT2RP3003469
 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999
 5 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%//P41217
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
 C-NT2RP3003559
 10 C-NT2RP3003614
 C-NT2RP3003729//HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.//5.80E-17//204aa//30%//Q03151
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130
 15 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381
 C-NT2RP3003963
 C-NT2RP3004000
 C-NT2RP3004025
 20 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894
 C-NT2RP3004075
 C-NT2RP3004083
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
 C-NT2RP3004119//PEREGRIN (BR140 PROTEIN).//7.30E-39//227aa//43%//P55201
 25 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
 C-NT2RP3004202
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118
 30 C-NT2RP3004321
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%//P15565
 C-NT2RP3004355
 35 C-NT2RP3004374
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544
 C-NT2RP3004481//BUTYROPHILIN PRECURSOR (BT).//8.50E-22//276aa//32%//Q62556
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//8.50E-24//263aa//33%//P17927
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292
 C-NT2RP3004625//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1339bp//99%//AF082516
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228
 45 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//X05608
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%//AF111105
 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
 50 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//AF131856
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
 55 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//AF127761
 C-NT2RP4001879
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//

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AF078850
 C-NT2RP4002451
 C-NT2RP4002715
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds//1.00E-310//
 5 2084bp//81%//U70859
 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds//4.30E-220//1158bp//94%//AF111856
 C-OVARC1000090
 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 10 LIGASE) (UBIQUITIN CARRIER PROTEIN)//4.20E-47//171aa//56%//P33296
 C-OVARC1000137
 C-OVARC1000208//Human calcium-dependent group X phospholipase A2 mRNA, complete cds//1.50E-61//
 365bp//90%//U95301
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase//0//1525bp//97%//Z29630
 15 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT)//9.90E-16//352aa//23%//P15924
 C-OVARC1000298
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02//3.00E-19//194aa//35%//Q50658
 C-OVARC1000313//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1)//3.00E-24//353aa//
 20 27%//Q12730
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-
 ASE)//9.40E-44//106aa//59%//P36959
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds//2.10E-63//744bp//69%//AF107253
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III//1.40E-
 33//143aa//53%//P34280
 25 C-OVARC1000467
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.40E-23//
 165aa//39%//P34244
 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-
 CULE) (THAM)//1.30E-23//169aa//40%//P28843
 30 C-OVARC1000775
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%//Q01177
 C-OVARC1000853
 C-OVARC1000873//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
 COSAMINE-6-SULFATASE)//1.00E-09//83aa//40%//P50426
 35 C-OVARC1000916//H.sapiens PISSLRE mRNA//7.30E-280//1117bp//95%//X78342
 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG
 PROTEIN)//2.20E-09//250aa//28%//P17437
 C-OVARC1000995
 C-OVARC1001030//Homo sapiens mRNA for KIAA0886 protein, complete cds//0//907bp//99%//AB020693
 40 C-OVARC1001049//TRANSCRIPTION FACTOR HES-1 (C-HAIRY1)//7.50E-14//96aa//36%//O57337
 C-OVARC1001086//Homo sapiens cyclin T2a mRNA, complete cds//0//1593bp//98%//AF048731
 C-OVARC1001132//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)(TCF-
 9)//2.30E-44//268aa//36%//P16383
 45 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I//2.30E-20//152aa//
 30%//Q09906
 C-OVARC1001222
 C-OVARC1001260
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds//0//1435bp//99%//AF111856
 50 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-)//8.80E-30//
 125aa//40%//P53104
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.50E-22//
 164aa//39%//P34244
 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds//0//1792bp//
 55 100%//AF190725
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds//0//1766bp//99%//
 AF126062
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds//0//

1836bp//96%//U15128
 C-OVARC1001725//Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.//0//
 1624bp//99%//AF064800
 C-OVARC1001727
 5 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds.//1.10E-243//1145bp//98%//L13740
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839
 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//8.30E-06//114aa//
 35%//Q01956
 10 C-OVARC1002058//Human 18S rRNA gene, complete.//1.50E-164//921bp//91%//M10098
 C-OVARC1002178
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR.//3.80E-17//190aa//28%//Q28295
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.//
 2.70E-101//947bp//74%//AF037272
 15 C-PLACE1000258//ZINC FINGER. PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.70E-55//431aa//
 35%//Q05481
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.00E-88//213aa//67%//P16415
 C-PLACE1000560
 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds.//5.60E-122//893bp//81%//M93661
 20 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//
 P51522
 C-PLACE1000912
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds.//7.50E-88//500bp//69%//AF045584
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X.//6.30E-21//123aa//
 25 37%//Q11079
 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//
 99%//AL117450
 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN).//6.80E-12//133aa//28%//
 P35500
 30 C-PLACE1001100//Homo sapiens nephrin (NPHS1) mRNA, complete cds.//3.10E-46//323bp//84%//AF035835
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN.//9.20E-06//389aa//31%//P03181
 C-PLACE1001123//INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).//
 5.00E-08//95aa//31%//Q04941
 C-PLACE1001183
 35 C-PLACE1001229
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
 cds.//2.20E-137//918bp//80%//AF026554
 C-PLACE1001340//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRI-
 40 AL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER)
 (TRANSLOCASE OF OUTER MEMBRANE TOM70).//1.20E-23//231aa//31%//P23231
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE
 FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740
 45 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%//
 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-
 50 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//
 Q28181
 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%//X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-
 plete cds.//0//1708bp//99%//AF043472
 55 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-
 SOR.//3.40E-20//159aa//40%//P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-

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BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E]//5.00E-27//134aa//47%/P10269
 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT) //2.30E-53//339aa//33%/P32802
 5 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38) //3.00E-75//315aa//44%/Q12697
 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691
 C-PLACE1002095
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791
 10 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 //6.50E-105//213aa//45%/Q08509
 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] //4.20E-12//131aa//40%/P01029
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP) //1.30E-313//1363bp//97%/X12451
 15 C-PLACE1002518//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.50E-14//396bp//64%/AF064801
 C-PLACE1002547//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) //2.30E-28//277aa//31%/P23231
 20 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC) //2.80E-202//926bp//82%/AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI) //2.40E-37//188aa//40%/P07106
 25 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR //4.50E-39//345aa//32%/P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGEC RECEPTOR, BETA-SUBUNIT) //4.60E-08//156aa//30%/Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-) //1.30E-47//210aa//49%/P08458
 30 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/AF069301
 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//99%/AF068227
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099
 35 C-PLACE1003438
 C-PLACE1003460
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT) //1.30E-09//281aa//22%/P11414
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN) //3.70E-16//226aa//26%/P20937
 40 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1 //1.80E-07//161aa//27%/P90917
 C-PLACE1003644
 C-PLACE1003737//TOLL PROTEIN PRECURSOR //5.40E-07//203aa//27%/P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) //2.40E-12//124aa//38%/P13983
 45 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//771bp//58%/AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) //3.40E-37//302aa//30%/Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%/AB018301
 50 C-PLACE1004028
 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%/D26549
 C-PLACE1004166//CREB-BINDING PROTEIN //1.80E-12//147aa//35%/P45481
 C-PLACE1004168//GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1 //9.10E-62//485aa//32%/P25655
 55 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III //1.40E-08//166aa//30%/P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL) //2.10E-11//

- 189aa//30%/P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%/P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%/U13666
 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 5 TIGEN CD13).//1.30E-91//562aa//35%/P15541
 C-PLACE1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%/AF097723
 C-PLACE1004492//VERPROLIN//3.30E-07//149aa//29%/P37370
 C-PLACE1004519
 10 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%/M20881
 C-PLACE1004630//Homo sapiens ten integrin EGF-like repeat domains protein precursor (ITGBL1) mRNA, com-
 plete cds.//1.00E-138//643bp//99%/AF072752
 C-PLACE1004637
 15 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.40E-18//395aa//25%/P08640
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%/D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTENN).//4.80E-33//179aa//47%/Q06003
 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-).//2.20E-52//269aa//41%/Q16651
 20 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%/AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%/P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, PH4-17).//1.80E-235//1010bp//84%/
 AJ2233511
 25 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%/AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%/AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%/M96629
 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 30 0//1629bp//95%/U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%/
 AF024636
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//
 3.10E-08//84aa//34%/Q00649
 35 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 1237bp//76%/U89915
 C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%/AJ132502
 C-PLACE1005601
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-
 40 33//143aa//53%/P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).//4.90E-09//183aa//33%/P
 20749
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 45 27%/Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%/E16311 C-PLACE1005745//ORM1
 PROTEIN.//2.40E-17//137aa//35%/P53224
 C-PLACE1005768
 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%/P
 50 23508
 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%/L16547
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//
 33%/Q09875
 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%/P
 55 02469
 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%/
 AB009598
 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%/

AF028233

C-PLACE1006093

C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AF047711

C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664

C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502

C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636

C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584

C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148

C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994

C-PLACE1006786

C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124

C-PLACE1006959

C-PLACE1007028//Homo sapiens TDAG51/lp1 homologue 1 (TIH1) mRNA, complete cds.//1.40E-307//1423bp//99%//AF151100

C-PLACE1007040

C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194

C-PLACE1007081//COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).//5.00E-20//247aa//34%//Q28107

C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GUTA.//2.70E-17//174aa//27%//O34368

C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885

C-PLACE1007591

C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439

C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335

C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//4.80E-14//158aa//40%//P43636

C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//42%//Q19425

C-PLACE1007971

C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//7.10E-274//627aa//82%//P33279

C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//P90648

C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069

C-PLACE1008469

C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//AF115403

C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549

C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//1888bp//99%//U15128

C-PLACE1008744//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//4.80E-32//338aa//30%//Q01102

C-PLACE1008984

C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107

C-PLACE1009067

C-PLACE1009196

C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//6.60E-86//1414bp//64%//E12965

C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//AJ133128

C-PLACE1009546

C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//88%//D88315

C-PLACE1009735

C-PLACE1009982//SALIVARY GILUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840

C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431

C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224

EP 1 130 094 A2

C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//AF027706

C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555

C-PLACE1010445

5 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850

C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//1146bp//99%//AF039686

10 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-19//163aa//34%//P49020

C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621

C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516

15 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640

C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815

C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451

C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013

20 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676

C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//139aa//34%//P53073

C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//AF034611

25 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424

C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%//Q05481

C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//P70315

30 C-PLACE2000219

C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//L11370

C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070

35 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927

C-PLACE4000455

C-SKNMC1000004

C-SKNMC1000014

40 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//130%//P29518

C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%//L41162

C-THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//1.40E-117//1126bp//74%//AB030505

45 C-THYRO1000099

C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272

C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//AL109665

C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676

50 C-THYRO1000584//EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE) (135 KD PROTEIN).//5.40E-127//335aa//71%//Q28949

C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585

C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377

C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114

55 C-THYRO1000846

C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963

C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642

C-THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//1.10E-

34//759bp//63%//AF091624
 C-THYRO1000999
 C-THYRO1001063
 5 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892
 C-THYRO1001102
 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%//AL096713
 10 C-THYRO1001128//Homo sapiens mRNA for hypothetical protein (C9orf9 gene).//6.40E-155//648bp//99%//AJ011375
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%//P21334
 15 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339
 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555
 20 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756
 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%//P04839
 25 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925
 30 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%//P27448
 C-THYRO1001608
 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855
 35 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%//AJ001616
 C-THYRO1001725
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-20//169aa//35%//P53974
 40 C-THYRO1001803
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247
 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 45 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//83%//U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%//U96386
 C-Y79AA1000521
 C-Y79AA1000750
 50 C-Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.//2.40E-161//820bp//85%//D87325
 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%//Q00808
 C-Y79AA1000876//PROTEIN DISULHDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%//P13667
 55 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973
 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%//AF093420
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-

NASE I).//1.00E-77//359aa//44%//Q14012

C-Y79AA1001013

C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535

C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
TEIN).//8.90E-12//132aa//38%//Q13829

C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1)
(NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT] (FRAG-
MENT).//4.50E-09//144aa//31%//Q63369

C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961

C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-
106//351aa//58%//Q10005

C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//
867bp//98%//AF172066

C-Y79AA1001328//Mus musculus mRNA for DII3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440

C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
6.20E-66//609aa//31%//P48751

C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
AF169481

C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938

C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
99%//AF119042

C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734

C-Y79AA1001592

C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795

C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
Q12697

C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325

C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061

C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500

C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851

C-Y79AA1001863

C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507

C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954

C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060

C-Y79AA1002129

C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
41%//Q03567

C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922

C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325

C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
304//1667bp//90%//U39045

C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
AF155100

C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.
2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence.3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO:4 and SEQ ID NO:830
SEQ ID NO:5 and SEQ ID NO:831
SEQ ID NO:6 and SEQ ID NO:832
SEQ ID NO:7 and SEQ ID NO:833
SEQ ID NO:8 and SEQ ID NO:834
SEQ ID NO:9 and SEQ ID NO:835
SEQ ID NO:11 and SEQ ID NO:836
SEQ ID NO:12 and SEQ ID NO:837
SEQ ID NO:13 and SEQ ID NO:838
SEQ ID NO:14 and SEQ ID NO:839
SEQ ID NO:15 and SEQ ID NO:840
SEQ ID NO:16 and SEQ ID NO:841
SEQ ID NO:17 and SEQ ID NO:842
SEQ ID NO:18 and SEQ ID NO:843
SEQ ID NO:20 and SEQ ID NO:844
SEQ ID NO:22 and SEQ ID NO:845
SEQ ID NO:23 and SEQ ID NO:846
SEQ ID NO:24 and SEQ ID NO:847
SEQ ID NO:25 and SEQ ID NO:848
SEQ ID NO:26 and SEQ ID NO:849
SEQ ID NO:27 and SEQ ID NO:850
SEQ ID NO:28 and SEQ ID NO:851
SEQ ID NO:29 and SEQ ID NO:852
SEQ ID NO:30 and SEQ ID NO:853
SEQ ID NO:31 and SEQ ID NO:854
SEQ ID NO:32 and SEQ ID NO:855
SEQ ID NO:33 and SEQ ID NO:856
SEQ ID NO:34 and SEQ ID NO:857
SEQ ID NO:35 and SEQ ID NO:858
SEQ ID NO:36 and SEQ ID NO:859
SEQ ID NO:37 and SEQ ID NO:860
SEQ ID NO:39 and SEQ ID NO:861
SEQ ID NO:40 and SEQ ID NO:862
SEQ ID NO:41 and SEQ ID NO:863
SEQ ID NO:42 and SEQ ID NO:864
SEQ ID NO:44 and SEQ ID NO:865
SEQ ID NO:45 and SEQ ID NO:866
SEQ ID NO:46 and SEQ ID NO:867
SEQ ID NO:47 and SEQ ID NO:868

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4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

EP 1 130 094 A2

set forth in any one of the following SEQ ID NOs:

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SEQ ID NO:4063, SEQ ID NO:4065, SEQ ID NO:4067, SEQ ID NO:4069, SEQ ID NO:4071,
SEQ ID NO:4073, SEQ ID NO:4075, SEQ ID NO:4077
SEQ ID NO:4079, SEQ ID NO:4081, SEQ ID NO:4083, SEQ ID NO:4085, SEQ ID NO:4087,
SEQ ID NO:4089, SEQ ID NO:4091, SEQ ID NO:4093, SEQ ID NO:4095, SEQ ID NO:4097,
50 SEQ ID NO:4100, SEQ ID NO:4102, SEQ ID NO:4104, SEQ ID NO:4106, SEQ ID NO:4108,
SEQ ID NO:4110, SEQ ID NO:4112, SEQ ID NO:4114, SEQ ID NO:4116, SEQ ID NO:4118,
SEQ ID NO:4120, SEQ ID NO:4122, SEQ ID NO:4124, SEQ ID NO:4126, SEQ ID NO:4128,
SEQ ID NO:4130, SEQ ID NO:4133, SEQ ID NO:4135, SEQ ID NO:4138, SEQ ID NO:4141,
SEQ ID NO:4143, SEQ ID NO:4145, SEQ ID NO:4147, SEQ ID NO:4149, SEQ ID NO:4151,
55 SEQ ID NO:4153, SEQ ID NO:4156, SEQ ID NO:4158, SEQ ID NO:4160, SEQ ID NO:4162,

SEQ ID NO:4164, SEQ ID NO:4166

SEQ ID NO:4169, SEQ ID NO:4171, SEQ ID NO:4173, SEQ ID NO:4175, SEQ ID NO:4177,
and SEQ ID NO:4179

- (c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
 - (d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
 - (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
 - (f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).
9. A substantially pure protein encoded by the polynucleotide of claim 8.
 10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.
 11. A vector comprising the polynucleotide of claim 5 or 8.
 12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
 14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
 16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
 18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
 19. A method for synthesizing a polynucleotide, the method comprising:
 - a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
 - b) recovering the synthesized product.
 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
 21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
 22. A method for detecting the polynucleotide of claim 8, the method comprising:
 - a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
 - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

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Figure 1

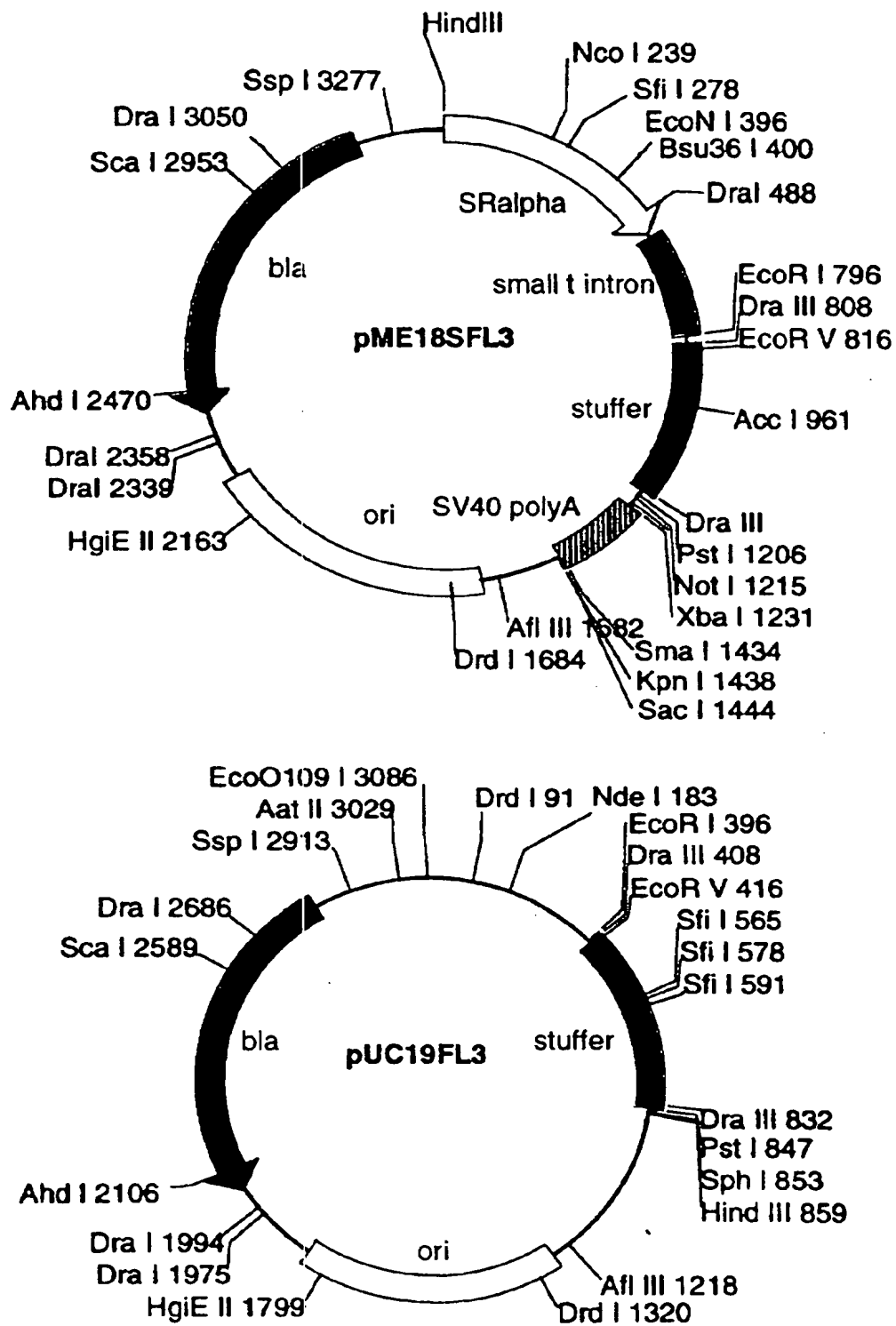


Figure 2

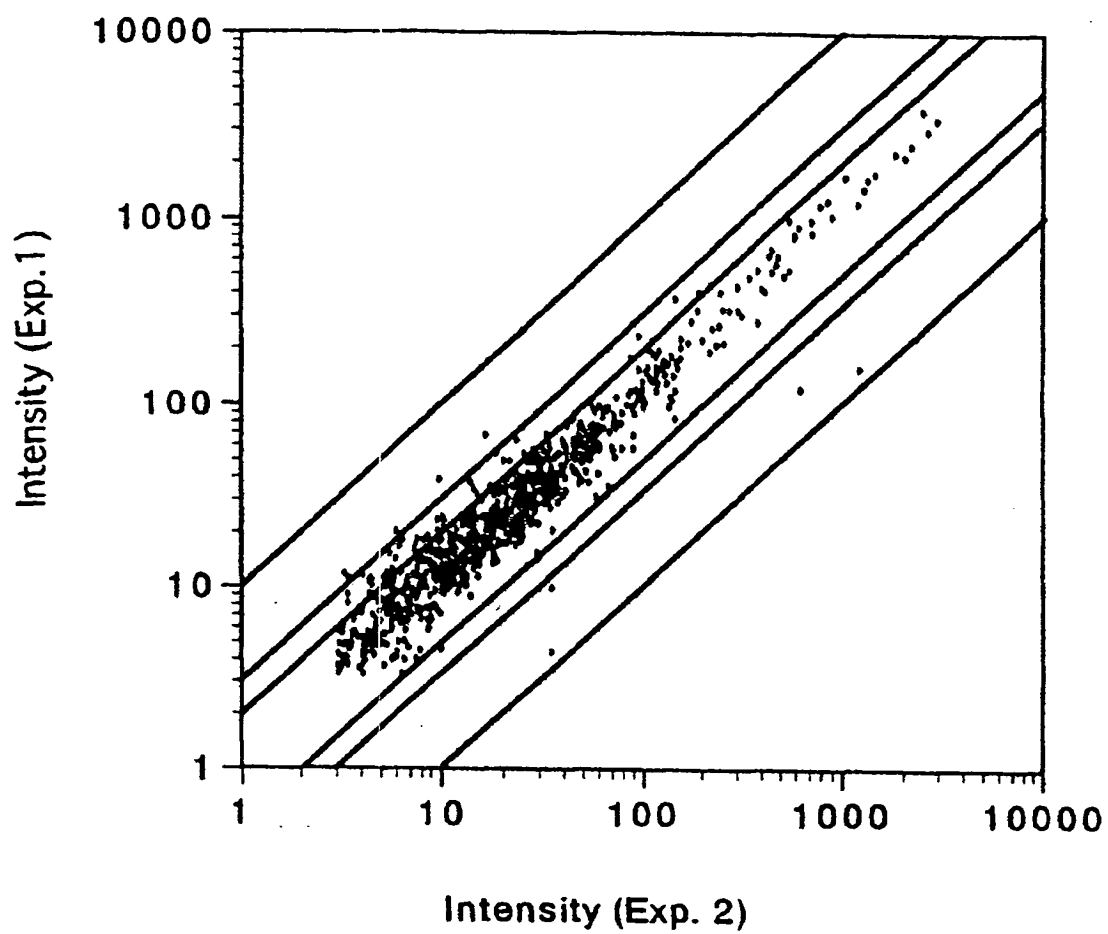
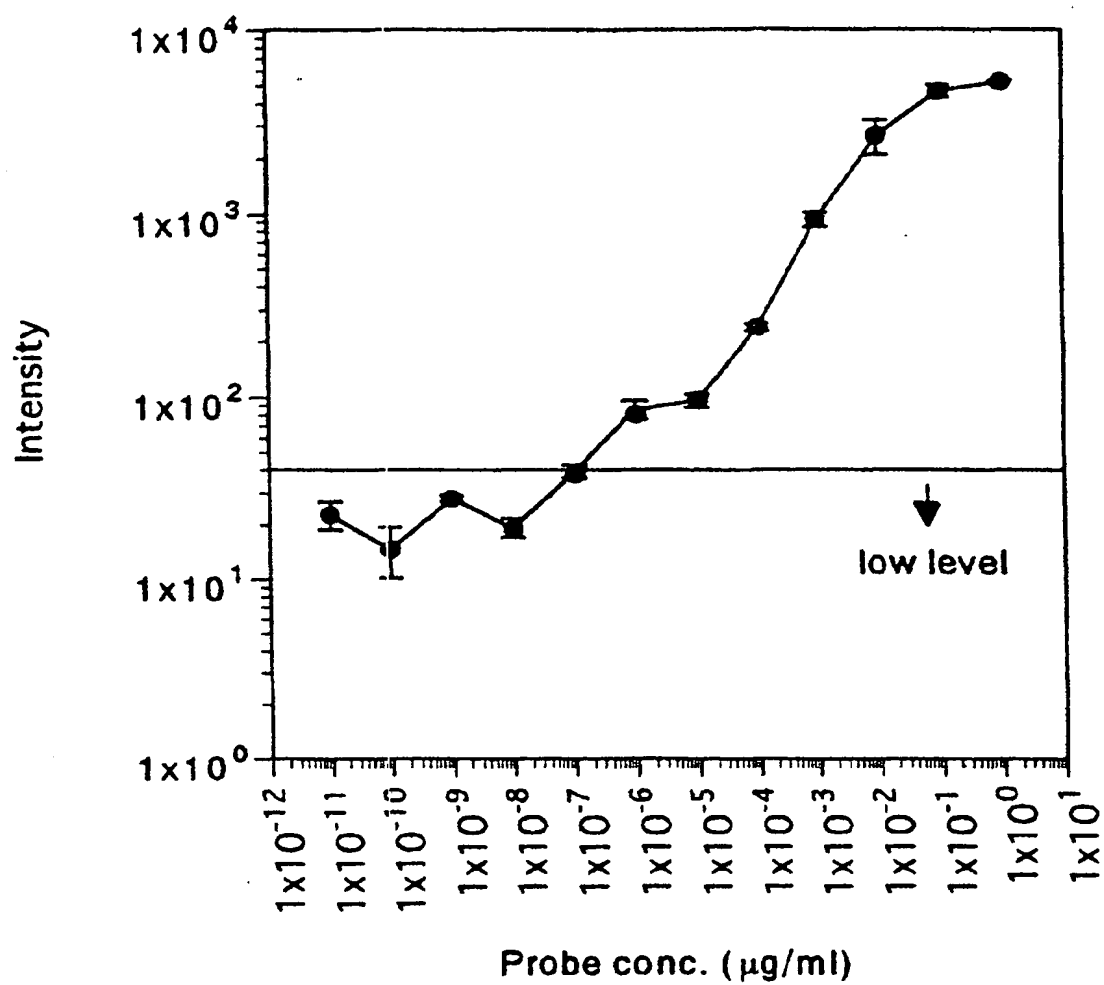
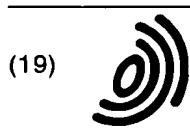


Figure 3



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(11) **EP 1 130 094 A3**

(12) **EUROPEAN PATENT APPLICATION**

(88) Date of publication A3:
21.11.2001 Bulletin 2001/47

(43) Date of publication A2:
05.09.2001 Bulletin 2001/36

(21) Application number: 00114089.6

(22) Date of filing: 07.07.2000

(51) Int Cl.7: **C12N 15/12, C12N 15/11, C12N 15/10, C12N 15/70, C12N 15/85, C12N 5/10, C12N 1/21, C07K 14/47, C07K 16/18, C12Q 1/68**

(84) Designated Contracting States:
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: 08.07.1999 JP 19448699
11.01.2000 JP 2000118774
02.05.2000 JP 2000183765

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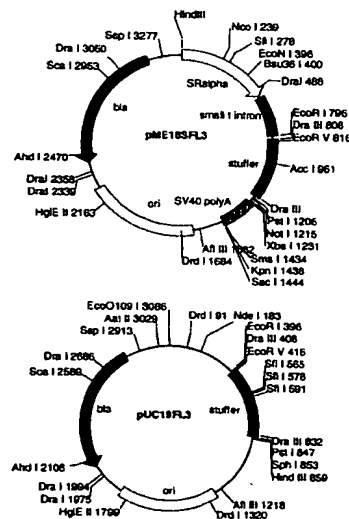
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(54) **Primers for synthesizing full length cDNA clones and their use**

(57) Primers for synthesizing full length cDNAs and their use are provided.

830 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA have been determined. Furthermore, primers for synthesizing the full length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

Figure 1



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EUROPEAN SEARCH REPORT

Application Number
EP 00 11 4089

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The present search report has been drawn up for all claims			
Place of search		Date of completion of the search	Examiner
THE HAGUE		19 June 2001	HORNIG H.
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document			

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CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

☒ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

1,2,4-22 - partially



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EUROPEAN SEARCH REPORT

Application Number
EP 00 11 4089

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-/-			
The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 19 June 2001	Examiner HORNIG H.
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

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LACK OF UNITY OF INVENTION
SHEET B

Application Number

EP 00 11 4089

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: (1,2,4-22)-partially

Use of an oligonucleotide as a primer for synthesizing the polynucleotide sequence of clone BNGH41000020 comprising the nucleotide sequence of SEQ ID No. 1, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides; a primer set for synthesizing polynucleotides, the primer set comprises an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide sequence SEQ ID No. 1; a polynucleotide which can be synthesized with said primer set; a protein coding for said polynucleotide; a partial peptide of said protein; an isolated polynucleotide comprises (a) a coding region of SEQ ID No. 3595 or (b) a polynucleotide comprises a nucleotide sequence encoding a protein comprising the amino acid SEQ ID No. 3596; an antibody against said protein; a vector comprises said polynucleotide; a transformant expressing said vector; an antisense polynucleotide against said polynucleotide; a method of synthesizing said polynucleotide; a method for detecting said polynucleotide;

2. Claims: (1,2,4-22)-partially

Idem as subject 1 but limited to BNGH41000087; SEQ ID No. 2, SEQ ID Nos. 4078 and 4079;

3. Claims: (1,2,4-22)-partially

Idem as subject 1 but limited to BNGH41000091; SEQ ID No. 3, SEQ ID Nos. 3597 and 3598;

4. Claims: (1-22)-partially and as far as applicable

Idem as subject 1 but limited to HEMBA1000006, respectively SEQ ID nos. 2547 and 2548; a primer set for synthesizing polynucleotides, the primer set comprises a combination of an oligonucleotide comprises a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotide comprises at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from SEQ ID Nos. 4 and 830;

5.-830. Claims: (1-23)-partially

Idem as subject 4 but limited to HEMBA1000121 to



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LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 00 11 4089

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

NT2RP2006580; (Invention 5 is limited to HEMBA1000121 respectively SEQ ID Nos. 5,831,2551 and 2552; Invention 6 is limited to HEMBA100128 respectively SEQ ID Nos. 6,832,2553 and 2554; Invention 830 is limited to NT2RP2006580 respectively SEQ ID Nos. 2545, 2546, 4178 and 4179).

831. Claim: 23-complete

A database of nucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotides of clone BNGH41000020 (SEQ ID Nos. 1, 3595 and 3596) to NT2RP2006580 (SEQ ID Nos. 2545,2546,4178 and 4179).



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Application Number
EP 00 11 4089

DOCUMENTS CONSIDERED TO BE RELEVANT			
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The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 19 June 2001	Examiner HORNIG H.
CATEGORY OF CITED DOCUMENTS		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document			

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ON EUROPEAN PATENT APPLICATION NO.

EP 00 11 4089

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The members are as contained in the European Patent Office EDP file on
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19-06-2001

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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82